

GenCore version 5.1.6  
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OW protein - protein search, using sw model

Run on: December 4, 2005, 04:09:54 ; Search time 95.5625 Seconds  
(without alignments)  
50.576 Million cell updates/sec

Title: US-10-632-706-198  
Perfect score: 59  
Sequence: 1 WGGCTVTVSS 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : A.GeneSeq\_21:\*

- 1: - geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*
- 9: geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	11	2	AAR85166 Human ONS
2	59	100.0	11	2	AAR97333 Humanised
3	59	100.0	11	4	AAU07452 Synthetic
4	59	100.0	11	5	AAE28561 scFv anti
5	59	100.0	11	5	AAU70517 Mouse hea
6	59	100.0	11	5	AAU70501 Mouse hea
7	59	100.0	11	5	AAU70485 Mouse hea
8	59	100.0	11	5	AAU70477 Mouse hea
9	59	100.0	11	6	ABO10719 Deimnitis
10	59	100.0	11	6	ABR44663 Murine J4
11	59	100.0	11	7	ABO33904 Anti-GPI-
12	59	100.0	11	7	ADG75671 Peptide o
13	59	100.0	11	8	ADH17960 Human mod
14	59	100.0	11	8	ADH18011 Human mod
15	59	100.0	11	8	ADG90791 Artificiala
16	59	100.0	11	8	ADR12645 Mammalian
17	59	100.0	11	8	ADR38796 Mouse hea
18	59	100.0	11	8	ADR38793 Mouse hea
19	59	100.0	11	8	ADR38802 Mouse hea
20	59	100.0	11	8	ADR38799 Mouse hea
21	59	100.0	11	8	ADU38427 Mouse ant
22	59	100.0	11	8	ADU67919 Mouse ant
23	59	100.0	11	9	ADW07403 Heavy cha
24	59	100.0	11	9	ADW07419 Heavy cha

25	59	100.0	11	9	ADM07407 Heavy cha
26	59	100.0	11	9	ADM07423 Heavy cha
27	59	100.0	11	9	ADM07427 Heavy cha
28	59	100.0	11	9	ADM07435 Heavy cha
29	59	100.0	11	9	ADM07439 Heavy cha
30	59	100.0	11	9	ADM07411 Heavy cha
31	59	100.0	11	9	ADM07443 Heavy cha
32	59	100.0	11	9	ADM07451 Heavy cha
33	59	100.0	11	9	ADM07415 Heavy cha
34	59	100.0	11	9	ADM07447 Heavy cha
35	59	100.0	11	9	ADM07431 Heavy cha
36	59	100.0	11	9	ADY31581 Human ant
37	59	100.0	11	9	ADZ35850 Anti-glic
38	59	100.0	11	9	ADZ83544 CD3 const
39	59	100.0	11	9	ADZ83542 CD3 const
40	59	100.0	11	9	ADZ83545 CD3 const
41	59	100.0	11	9	ADZ83543 CD3 const
42	59	100.0	11	9	AEA21481 Human ant
43	59	100.0	11	9	AEA21445 Human ant
44	59	100.0	11	9	AEA45691 Apolipop
45	59	100.0	11	9	AEA44171 Anti-TP0

## ALIGNMENTS

RESULT 1  
AAR85166 standard; protein; 11 AA.

AC AAR85166;

DT 18-JAN-1996 (first entry)

DE Human ONS-M21 antibody heavy variable region FR 4.

XX Human; ONS-M21 antibody; heavy variable region; chimeric protein;

KW framework region; FR 4; medulloblastoma; brain tumour; treatment;

XX diagnosis.

OS Homo sapiens.

XX MO9514041-A1.

XX 26-MAY-1995.

XX 19-OCT-1994; 94WO-JP001763.

XX 19-NOV-1993; 93JP-00291078.

XX (CHUS ) CHUGAI SEIYAKU KK.

XX Ohtomo T, Sato K, Tsuchiya M;

XX WPI; 1995-200347/26.

XX Reconstituted antibody against human medullo:blastoma cells - contains

XX high proportion of human antibody origin and has low antigenicity.

XX Claim 18; Page 102; 120pp; Japanese.

XX AAR85163-85166 are human antibody ONS-M21 heavy variable region

XX framework regions (FRs). They were used in the construction of a

XX human/murine chimeric antibody, reactive with human medullo: blastoma (a

XX brain tumour) cells. The chimeric antibody can be used in the diagnosis

XX and treatment of this disease

XX Sequence 11 AA;

XX Query Match 100.0%; Score 59; DB 2; Length 11;

XX Best local Similarity 100.0%; Pred. No. 0.011;

XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11  
 |||||  
 DB 1 WGGGTTTVSS 11

## RESULT 2

AAE97333  
 ID AAE97333 standard; peptide; 11 AA.

AAE97333;

15-OCT-1996 (first entry)

Humanised monoclonal antibody heavy chain framework region.

Monoclonal antibody; humanised; mouse; framework region; FR; CDR; complementary determining region; anti-carcinoma/embryonic antigen; CEA; diagnosis; imaging; therapy; immune response.

Homo sapiens.

MO9611013-A1.

18-APR-1996.

28-SEP-1995; 95WO-US011964.

05-OCT-1994; 94US-00318157.

(IMMU-) IMMUNOMEDICS INC.

Hansen HJ, Armour KL;

WPI; 1996-209653/21.

New humanised anti-CEA monoclonal antibody - having engrafted murine CDR, used for diagnosis, imaging and therapy of CEA-producing cancers.

Claim 7, Page 40; 62pp; English.

New humanised monoclonal antibodies (MAbs) comprising the complementary determining regions (CDRs) of a parental murine class III anti-carcinoma/embryonic (CEA) MAb engrafted to the framework regions (FRs) of a human, retain the anti-CEA binding specificity of the parental murine MAb but are less immunogenic in a human subject than the parental MAb. The humanised antibodies can be used in diagnosis, imaging and therapy of CEA-producing cancers and patients receiving the humanised antibodies and conjugates show improved therapeutic results, decreased immune responses and decreased immune-mediated adverse effects compared to the parent antibody. This sequence corresponds to the fourth framework region of the heavy chain of the humanised MAb. See AAE97333-97333

Sequence 11 AA;

Query Match 100.0%; Score 59; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.011;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11  
 |||||  
 DB 1 WGGGTTTVSS 11

## RESULT 3

AAU07452  
 ID AAU07452 standard; peptide; 11 AA.

AAU07452;

24-OCT-2001 (first entry)

Synthetic peptide H-FR4-F8.

H-FR4-F8; antimicrobial; antiviral; cytostatic; immunomodulatory; antibody; gene therapy; HIV; human immunodeficiency virus; tumour; metabolic disorder; immune disorder; auto-immune disorder.

Synthetic.

WO200149713-A2.

12-JUL-2001.

29-DEC-2000; 2000WO-IT000554.

30-DEC-1999; 99IT-RM000803.

(CNEB) ENBA ENTE NDOVE TECNOLOGIE ENERGIA.

(CONS) SOC CONSORTILE METAPONTUM AGROBIOS SRL.

Benvenuto E, Francini R, Desiderio A, Taviadoraki P;

WPI; 2001-502555/55.

N-PSDB; AAS11874.

Peptides which are able to confer stability and solubility to an antibody comprising these peptides, useful for treating pathologies (e.g. tumor) associated with accumulation of a molecule inside or outside a human, or animal cell.

Claim 1, Page 57; 109pp; English.

The invention relates to peptides which are able to confer stability and solubility to an antibody comprising these peptides. The peptides are especially H-FR1, H-FR2, H-FR3, H-FR4, L-FR1, L-FR2 or L-FR4 present within a variable region of an antibody which makes the antibody soluble and stable in cytoplasm. Peptides having the sequences of HFR1 to H-FR4 are present within the variable region of the heavy chain of an antibody, covalently linked to the H-CDR1, H-CDR2, H-CDR3 in the order (H-CDR1)-(H-CDR2)-(H-CDR3)-(H-CDR4) and peptides having the sequences of L-FR1 to L-FR4 are present within the variable region of the light chain of an antibody, covalently linked to the L-CDR1, L-CDR2, L-CDR3 in the order (L-CDR1)-(L-CDR2)-(L-CDR3)-(L-CDR4). The antibodies and polynucleotides are useful (e.g. by gene therapy) for the manufacture of a medicament for the treatment of pathologies associated with accumulation of a molecule inside or outside a human, animal cell or plant cell. The pathologies are infectious (e.g. viral infections such as HIV, human immunodeficiency virus, infections), tumour, metabolic and immune (especially auto-immune) pathologies. The present sequence represents the peptide H-FR4-F8 (also known as H-FR4)

Sequence 11 AA;

Query Match 100.0%; Score 59; DB 4; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.011;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11  
 |||||  
 DB 1 WGGGTTTVSS 11

## RESULT 4

AAE28561  
 ID AAE28561 standard; peptide; 11 AA.

AAE28561;

27-DEC-2002 (first entry)

scFv antibody heavy chain framework region 4 from S18 clone.

Human; sugar-nucleic acid interaction; single chain human antibody; scFv; L-peptide binder; D-nucleic acid binder; sugar-protein interaction; FR4;

KW frame work region 4.  
XX Homo sapiens.  
XX MO200267860-A2.  
XX  
XX 06-SEP-2002.  
XX  
XX 22-FEB-2002; 2002MO-US005193.  
XX  
XX 22-FEB-2001; 2001US-0271377P.  
XX  
XX (SCRI ) SCRIPPS RES INST.  
XX  
XX Wong C;  
XX  
XX WPI; 2002-691633/74.  
XX  
XX Selecting L-peptide or D-nucleic acid binders that binds to enantiomers  
PT of naturally occurring carbohydrate, comprises providing enantiomers of  
PT naturally occurring carbohydrate, and screening library against  
PT enantiomers.  
XX  
XX Disclosure; Fig 6B; 46pp; English.  
XX  
XX The present invention relates to a novel method of selecting L-peptide or  
CC D-nucleic acid binders that bind to enantiomers of naturally occurring  
CC sugar or carbohydrate. The method involves providing enantiomers of  
CC naturally occurring sugar or carbohydrate employable for screening the  
CC library and then screening the library against the enantiomers for  
CC identifying a L-peptide binder or D-nucleic acid binder having binding  
CC activity with respect to enantiomers. The method is useful for selecting  
CC L-peptide binder or D-nucleic acid binder that binds to enantiomer of  
CC naturally occurring sugar or carbohydrate. It is useful for selecting L-  
CC peptide binders and/or L-nucleic acid binders that are resistant to  
CC enzymatic degradation due to their non-naturally occurring chirality, for  
CC blocking or activating the biological function of the naturally occurring  
CC sugar or carbohydrate to which they are targeted. The naturally occurring  
CC sugar or carbohydrate include bacterial or viral cell surface sugars  
CC or carbohydrates, heparin sulphates involved in viral entry, thrombosin  
CC and angiotensin. The method is useful for identifying D-peptides, for  
CC studying sugar-protein and sugar-nucleic acid interaction and for  
CC designing high-affinity and hydrolase resistant molecules as artificial  
CC receptors capable of binding natural carbohydrates. The immobilised  
CC enantiomers are useful for screening phage expressing a peptide library  
CC on the coat proteins to identify specific clones that bind to an  
CC immobilised enantiomer. The present sequence is single chain human  
CC antibody (scfv) heavy chain frame work region 4 (PR4) from S18 clone.  
CC This sequence is used to illustrate the method of the invention  
XX  
XX Sequence 11 AA;  
SO  
Query Match 100.0%; Score 59; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 WGGGTTTVSS 11  
DB 1 WGGGTTTVSS 11  
RESULT 5  
AAU70517 standard; peptide; 11 AA.  
XX  
XX AAU70517;  
XX  
XX 14-FEB-2002 (first entry)  
XX  
XX Mouse heavy chain immunoglobulin framework region 4 #11.  
XX  
XX Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;  
KW complementarity determining region; framework region; IgBP;  
KW

KW transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA;  
XX IgB; IgE; IgY; IgM; kappa; lambda; CHBP.  
XX  
XX Mus musculus.  
XX  
XX MO200183806-A1.  
XX  
XX 08-NOV-2001.  
XX  
XX 02-MAY-2001; 2001MO-US014349.  
XX  
XX 02-MAY-2000; 2000US-00563222.  
XX  
XX (EPIC-) EPICYTE PHARM INC.  
XX  
XX Hiatt AC, Hein MB;  
XX  
XX WPI; 2002-055482/07.  
XX  
XX Preparing immunoglobulin binding protein array in plant cells by  
PT transforming the cells with different polynucleotides encoding binding  
PT protein polypeptides specific to ligand, selecting plant cells for  
PT preparing array.  
XX  
XX Disclosure; Fig 1B; 129pp; English.  
XX  
XX The invention relates to transforming a population of cells (e.g. plant  
CC cells), comprising using a library of two different polynucleotides  
CC encoding different immunoglobulin binding protein (IgBP) polypeptides  
CC that specifically bind to a ligand or form one or more disulphide bonds  
CC with polypeptides in transfected cells, to generate an IgBP that binds to  
CC a ligand, and transformed plant cells are selected, and preparing an IgBP  
CC array in plant cells. At least one peptide sequence has at least 75%  
CC sequence identity to a framework region (FR) of a native IgM, IgG, IgA,  
CC IgB, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is  
CC useful for preparing an immunoglobulin binding protein array, preferably  
CC heavy chain binding protein (CHBP) array in eukaryotic cells especially  
CC plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic  
CC cells (e.g. insect cells or mammalian cells). The CHBP is useful for  
CC discovery of e.g. screening assays of IgBPs having desired  
CC characteristics. The present sequence is a mammalian immunoglobulin  
CC derived peptide that may be incorporated into an IgBP of the invention  
XX  
XX Sequence 11 AA;  
SO  
Query Match 100.0%; Score 59; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 WGGGTTTVSS 11  
DB 1 WGGGTTTVSS 11  
RESULT 6  
AAU70501 standard; peptide; 11 AA.  
XX  
XX AAU70501;  
XX  
XX 14-FEB-2002 (first entry)  
XX  
XX Mouse heavy chain immunoglobulin framework region 4 #7.  
XX  
XX Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;  
KW complementarity determining region; framework region; IgBP;  
KW transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA;  
KW IgB; IgE; IgY; IgM; kappa; lambda; CHBP.  
XX  
XX Mus musculus.  
XX  
XX MO200183806-A1.  
XX

PD 08-NOV-2001.  
XX  
XX 02-MAY-2001; 2001WO-US014349.  
XX  
XX 02-MAY-2000; 2000US-00563222.  
PR  
XX (EPIC-) EPICYTE PHARM INC.  
PA  
XX Hiact AC, Hein MB;  
PI  
XX WPI; 2002-055482/07.  
DR  
XX  
PT Preparing immunoglobulin binding protein array in plant cells by  
PT transforming the cells with different polynucleotides encoding binding  
PT protein polypeptides specific to ligand, selecting plant cells for  
PT preparing array.  
XX  
XX PS Disclosure; Fig 1B; 129pp; English.  
XX  
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XX cells), comprising using a library of two different polynucleotides  
XX encoding different immunoglobulin binding protein (IgBP) polypeptides  
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XX with polypeptides in transfected cells, to generate an IgBP that binds to  
XX a ligand, and transformed plant cells are selected, and preparing an IgBP  
XX array in plant cells. At least one peptide sequence has at least 75%  
XX sequence identity to a framework region (FR) of a native IgM, IgG, IgA,  
XX IgD, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is  
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XX cells (e.g. insect cells or mammalian cells). The CHBP is useful for  
XX discovery of e.g. screening assays of IgBPs having desired  
XX characteristics. The present sequence is a mammalian immunoglobulin  
XX derived peptide that may be incorporated into an IgBP of the invention  
XX  
SQ Sequence 11 AA;  
  
Query Match 100.0%; Score 59; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 WGGGTTTVVSS 11  
Db 1 WGGGTTTVVSS 11  
  
RESULT 7  
AAU70485 standard; peptide; 11 AA.  
ID  
XX  
XX AAU70485;  
AC  
XX  
XX 14-FEB-2002 (first entry)  
DT  
XX  
XX Mouse heavy chain immunoglobulin framework region 4 #3.  
DE  
XX  
XX Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;  
XX complementarity determining region; framework region; IgBP;  
XX transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA;  
XX IgD; IgE; IgY; IgM; kappa; lambda; CHBP.  
KM  
XX  
XX Mus musculus.  
OS  
XX  
XX WO200183806-A1.  
PN  
XX  
XX 08-NOV-2001.  
PD  
XX  
XX 02-MAY-2001; 2001WO-US014349.  
PF  
XX  
XX 02-MAY-2000; 2000US-00563222.  
PR  
XX  
XX (EPIC-) EPICYTE PHARM INC.  
PA

XX  
XX Hiact AC, Hein MB;  
PI  
XX  
XX WPI; 2002-055482/07.  
DR  
XX  
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PT transforming the cells with different polynucleotides encoding binding  
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XX  
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XX with polypeptides in transfected cells, to generate an IgBP that binds to  
XX a ligand, and transformed plant cells are selected, and preparing an IgBP  
XX array in plant cells. At least one peptide sequence has at least 75%  
XX sequence identity to a framework region (FR) of a native IgM, IgG, IgA,  
XX IgD, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is  
XX useful for preparing an immunoglobulin binding protein array, preferably  
XX heavy chain binding protein (CHBP) array in eukaryotic cells especially  
XX plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic  
XX cells (e.g. insect cells or mammalian cells). The CHBP is useful for  
XX discovery of e.g. screening assays of IgBPs having desired  
XX characteristics. The present sequence is a mammalian immunoglobulin  
XX derived peptide that may be incorporated into an IgBP of the invention  
XX  
SQ Sequence 11 AA;  
  
Query Match 100.0%; Score 59; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 WGGGTTTVVSS 11  
Db 1 WGGGTTTVVSS 11  
  
RESULT 8  
AAU70477 standard; peptide; 11 AA.  
ID  
XX  
XX AAU70477;  
AC  
XX  
XX 14-FEB-2002 (first entry)  
DT  
XX  
XX Mouse heavy chain immunoglobulin framework region 4 #1.  
DE  
XX  
XX Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;  
XX complementarity determining region; framework region; IgBP;  
XX transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA;  
XX IgD; IgE; IgY; IgM; kappa; lambda; CHBP.  
KM  
XX  
XX Mus musculus.  
OS  
XX  
XX WO200183806-A1.  
PN  
XX  
XX 08-NOV-2001.  
PD  
XX  
XX 02-MAY-2001; 2001WO-US014349.  
PF  
XX  
XX 02-MAY-2000; 2000US-00563222.  
PR  
XX  
XX (EPIC-) EPICYTE PHARM INC.  
PA  
XX  
XX Hiact AC, Hein MB;  
PI  
XX  
XX WPI; 2002-055482/07.  
DR  
XX  
XX Preparing immunoglobulin binding protein array in plant cells by  
PT transforming the cells with different polynucleotides encoding binding



PT protein polypeptides specific to ligand, selecting plant cells for  
PT preparing array.  
XX  
PS Disclosure; Fig 1B; 123pp; English.  
XX  
CC The invention relates to transforming a population of cells (e.g. plant  
CC cells), comprising using a library of two different polynucleotides  
CC encoding different immunoglobulin binding protein (IGBP) polypeptides  
CC that specifically bind to a ligand or form one or more disulphide bonds  
CC with polypeptides in transfected cells, to generate an IGBP that binds to  
CC a ligand, and transformed plant cells are selected, and preparing an IGBP  
CC array in plant cells. At least one peptide sequence has at least 75%  
CC sequence identity to a framework region (FR) of a native IGH, IGH, IGH,  
CC IGH, IGH, IGH, kappa or lambda immunoglobulin molecule. The method is  
CC useful for preparing an immunoglobulin binding protein array, preferably  
CC heavy chain binding protein (CHBP) array in eukaryotic cells especially  
CC plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic  
CC cells (e.g. insect cells or mammalian cells). The CHBP is useful for  
CC discovery of e.g. screening assays of IGBPs having desired  
CC characteristics. The present sequence is a mammalian immunoglobulin  
CC derived peptide that may be incorporated into an IGBP of the invention  
XX  
SQ Sequence 11 AA;  
Query Match 100.0%; Score 59; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WGGGTTVTSS 11  
Db 1 WGGGTTVTSS 11  
RESULT 9  
ABO10719  
ID ABO10719 standard; peptide; 11 AA.  
XX  
AC ABO10719;  
XX  
DT 20-AUG-2003 (first entry)  
XX  
DE Deimmunised murine J415-4 antibody framework sequence VHFR4.  
XX  
XX Modified antibody; deimmunised antibody; anti-PMMA antibody;  
KM prostate specific membrane antigen; immunogenic; CDR; murine;  
KM complementarity determining region; J591; J415; J533; E99; mouse;  
KM prostatic disorder; cancerous disorder; genitourinary inflammation;  
KM prostaticitis; benign enlargement; prostatic cancer; testicular cancer;  
KM solid tumour; soft tissue tumour; metastatic lesion; pain; analgesic;  
KM antiinflammatory; cytostatic; framework region; variable heavy chain;  
KM variable light chain; VH; VL; variable region; mutant; nuclein.  
XX  
XX Mus musculus.  
OS Synthetic.  
XX  
XX WO200298897-A2.  
XX  
XX 12-DEC-2002.  
XX  
XX 30-MAY-2002; 2002WO-US017068.  
XX  
XX 01-JUN-2001; 2001US-0295214P.  
XX 20-SEP-2001; 2001US-0323585P.  
XX 08-MAR-2002; 2002US-0362810P.  
XX  
XX (CORR ) CORNELL RES FOUND INC.  
XX  
XX Bander N, Carr FJ, Hamilton A;  
XX  
XX WPI; 2003-156839/15.  
XX  
XX New modified anti-prostate specific membrane antigen (PSMA)  
PT immunoglobulins, useful for treating or preventing a prostatic or

PT cancerous disorder, e.g. genitourinary inflammation, prostatitis, or  
PT prostatic or testicular cancer.  
XX  
PS Disclosure; Page 21; 254pp; English.  
XX  
XX The present invention relates to modified (e.g. deimmunised) antibodies  
CC to prostate specific membrane antigen (PSMA). The modified anti-PSMA  
CC antibodies are less immunogenic compared to the unmodified anti-PSMA  
CC antibodies. The modified antibodies comprise complementarity determining  
CC regions (CDRs) from a non-human antibody (e.g. murine antibody J591, J415,  
CC J533 or E99), and framework sequences that are less immunogenic in humans  
CC (e.g. less antigenic than the murine frameworks in which a murine CDR  
CC naturally occurs). The modified antibodies bind with PMSA, preferably  
CC human PMSA, with high affinity and specificity. The anti-PMMA antibodies  
CC are useful for treating or preventing a prostatic or cancerous disorder,  
CC e.g. genitourinary inflammation, prostatitis, benign enlargement,  
CC prostatic cancer or testicular cancer, or solid tumours, soft tissue  
CC tumours or metastatic lesions, and its associated pain. The present  
CC sequence represents a deimmunised murine framework region  
XX  
SQ Sequence 11 AA;  
Query Match 100.0%; Score 59; DB 6; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WGGGTTVTSS 11  
Db 1 WGGGTTVTSS 11  
RESULT 10  
ABR44663  
ID ABR44663 standard; peptide; 11 AA.  
XX  
AC ABR44663;  
XX  
DT 25-JUL-2003 (first entry)  
XX  
DE Murine J415-4 antibody VH FR4 amino acid sequence SEQ ID NO:40.  
XX  
XX Mouse; murine; antibody; skin disorder; binding agent; PSMA; cytostatic;  
KM prostate specific membrane antigen; antiproliferic; antiarthritic;  
KM dermatological; antiinflammatory; antiallergic; vaccine; dermal disorder;  
KM epidermal disorder; psoriasis; inflammatory disorder; epidermis; dermis;  
KM neoplastic disorder.  
OS  
XX Mus musculus.  
OS Synthetic.  
XX  
XX WO2003024388-A2.  
XX  
XX 27-MAR-2003.  
XX  
XX 30-MAY-2002; 2002WO-US017204.  
XX  
XX 20-SEP-2001; 2001US-0324100P.  
XX 08-MAR-2002; 2002US-0362612P.  
XX  
XX (CORR ) CORNELL RES FOUND INC.  
XX  
XX Bander N;  
XX  
XX WPI; 2003-313319/30.  
XX  
XX Ablating/killing aberrant prostate specific membrane antigen-expressing  
PT cells for treating skin disorders, by contacting the cell with an  
PT antibody that binds to the extracellular domain of prostate specific  
PT membrane antigen.  
XX  
XX Disclosure; Page 68; 225pp; English.  
XX  
XX The present invention describes a method (M1) for ablating or killing an



CC excessive T cell or neutrophil activity. Accordingly, these IL-9  
CC antagonists exhibit antiallergic, antiasthmatic and cytostatic  
CC activities. This peptide sequence is a peptide from the human heavy chain  
CC framework region 4, used in an exemplification of the invention.

XX SQ Sequence 11 AA;

Query Match 100.0%; Score 59; DB 7; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WGGGTTVTSS 11  
Db 1 WGGGTTVTSS 11

#### RESULT 13

ADH17960  
ID ADH17960 standard; peptide; 11 AA.

XX AC ADH17960;

DT 11-MAR-2004 (first entry)

XX DE Human modified 15H12/19D12 HCA framework region 4 peptide.

XX insulin-like growth factor receptor 1; IGFRI; cytosolic; osteopathic;  
XX antidiatherosclerotic; antiposoriatic; vasotropic; antidiatheroeal;  
XX acromegaly; bladder cancer; Wilms tumour; ovarian; pancreatic;  
XX benign prostatic hyperplasia; breast; prostate; bone; lung; colorectal;  
XX cervical; synovial sarcoma; diarrhoea; carcinoid syndrome;  
XX vasoactive intestinal peptide; gigantism; psoriasis; atherosclerosis;  
XX smooth muscle restenosis; blood vessel; microvascular proliferation;  
XX gene therapy; human; 15H12/19D12; heavy chain A; HCA; framework region.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO2003100008-A2.

XX PD 04-DEC-2003.

XX PF 22-MAY-2003; 2003WO-US016283.

XX PR 24-MAY-2002; 2002US-0383459P.

XX PR 02-JUL-2002; 2002US-0393214P.

XX PR 23-DEC-2002; 2002US-0436254P.

XX PA (SCHE ) SCHERING CORP.

XX PI Wang Y, Greenberg R, Presta L, Pachter JA, Hailey J, Brams P;  
PI Williams D, Srinivasan M, Feingersh D;

XX DR WPI; 2004-042807/04.

XX DR N-PSDB; ADH17959.

XX PT New binding composition that specifically binds to insulin-like growth  
XX factor receptor 1, useful for treating or preventing a medical condition  
XX that is mediated by elevated expression or activity of IGFRI.

XX PS Disclosure; SEQ ID NO 69; 144pp; English.

XX The invention relates to a novel binding composition that specifically  
XX binds to insulin-like growth factor receptor 1 (IGFRI). The composition  
XX of the invention demonstrates cytostatic, osteopathic,  
XX antidiatherosclerotic, antiposoriatic, vasotropic and antidiatheroeal  
XX activities and may be useful for preventing or treating a medical  
XX condition selected from acromegaly, bladder cancer, Wilms cancer,  
XX ovarian cancer, pancreatic cancer, benign prostatic hyperplasia, breast  
XX cancer, prostate cancer, bone cancer, lung cancer, colorectal cancer,  
XX cervical cancer, synovial sarcoma, diarrhoea associated with carcinoid  
XX syndrome, vasoactive intestinal peptide secreting tumours, gigantism,  
XX psoriasis, atherosclerosis, smooth muscle restenosis of blood vessels and

CC inappropriate microvascular proliferation. The composition may also have  
CC gene therapy applications. The current sequence is that of the human  
CC 15H12/19D12 heavy chain A (HCA) framework region peptide of the  
CC invention.

XX SQ Sequence 11 AA;

Query Match 100.0%; Score 59; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WGGGTTVTSS 11  
Db 1 WGGGTTVTSS 11

#### RESULT 14

ADH18011  
ID ADH18011 standard; peptide; 11 AA.

XX AC ADH18011;

DT 11-MAR-2004 (first entry)

XX DE Human modified 15H12/19D12 HCB framework region 4 peptide.

XX insulin-like growth factor receptor 1; IGFRI; cytosolic; osteopathic;  
XX antidiatherosclerotic; antiposoriatic; vasotropic; antidiatheroeal;  
XX acromegaly; bladder cancer; Wilms tumour; ovarian; pancreatic;  
XX benign prostatic hyperplasia; breast; prostate; bone; lung; colorectal;  
XX cervical; synovial sarcoma; diarrhoea; carcinoid syndrome;  
XX vasoactive intestinal peptide; gigantism; psoriasis; atherosclerosis;  
XX smooth muscle restenosis; blood vessel; microvascular proliferation;  
XX gene therapy; human; 15H12/19D12; heavy chain B; HCB; framework region.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO2003100008-A2.

XX PD 04-DEC-2003.

XX PF 22-MAY-2003; 2003WO-US016283.

XX PR 24-MAY-2002; 2002US-0383459P.

XX PR 02-JUL-2002; 2002US-0393214P.

XX PR 23-DEC-2002; 2002US-0436254P.

XX PA (SCHE ) SCHERING CORP.

XX PI Wang Y, Greenberg R, Presta L, Pachter JA, Hailey J, Brams P;  
PI Williams D, Srinivasan M, Feingersh D;

XX DR WPI; 2004-042807/04.

XX DR N-PSDB; ADH18010.

XX PT New binding composition that specifically binds to insulin-like growth  
XX factor receptor 1, useful for treating or preventing a medical condition  
XX that is mediated by elevated expression or activity of IGFRI.

XX PS Disclosure; SEQ ID NO 120; 144pp; English.

XX The invention relates to a novel binding composition that specifically  
XX binds to insulin-like growth factor receptor 1 (IGFRI). The composition  
XX of the invention demonstrates cytostatic, osteopathic,  
XX antidiatherosclerotic, antiposoriatic, vasotropic and antidiatheroeal  
XX activities and may be useful for preventing or treating a medical  
XX condition selected from acromegaly, bladder cancer, Wilms cancer,  
XX ovarian cancer, pancreatic cancer, benign prostatic hyperplasia, breast  
XX cancer, prostate cancer, bone cancer, lung cancer, colorectal cancer,  
XX cervical cancer, synovial sarcoma, diarrhoea associated with carcinoid  
XX syndrome, vasoactive intestinal peptide secreting tumours, gigantism,  
XX psoriasis, atherosclerosis, smooth muscle restenosis of blood vessels and

CC inappropriate microvascular proliferation. The composition may also have  
 CC gene therapy applications. The current sequence is that of the human  
 CC 15112/19D12 heavy chain B (HCB) framework region peptide of the  
 CC invention.

XX  
 SQ Sequence 11 AA;

Query Match 100.0%; Score 59; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.011;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTVTSS 11  
 |||||  
 Db 1 WGGGTTVTSS 11

# RESULT 15

ADQ90791  
 ID ADQ90791 standard; protein; 11 AA.

AC ADQ90791;

DT 07-OCT-2004 (first entry)

DE Artificially deimmunised framework sequence #14.

KW insulin-related disorder; prostate specific membrane antigen; PSMA;

KW obesity; hyperglycaemia; hypoglycaemia; hyperinsulinaemia;

KW insulin-resistance; impaired glucose tolerance; impaired fasting glucose;

KW Type 1 diabetes mellitus; Type 2 diabetes mellitus; gestational diabetes.

XX Synthetic.

OS  
 XX US2004136998-A1.

XX PD 15-JUL-2004.

XX PF 17-OCT-2003; 2003US-00668015.

XX PR 30-OCT-2002; 2002US-0422396P.

XX PA (BAND/) BANDER N H.

XX PI Bander NH;

XX DR WPI; 2004-533338/51.

PT Use of anti-prostate specific membrane antigen antibodies for treating or  
 PT preventing insulin-related disorders, e.g. obesity, hyperglycemia,  
 PT hypoglycemia, hyperinsulinemia, insulin-resistance, or Type 1 or 2  
 PT diabetes mellitus.

PS Disclosure; SEQ ID NO 40; 89pp; English.

XX The invention relates to a method of treating or preventing an insulin-  
 CC related disorder in a subject which comprises administering an antibody  
 CC or its antigen-binding portion specific for prostate specific membrane  
 CC antigen (PSMA). The method is useful for treating an insulin-related  
 CC disorder, including obesity, hyperglycaemia, hypoglycaemia,  
 CC hyperinsulinaemia, insulin-resistance, impaired glucose tolerance,  
 CC impaired fasting glucose, Type 1 diabetes mellitus, Type 2 diabetes  
 CC mellitus, and gestational diabetes. The present sequence represents an  
 CC artificially deimmunised framework sequence.

XX SQ Sequence 11 AA;

Query Match 100.0%; Score 59; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.011;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTVTSS 11  
 |||||  
 Db 1 WGGGTTVTSS 11

Search completed: December 4, 2005, 04:45:01  
 Job time : 97.5625 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:31:45 ; Search time 15.5833 Seconds  
(without alignments)  
67.918 Million cell updates/sec

Title: US-10-632-706-198

Perfect score: 59

Sequence: 1 WGCGTIVTSS 11

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	74	2 S26793	Ig heavy chain V r
2	59	100.0	110	2 PH1655	Ig heavy chain V r
3	59	100.0	113	2 S55533	Ig heavy chain V r
4	59	100.0	113	2 S55535	Ig heavy chain V r
5	59	100.0	113	2 S55530	Ig heavy chain V r
6	59	100.0	113	2 S55534	Ig heavy chain V r
7	59	100.0	113	2 S55528	Ig heavy chain V r
8	59	100.0	113	2 S55532	Ig heavy chain V r
9	59	100.0	113	2 S55531	Ig heavy chain V r
10	59	100.0	114	2 S46392	Ig heavy chain V r
11	59	100.0	114	2 S20707	Ig heavy chain V r
12	59	100.0	115	2 S20706	Ig heavy chain V r
13	59	100.0	116	2 S15672	Ig heavy chain V r
14	59	100.0	116	2 S55542	Ig heavy chain V r
15	59	100.0	117	2 S55541	Ig heavy chain V r
16	59	100.0	118	2 PH1666	Ig heavy chain V r
17	59	100.0	118	2 PH1660	Ig heavy chain V r
18	59	100.0	118	2 S32786	Ig heavy chain (an
19	59	100.0	119	2 PH0964	Ig heavy chain V r
20	59	100.0	120	2 PH1650	Ig heavy chain V r
21	59	100.0	120	2 S49590	Ig heavy chain V r
22	59	100.0	120	2 PD0008	Ig heavy chain V r
23	59	100.0	120	2 S55538	Ig heavy chain V r
24	59	100.0	120	2 S55539	Ig heavy chain V r
25	59	100.0	120	2 S55537	Ig heavy chain V r
26	59	100.0	120	2 S55536	Ig heavy chain V r
27	59	100.0	120	2 S12953	Ig heavy chain V r
28	59	100.0	121	2 S31106	Ig heavy chain - h
29	59	100.0	121	2 S55540	Ig heavy chain V r

30	59	100.0	122	2 E36005	Ig heavy chain V r
31	59	100.0	122	2 PH0958	Ig heavy chain V r
32	59	100.0	123	2 S26794	Ig heavy chain V r
33	59	100.0	124	2 S20775	Ig heavy chain V r
34	59	100.0	125	2 S37455	Ig mu chain - huma
35	59	100.0	125	2 S37455	Ig heavy chain V6
36	59	100.0	127	2 S24689	Ig heavy chain V r
37	59	100.0	127	2 S24689	Ig heavy chain V6
38	59	100.0	128	2 S48797	Ig heavy chain V r
39	59	100.0	131	2 S66537	Ig heavy chain V r
40	59	100.0	132	2 PH0954	Ig heavy chain V r
41	59	100.0	133	2 C33548	Ig heavy chain V-I
42	59	100.0	135	2 B32274	Ig heavy chain pre
43	59	100.0	135	2 S78051	Ig heavy chain pre
44	59	100.0	136	2 PH0960	Ig heavy chain V r
45	59	100.0	137	2 S31676	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S26793  
Ig heavy chain V region - human

C/Species: Homo sapiens (man)

C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Jun-2000

C/Accession: S26793

R/Mottari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.

Eur. J. Immunol. 22, 241-245, 1992

A/Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene fami

A/Reference number: S26786; MUID:9211632; PMID:1730251

A/Accession: S26793

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-74 <MOR>

A/References: UNIPARC:UPI000015FCA; EMBL:X61019; NID:G32787; PIDN:CAA43353.1; PID

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 59; DB 2; Length 74;

Best Local Similarity 100.0%; Pred. No. 0.0021;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGCGTIVTSS 11  
Db 64 WGCGTIVTSS 74

RESULT 2

PH1655  
Ig heavy chain V region (clone 2B8) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 16-Aug-1996

C/Accession: PH1655

J.Hillson, J.L.; Kair, N.S.; Opplinger, I.R.; Mannik, M.; Saseo, E.H.

J. Exp. Med. 178, 331-336, 1993

A/Title: The structural basis of germline-encoded VH3 immunoglobulin binding to streptoly

A/Reference number: PH1642; MUID:93301610; PMID:8315388

A/Accession: PH1655

A/Molecule type: mRNA

A/Residues: 1-110 <Hil>

A/Cross-references: UNIPARC:UPI0000176BDC

A/Experimental source: B cell

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/7-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 110;

Best Local Similarity 100.0%; Pred. No. 0.0032;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGCGTIVTSS 11  
Db 11 WGCGTIVTSS 11

Db 100 WGGGTTVTSS 110

## RESULT 3

S55533

Ig heavy chain V region pe25 - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 21-Jan-2000

C/Accession: S55533

R/Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.

J. Mol. Biol. 247, 932-946, 1995

A/Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using

A/Reference number: S55528; MUID:95239763; PMID:7536850

A/Accession: S55533

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-113 &lt;BOB&gt;

A/Cross-references: UNIPARC:UPI0000116205; EMBL:X82594; NID:9854314; PIDN:CAA57930.1; PI

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/14-97/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 100.0%; Score 59; DB 2; Length 113;

Best Local Similarity 100.0%; Pred. No. 0.0033;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTVTSS 11

Db 103 WGGGTTVTSS 113

## RESULT 4

S55535

Ig heavy chain V region pe23 - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 21-Jan-2000

C/Accession: S55535

R/Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.

J. Mol. Biol. 247, 932-946, 1995

A/Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using

A/Reference number: S55528; MUID:95239763; PMID:7536850

A/Accession: S55535

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-113 &lt;BOB&gt;

A/Cross-references: UNIPARC:UPI0000116203; EMBL:X82592; NID:9854310; PIDN:CAA57928.1; PI

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/14-97/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 100.0%; Score 59; DB 2; Length 113;

Best Local Similarity 100.0%; Pred. No. 0.0033;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTVTSS 11

Db 103 WGGGTTVTSS 113

## RESULT 5

S55530

Ig heavy chain V region pe17 - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 21-Jan-2000

C/Accession: S55530

R/Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.

J. Mol. Biol. 247, 932-946, 1995

A/Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using

A/Reference number: S55528; MUID:95239763; PMID:7536850

A/Accession: S55530

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-113 &lt;BOB&gt;

A/Cross-references: UNIPARC:UPI00001161FD; EMBL:X82586; NID:9854296; PIDN:CAA57922.1; PI

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/14-97/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 100.0%; Score 59; DB 2; Length 113;

Best Local Similarity 100.0%; Pred. No. 0.0033;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTVTSS 11

Db 103 WGGGTTVTSS 113

## RESULT 6

S55534

Ig heavy chain V region pe15 - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 21-Jan-2000

C/Accession: S55534

R/Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.

J. Mol. Biol. 247, 932-946, 1995

A/Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using

A/Reference number: S55528; MUID:95239763; PMID:7536850

A/Accession: S55534

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-113 &lt;BOB&gt;

A/Cross-references: UNIPARC:UPI00001161FC; EMBL:X82584; NID:9854292; PIDN:CAA57920.1; PI

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/14-97/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 100.0%; Score 59; DB 2; Length 113;

Best Local Similarity 100.0%; Pred. No. 0.0033;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTVTSS 11

Db 103 WGGGTTVTSS 113

## RESULT 7

S55528

Ig heavy chain V region (pe16/pe14) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 21-Jan-2000

C/Accession: S55528; S55529

R/Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.

J. Mol. Biol. 247, 932-946, 1995

A/Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using

A/Reference number: S55528; MUID:95239763; PMID:7536850

A/Accession: S55528

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-113 &lt;BOB&gt;

A/Cross-references: UNIPARC:UPI00001161FB; EMBL:X82585; NID:9854294; PIDN:CAA57921.1; PI

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/14-97/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 100.0%; Score 59; DB 2; Length 113;

Best Local Similarity 100.0%; Pred. No. 0.0033;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WGGGTTVTSS 11  
Db 103 WGGGTTVTSS 113

## RESULT 8

S55532  
Ig heavy chain V region pe19 - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 21-Jan-2000  
C/Accession: S55532  
R/Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.  
J. Mol. Biol. 247, 932-946, 1995  
A/Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using  
utations in the variable region genes.  
A/Reference number: S55528; PMID:95239763; PMID:7536850  
A/Accession: S55532  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-113 <BOB>  
A/Cross-references: UNIPARC:UPI00001161F; EMBL:X82588; NID:9854300; PIDN:CAAS7924.1; P  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F;14-97/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 113;  
Best Local Similarity 100.0%; Pred. No. 0.0033;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTVTSS 11  
Db 103 WGGGTTVTSS 113

## RESULT 9

S55531  
Ig heavy chain V region pe18 - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 21-Jan-2000  
C/Accession: S55531  
R/Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.  
J. Mol. Biol. 247, 932-946, 1995  
A/Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using  
utations in the variable region genes.  
A/Reference number: S55528; PMID:95239763; PMID:7536850  
A/Accession: S55531  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-113 <BOB>  
A/Cross-references: UNIPARC:UPI00001161F; EMBL:X82587; NID:9854298; PIDN:CAAS7923.1; P  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F;14-97/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 113;  
Best Local Similarity 100.0%; Pred. No. 0.0033;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTVTSS 11  
Db 103 WGGGTTVTSS 113

## RESULT 10.

S46392  
Ig heavy chain V region (VH-28) - human  
C/Species: Homo sapiens (man)  
C/Date: 27-Jan-1995 #sequence\_revision 27-Jan-1995 #text\_change 20-Jun-2000  
C/Accession: S46392  
R/Fligint, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.  
J. Mol. Biol. 239, 68-78, 1994

A/Title: In vitro assembly of repertoires of antibody chains on the surface of phage by  
A/Reference number: S46390; PMID:94254092; PMID:8196048

A/Accession: S46392  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-114 <FIG>  
A/Cross-references: UNIPARC:UPI00001137D6; EMBL:Z31688; NID:9499306; PIDN:CAAS493.1; P  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 114;  
Best Local Similarity 100.0%; Pred. No. 0.0033;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTVTSS 11  
Db 104 WGGGTTVTSS 114

## RESULT 11

S20707  
Ig heavy chain V region - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jan-2000  
C/Accession: S20707  
R/Brenand, D.M.; Hinde, M.G.; Welsh, J.H.; Tempest, P.R.; Harris, W.J.; Carr, F.J.; Osbc  
submitted to the EMBL Data Library, April 1992  
A/Description: Binding specificity and variable region sequences of two monoclonal antic  
A/Reference number: S20706  
A/Accession: S20707  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-114 <BRE>  
A/Cross-references: UNIPARC:UPI0000176B37; EMBL:Z11916  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F;12-95/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 114;  
Best Local Similarity 100.0%; Pred. No. 0.0033;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTVTSS 11  
Db 104 WGGGTTVTSS 114

## RESULT 12

S20706  
Ig heavy chain V region - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C/Accession: S20706  
R/Brenand, D.M.; Hinde, M.G.; Welsh, J.H.; Tempest, P.R.; Harris, W.J.; Carr, F.J.; Osbc  
submitted to the EMBL Data Library, April 1992  
A/Description: Binding specificity and variable region sequences of two monoclonal antic  
A/Reference number: S20706  
A/Accession: S20706  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-115 <BRE>  
A/Cross-references: UNIPARC:QBR3V9; UNIPARC:UPI0000176C45; EMBL:Z11914  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F;12-97/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 115;  
Best Local Similarity 100.0%; Pred. No. 0.0033;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTVTSS 11  
Db 104 WGGGTTVTSS 114

Db 105 WGGTTTVSS 115

# RESULT 13

IG heavy chain V region - mouse (fragment)

C:Species: Mus musculus (house mouse)  
C:Date: 18-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000  
C:Accession: S15672  
R:Tempest, P.R.; Bremner, P.; Lambert, M.; Taylor, G.; Furze, J.M.; Carr, F.J.; Harris, B.; Technology 9, 266-271, 1991  
A:Title: Reshaping a human monoclonal antibody to inhibit human respiratory syncytial virus  
A:Reference number: S15672; MUID:91337412; PMID:1367535  
A:Accession: S15672  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-116 <TEM>  
A:Cross-references: UNIPARC:UPI0000115F4C; EMBL:X58835; NID:951978; PIDN:CAA41644.1; PI  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 116;  
Best Local Similarity 100.0%; Pred. No. 0.0033;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGTTTVSS 11  
|||||  
Db 106 WGGTTTVSS 116

# RESULT 14

IG heavy chain V region pe2 - mouse (fragment)

C:Species: Mus musculus (house mouse)  
C:Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S55542  
R:Boeltger, V.; Boeltger, A.; Lane, E.B.; Spruce, B.A.  
J. Mol. Biol. 247, 932-946, 1995  
A:Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using variations in the variable region genes.  
A:Reference number: S55528; MUID:95239763; PMID:7536850  
A:Accession: S55542  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-116 <BOB>  
A:Cross-references: UNIPARC:UPI00001161F9; EMBL:X82581; NID:9854302; PIDN:CAA57917.1; PI  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:14-97/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 116;  
Best Local Similarity 100.0%; Pred. No. 0.0033;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGTTTVSS 11  
|||||  
Db 106 WGGTTTVSS 116

# RESULT 15

IG heavy chain V region pe1 - mouse (fragment)

C:Species: Mus musculus (house mouse)  
C:Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S55541  
R:Boeltger, V.; Boeltger, A.; Lane, E.B.; Spruce, B.A.  
J. Mol. Biol. 247, 932-946, 1995  
A:Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using variations in the variable region genes.  
A:Reference number: S55528; MUID:95239763; PMID:7536850  
A:Accession: S55541  
A:Status: preliminary

A:Molecule type: mRNA  
A:Residues: 1-117 <BOB>  
A:Cross-references: UNIPARC:UPI00001161F8; EMBL:X82580; NID:9854286; PIDN:CAA57916.1; PI  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:14-97/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 117;  
Best Local Similarity 100.0%; Pred. No. 0.0034;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGTTTVSS 11  
|||||  
Db 107 WGGTTTVSS 117

Search completed: December 4, 2005, 04:53:46  
Job time : 15.5833 secs



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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:08:08 ; Search time 3.20833 Seconds  
(without alignments)  
16.417 Million cell updates/sec

Title: US-10-632-706-198

Sequence: 1 WGGTIVVSS 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.New.\*  
1: /cgn2\_6/prodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
2: /cgn2\_6/prodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
3: /cgn2\_6/prodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
4: /cgn2\_6/prodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
5: /cgn2\_6/prodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
6: /cgn2\_6/prodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
7: /cgn2\_6/prodata/1/pubpaa/US11\_NEW\_PUB.pep.\*  
8: /cgn2\_6/prodata/1/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	100.0	11	US-10-839-799-114	Sequence 114, App
2	59	100.0	11	US-10-839-799-129	Sequence 129, App
3	59	100.0	11	US-11-108-135-7	Sequence 7, Appl1
4	59	100.0	20	US-11-040-159-4	Sequence 4, Appl1
5	59	100.0	20	US-11-054-669-107	Sequence 107, App
6	59	100.0	113	US-11-144-248-20	Sequence 20, Appl
7	59	100.0	116	US-11-174-186-20	Sequence 20, Appl
8	59	100.0	116	US-11-174-186-21	Sequence 21, Appl
9	59	100.0	116	US-11-174-186-22	Sequence 22, Appl
10	59	100.0	116	US-11-174-186-23	Sequence 23, Appl
11	59	100.0	116	US-11-174-186-24	Sequence 24, Appl
12	59	100.0	116	US-11-174-186-25	Sequence 25, Appl
13	59	100.0	117	US-10-839-799-132	Sequence 132, App
14	59	100.0	117	US-11-054-669-120	Sequence 120, App
15	59	100.0	118	US-10-932-334-75	Sequence 75, Appl
16	59	100.0	118	US-11-012-353-71	Sequence 71, Appl
17	59	100.0	120	US-10-932-334-71	Sequence 71, Appl
18	59	100.0	120	US-11-096-074-2	Sequence 2, Appl1
19	59	100.0	121	US-11-108-135-24	Sequence 24, Appl
20	59	100.0	124	US-10-932-334-13	Sequence 13, Appl
21	59	100.0	124	US-11-144-248-8	Sequence 8, Appl1
22	59	100.0	124	US-11-040-159-6	Sequence 6, Appl1
23	59	100.0	124	US-11-040-159-8	Sequence 8, Appl1
24	59	100.0	124	US-11-096-074-14	Sequence 14, Appl
25	59	100.0	125	US-11-144-248-16	Sequence 16, Appl

26	59	100.0	125	US-11-084-554-8	Sequence 8, Appl1
27	59	100.0	136	US-10-839-799-99	Sequence 99, Appl
28	59	100.0	136	US-10-788-273-4	Sequence 4, Appl1
29	59	100.0	143	US-11-096-074-6	Sequence 6, Appl1
30	59	100.0	143	US-11-096-074-10	Sequence 10, Appl
31	59	100.0	143	US-11-096-074-12	Sequence 12, Appl
32	59	100.0	143	US-11-096-074-16	Sequence 16, Appl
33	59	100.0	143	US-11-096-074-18	Sequence 18, Appl
34	59	100.0	145	US-10-721-763-29	Sequence 29, Appl
35	59	100.0	154	US-10-721-763-25	Sequence 25, Appl
36	59	100.0	174	US-11-144-248-4	Sequence 4, Appl1
37	59	100.0	237	US-10-073-301A-9	Sequence 9, Appl1
38	59	100.0	237	US-11-054-515-2104	Sequence 2104, Ap
39	59	100.0	240	US-11-054-515-2105	Sequence 2105, Ap
40	59	100.0	240	US-11-054-515-2113	Sequence 2113, Ap
41	59	100.0	243	US-11-054-515-1927	Sequence 1927, Ap
42	59	100.0	243	US-11-054-515-1945	Sequence 1945, Ap
43	59	100.0	244	US-11-054-515-2058	Sequence 2058, Ap
44	59	100.0	247	US-11-054-515-1434	Sequence 1434, Ap
45	59	100.0	248	US-11-054-515-1008	Sequence 1008, Ap

#### ALIGNMENTS

RESULT 1  
US-10-839-799-114  
; Sequence 114, Application US/10839799  
; Publication No. US20050249726A1  
; GENERAL INFORMATION:  
APPLICANT: OHTOMO, Toshihiko  
SATO, Koh  
TSUCHIYA, Masayuki  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
MEDULLOBLASTOMA CELLS  
NUMBER OF SEQUENCES: 132  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/839,799  
FILING DATE: 06-May-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,265  
FILING DATE: 09-SEP-1996  
APPLICATION NUMBER: WO PCT/JP94/01763  
FILING DATE: 19-OCT-1994  
APPLICATION NUMBER: JP 5-291078  
FILING DATE: 19-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/184  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 114:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 114:  
US-10-839-799-114

Query Match 100.0%; Score 59; DB 6; Length 11;  
Best Local Similarity 100.0%; Pred. NO. 0.0001;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVVSS 11  
|||  
Db 1 WGGGTTTVVSS 11

## RESULT 2

US-10-839-799-129  
; Sequence 129, Application US/10839799  
; Publication No. US20050249726A1  
; GENERAL INFORMATION:  
; APPLICANT: OHTOMO, Toshihiko  
; SATO, Koh  
; TSUCHIYA, Masayuki  
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
; MEDIOBLASTOMA CELLS  
; NUMBER OF SEQUENCES: 132  
; CORRESPONDENCE ADDRESS:  
; ADDRESSSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/839,799  
; FILING DATE: 06-May-2004  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/646,265  
; FILING DATE: 09-SEP-1996  
; APPLICATION NUMBER: WO PCT/JP94/01763  
; FILING DATE: 19-OCT-1994  
; APPLICATION NUMBER: JP 5-291078  
; FILING DATE: 19-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WEGNER, Harold C.  
; REGISTRATION NUMBER: 25,258  
; REFERENCE/DOCKET NUMBER: 53466/184  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 129:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: 1linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 129:  
US-10-839-799-129

Query Match 100.0%; Score 59; DB 6; Length 11;  
Best Local Similarity 100.0%; Pred. NO. 0.0001;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVVSS 11  
|||  
Db 1 WGGGTTTVVSS 11

## RESULT 3

US-11-108-135-7  
; Sequence 7, Application US/11108135  
; Publication No. US20050260213A1  
; GENERAL INFORMATION:  
; APPLICANT: Koenig, Scott  
; APPLICANT: Verti, Maria Concetta  
; APPLICANT: Tuallion, Nadine  
; APPLICANT: Bonvini, Ezio  
; APPLICANT: Stavenhagen, Jeffrey  
; APPLICANT: Rankin, Christopher  
; TITLE OF INVENTION: Fc-gamma-RIIb-specific antibodies and methods of use thereof  
; FILE REFERENCE: 11183-014-999  
; CURRENT APPLICATION NUMBER: US/11/108,135  
; CURRENT FILING DATE: 2005-04-15  
; PRIOR APPLICATION NUMBER: US 60/562,804  
; PRIOR FILING DATE: 2004-04-16  
; PRIOR APPLICATION NUMBER: US 60/582,044  
; PRIOR FILING DATE: 2004-06-21  
; PRIOR APPLICATION NUMBER: US 60/582,045  
; PRIOR FILING DATE: 2004-06-21  
; PRIOR APPLICATION NUMBER: US 60/654,713  
; PRIOR FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Framework sequence from human germline VH1-18 and JH6 - FR4  
US-11-108-135-7

Query Match 100.0%; Score 59; DB 7; Length 11;  
Best Local Similarity 100.0%; Pred. NO. 0.0001;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVVSS 11  
|||  
Db 1 WGGGTTTVVSS 11

RESULT 4  
US-11-040-159-4  
; Sequence 4, Application US/11040159  
; Publication No. US2005025552A1  
; GENERAL INFORMATION:  
; APPLICANT: Flynn, Peter  
; APPLICANT: Luehrs, Kenneth  
; APPLICANT: Ballint, Robert F.  
; APPLICANT: Her, Jeng-Hong  
; APPLICANT: Bebbington, Christopher R.  
; APPLICANT: Yarranton, Geoffrey T.  
; APPLICANT: Kaiobios, Inc.  
; TITLE OF INVENTION: Antibody Specificity Transfer Using Minimal Essential  
; FILE REFERENCE: 021167-001730US  
; CURRENT APPLICATION NUMBER: US/11/040,159  
; CURRENT FILING DATE: 2005-01-20  
; PRIOR APPLICATION NUMBER: US 60/537,364  
; PRIOR FILING DATE: 2004-01-20  
; PRIOR APPLICATION NUMBER: US 60/546,216  
; PRIOR FILING DATE: 2004-02-23  
; NUMBER OF SEQ ID NOS: 133  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:JH6  
US-11-040-159-4

Query Match 100.0%; Score 59; DB 7; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.00018;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11  
|||||  
Db 10 WGGGTTTVSS 20

## RESULT 5

US-11-054-669-107  
; Sequence 107, Application US/11054669  
; Publication No. US20050261480A1  
; GENERAL INFORMATION:  
; APPLICANT: Foote, Jefferson  
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES  
; FILE REFERENCE: 30219/US/3  
; CURRENT APPLICATION NUMBER: US/11/054,669  
; CURRENT FILING DATE: 2005-02-08  
; PRIOR APPLICATION NUMBER: US 10/194,975  
; PRIOR FILING DATE: 2002-07-12  
; PRIOR APPLICATION NUMBER: US 60/305,111  
; PRIOR FILING DATE: 2001-07-12  
; NUMBER OF SEQ ID NOS: 124  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 107  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-054-669-107

Query Match 100.0%; Score 59; DB 7; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.00018;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11  
|||||  
Db 10 WGGGTTTVSS 20

## RESULT 6

US-11-144-248-20  
; Sequence 20, Application US/11144248  
; Publication No. US20050244408A1  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Bruce D.  
; APPLICANT: Beebe, Jean  
; APPLICANT: Miller, Penelope E.  
; APPLICANT: Moyer, James D.  
; APPLICANT: Corvalan, Jose R.  
; APPLICANT: Gallo, Michael  
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR  
; FILE REFERENCE: ABX-PF2  
; CURRENT APPLICATION NUMBER: US/11/144,248  
; CURRENT FILING DATE: 2005-06-02  
; PRIOR APPLICATION NUMBER: US/10/038,591  
; PRIOR FILING DATE: 2002-01-04  
; PRIOR APPLICATION NUMBER: 60/259,927  
; PRIOR FILING DATE: 2001-01-05  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 113  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-144-248-20

Query Match 100.0%; Score 59; DB 7; Length 113;  
Best Local Similarity 100.0%; Pred. No. 0.00086;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11  
|||||  
Db 103 WGGGTTTVSS 113

## RESULT 7

US-11-174-186-20  
; Sequence 20, Application US/11174186  
; Publication No. US20050244418A1  
; GENERAL INFORMATION:  
; APPLICANT: Gillies, Stephen  
; APPLICANT: Lo, Kin-Ming  
; APPLICANT: Qian, Xiyu  
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof  
; FILE REFERENCE: LEX-019  
; CURRENT APPLICATION NUMBER: US/11/174,186  
; CURRENT FILING DATE: 2005-07-01  
; PRIOR APPLICATION NUMBER: US 60/288,564  
; PRIOR FILING DATE: 2001-05-03  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 20  
; LENGTH: 116  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: KS VH veneered  
US-11-174-186-20

Query Match 100.0%; Score 59; DB 7; Length 116;  
Best Local Similarity 100.0%; Pred. No. 0.00086;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11  
|||||  
Db 106 WGGGTTTVSS 116

## RESULT 8

US-11-174-186-21  
; Sequence 21, Application US/11174186  
; Publication No. US20050244418A1  
; GENERAL INFORMATION:  
; APPLICANT: Gillies, Stephen  
; APPLICANT: Lo, Kin-Ming  
; APPLICANT: Qian, Xiyu  
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof  
; FILE REFERENCE: LEX-019  
; CURRENT APPLICATION NUMBER: US/11/174,186  
; CURRENT FILING DATE: 2005-07-01  
; PRIOR APPLICATION NUMBER: US 60/288,564  
; PRIOR FILING DATE: 2001-05-03  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 21  
; LENGTH: 116  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: KS de-immunized VH1  
US-11-174-186-21

Query Match 100.0%; Score 59; DB 7; Length 116;  
Best Local Similarity 100.0%; Pred. No. 0.00086;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11  
|||||  
Db 106 WGGGTTTVSS 116

## RESULT 9

US-11-174-186-22  
; Sequence 22, Application US/11174186  
; Publication No. US20050244418A1  
; GENERAL INFORMATION:

```

: APPLICANT: Gillies, Stephen
: APPLICANT: Lo, Kin-Ming
: APPLICANT: Qian, Xingui
: TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
: FILE REFERENCE: LXX-019
: CURRENT APPLICATION NUMBER: US/11/174,186
: CURRENT FILING DATE: 2005-07-01
: PRIOR APPLICATION NUMBER: US 60/288,564
: PRIOR FILING DATE: 2001-05-03
: NUMBER OF SEQ ID NOS: 42
: SOFTWARE: PatentIn version 3.3
: SEQ ID NO 22
: LENGTH: 116
: TYPE: PRT
: ORGANISM: Artificial
: FEATURE:
: OTHER INFORMATION: KS de-immunized VH2
: US-11-174-186-22

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Query Match	100.0%;	Score 59;	DB 7;	Length 116;
Best Local Similarity	100.0%;	Pred. No. 0.00088;		
Matches 11;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	WGQGTIVTVSS	11
Db	106	WGQGTIVTVSS	116

```

RESULT 10
US-11-174-186-23
: Sequence 23. Application US/11174186
: Publication No. US20050244418A1
: GENERAL INFORMATION:
: APPLICANT: Gillies, Stephen
: APPLICANT: Lo, Kin-Ming
: TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
: FILE REFERENCE: LEX-019
: CURRENT APPLICATION NUMBER: US/11/174,186
: CURRENT FILING DATE: 2005-07-01
: PRIORITY APPLICATION NUMBER: US 60/288,564
: PRIORITY FILING DATE: 2001-05-03
: NUMBER OF SEQ ID NOS: 42
: SOFTWARE: PatentIn version 3.3
: SEQ ID NO 23
: LENGTH: 116
: TYPE: PRT
: ORGANISM: Artificial
: FEATURE:
: OTHER INFORMATION: KS de-immunized VH3
: US-11-174-186-23

```

Query Match	100.0%;	Score 59;	DB 7;	Length 116;
Best Local Similarity	100.0%;	Pred. No. 0.00088;		
Matches	11;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0

```
QY      1  WGQGTIVTVSS  11
         |||||
Db      106 WGQGTIVTVSS  116
```

```

RESULT 11
US-11-174-186-24
: Sequence 24. Application US/11/74186
: Publication No. US2005024441A1
: GENERAL INFORMATION:
: APPLICANT: Gillies, Stephen
: APPLICANT: Lo, Kin-Ming
: APPLICANT: Qian, Xiyu1
: TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
: FILE REFERENCE: LEX-019
: CURRENT APPLICATION NUMBER: US/11/174,186
: CURRENT FILING DATE: 2005-07-01

```

```

: PRIOR APPLICATION NUMBER: US 60/288,566
:
: PRIOR FILING DATE: 2001-05-03
:
: NUMBER OF SEQ ID NOS: 42
:
: SOFTWARE: PatentIn version 3.3
: SEQ ID NO 24
:
: LENGTH: 116
:
: TYPE: PRT
:
: ORGANISM: Artificial
:
: FEATURE:
:
: OTHER INFORMATION: KS - delimmunized vha
US-11-174-186-24

```

Query Match	100.0%;	Score 59;	DB 7;	Length 116;
Best Local Similarity	100.0%;	Pred. No. 0.00088;		
Matches 11;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	WGQGTIVTVSS	11
Db	106	WGQGTIVTVSS	116

```

RESULT 12
US-11-174-186-25
; Sequence 25, Application US/11/174,186
; Publication No. US20050244418A1
GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
APPLICANT: Lo, Kin-Ming
APPLICANT: Qian, Xiang
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
CURRENT APPLICATION NUMBER: US/11/174,186
CURRENT FILING DATE: 2005-07-01
PRIORITY APPLICATION NUMBER: US 60/288,564
PRIORITY FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
SEQ ID NO 25
; LENGTH: 116
; TYPE: PRT
ORGANISM: Artificial
FEATURE:
; OTHER INFORMATION: KS de-immunized VHS
US-11-174-186-25

```

Query Match	100.04;	Score 59;	DB 7;	Length 116;
Best Local Similarity	100.04;	Pred. No. 0.00088;		
Matches 11;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

```

QY      1  WGQGTVTVSS  11
         |||||
Db      106 WGQGTVTVSS  116

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RESULT 13  
 US-10-839-799-132  
 : Sequence 132, Application US/10839799  
 : Publication No. US20050249726A1  
 :  
 : GENERAL INFORMATION:  
 :  
 : APPLICANT: OHTOMO, Toshihiko  
 : SATO, Koh  
 : TSUCHIYA, Masayuki  
 : TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
 : MEDULLOBLASTOMA CELLS  
 :  
 : NUMBER OF SEQUENCES: 132  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESS: Foley & Lardner  
 : STREET: 3000 K Street, N.W., Suite 500  
 : CITY: Washington  
 : STATE: D.C.  
 :  
 : COUNTRY: USA  
 : ZIP: 20007-5109  
 :  
 : COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/839,799  
FILING DATE: 06-May-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,265  
FILING DATE: 09-SEP-1996  
APPLICATION NUMBER: WO PCT/JP94/01763  
FILING DATE: 19-OCT-1994  
APPLICATION NUMBER: JP 5-291078  
FILING DATE: 19-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/184  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 132:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 117 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 132:  
US-10-839-799-132

Query Match 100.0%; Score 59; DB 6; Length 117;  
Best Local Similarity 100.0%; Pred. No. 0.00089;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11  
|||||  
Db 107 WGGGTTTVSS 117

RESULT 14  
US-11-054-669-120  
Sequence 120, Application US/11054669  
Publication No. US20050261480A1  
GENERAL INFORMATION:  
APPLICANT: Foote, Jefferson  
TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES  
FILE REFERENCE: 30219/US/3  
CURRENT APPLICATION NUMBER: US/11/054,669  
CURRENT FILING DATE: 2005-02-08  
PRIOR APPLICATION NUMBER: US 10/194,975  
PRIOR FILING DATE: 2002-07-12  
PRIOR APPLICATION NUMBER: US 60/305,111  
PRIOR FILING DATE: 2001-07-12  
NUMBER OF SEQ ID NOS: 124  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 120  
LENGTH: 117  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-054-669-120

Query Match 100.0%; Score 59; DB 7; Length 117;  
Best Local Similarity 100.0%; Pred. No. 0.00089;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11  
|||||  
Db 107 WGGGTTTVSS 117

RESULT 15

US-10-932-334-75  
Sequence 75, Application US/10932334  
Publication No. US20050249728A1  
GENERAL INFORMATION:  
APPLICANT: Immunogen, Inc.  
TITLE OF INVENTION: ANTI-IGF-1 RECEPTOR ANTIBODY  
FILE REFERENCE: A8689  
CURRENT APPLICATION NUMBER: US/10/932,334  
CURRENT FILING DATE: 2004-09-02  
PRIOR APPLICATION NUMBER: US/10/729,441  
PRIOR FILING DATE: 2003-12-08  
PRIOR APPLICATION NUMBER: 10/170,390  
PRIOR FILING DATE: 2002-06-14  
NUMBER OF SEQ ID NOS: 96  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 75  
LENGTH: 118  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic antibody structure  
US-10-932-334-75

Query Match 100.0%; Score 59; DB 6; Length 118;  
Best Local Similarity 100.0%; Pred. No. 0.0009;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11  
|||||  
Db 108 WGGGTTTVSS 118

Search completed: December 4, 2005, 04:37:50  
Job time : 3.20833 secs

**This Page Blank (uspo10)**

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OM protein - protein search, using SW model

Run on: December 4, 2005, 04:08:08 ; Search time 3.20833 Seconds  
(without alignments)  
16.417 Million cell updates/sec

Title: US-10-632-706-198  
Perfect score: 59  
Sequence: 1 WGGCTVTVSS 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
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7: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	11	6	US-10-839-799-114
2	59	100.0	11	6	US-10-839-799-129
3	59	100.0	11	7	US-11-108-135-7
4	59	100.0	20	7	US-11-040-159-4
5	59	100.0	20	7	US-11-054-669-107
6	59	100.0	113	7	US-11-144-248-20
7	59	100.0	116	7	US-11-174-186-20
8	59	100.0	116	7	US-11-174-186-21
9	59	100.0	116	7	US-11-174-186-22
10	59	100.0	116	7	US-11-174-186-23
11	59	100.0	116	7	US-11-174-186-24
12	59	100.0	116	7	US-11-174-186-25
13	59	100.0	117	6	US-10-839-799-112
14	59	100.0	117	7	US-11-054-669-110
15	59	100.0	118	6	US-10-932-334-75
16	59	100.0	118	6	US-11-012-353-71
17	59	100.0	120	6	US-10-932-334-71
18	59	100.0	120	7	US-11-096-074-2
19	59	100.0	121	7	US-11-108-135-24
20	59	100.0	124	6	US-10-932-334-13
21	59	100.0	124	7	US-11-144-248-8
22	59	100.0	124	7	US-11-040-159-6
23	59	100.0	124	7	US-11-040-159-8
24	59	100.0	124	7	US-11-096-074-14
25	59	100.0	125	7	US-11-144-248-16

26	59	100.0	125	7	US-11-084-554-8	Sequence 8, Appl1
27	59	100.0	136	6	US-10-839-799-99	Sequence 99, Appl1
28	59	100.0	138	6	US-10-789-273-4	Sequence 4, Appl1
29	59	100.0	143	7	US-11-096-074-6	Sequence 6, Appl1
30	59	100.0	143	7	US-11-096-074-10	Sequence 10, Appl1
31	59	100.0	143	7	US-11-096-074-12	Sequence 12, Appl1
32	59	100.0	143	7	US-11-096-074-16	Sequence 16, Appl1
33	59	100.0	143	7	US-11-096-074-18	Sequence 18, Appl1
34	59	100.0	145	6	US-10-721-763-29	Sequence 29, Appl1
35	59	100.0	154	6	US-10-721-763-25	Sequence 25, Appl1
36	59	100.0	174	7	US-11-144-248-4	Sequence 4, Appl1
37	59	100.0	237	6	US-10-073-301A-9	Sequence 9, Appl1
38	59	100.0	237	7	US-11-054-515-2104	Sequence 2104, Ap
39	59	100.0	240	7	US-11-054-515-2105	Sequence 2105, Ap
40	59	100.0	240	7	US-11-054-515-2113	Sequence 2113, Ap
41	59	100.0	243	7	US-11-054-515-1927	Sequence 1927, Ap
42	59	100.0	243	7	US-11-054-515-1945	Sequence 1945, Ap
43	59	100.0	244	7	US-11-054-515-2058	Sequence 2058, Ap
44	59	100.0	247	7	US-11-054-515-1434	Sequence 1434, Ap
45	59	100.0	248	7	US-11-054-515-1008	Sequence 1008, Ap

## ALIGNMENTS

RESULT 1  
US-10-839-799-114  
Sequence 114, Application US/10839799  
Publication No. US20050249726A1  
GENERAL INFORMATION:  
APPLICANT: OHTOMO, Toeshihiko  
SATO, Koh  
TSUCHIYA, Masayuki  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
MEDULLOBLASTOMA CELLS  
NUMBER OF SEQUENCES: 132  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/839,799  
FILING DATE: 06-May-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,265  
FILING DATE: 09-SEP-1996  
APPLICATION NUMBER: WO PCT/JP94/01763  
FILING DATE: 19-OCT-1994  
APPLICATION NUMBER: JP 5-291078  
FILING DATE: 19-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/184  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 114:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 114;  
US-10-839-799-114

Query Match 100.0%; Score 59; DB 6; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0001;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVSS 11  
Db 1 WGGGTTTVSS 11

## RESULT 2

US-10-839-799-129  
Sequence 129, Application US/10839799  
Publication No. US20050249726A1  
GENERAL INFORMATION:  
APPLICANT: OHTOMO, Toshiniko  
SATO, Koh  
TSUCHIYA, Masayuki  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
MEDULLOBLASTOMA CELLS  
NUMBER OF SEQUENCES: 132  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/839,799  
FILING DATE: 06-May-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,265  
FILING DATE: 09-SEP-1996  
APPLICATION NUMBER: WO PCT/JP94/01763  
FILING DATE: 19-OCT-1994  
APPLICATION NUMBER: JP 5-291078  
FILING DATE: 19-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/184  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 129:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 129:  
US-10-839-799-129

Query Match 100.0%; Score 59; DB 6; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0001;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVSS 11  
Db 1 WGGGTTTVSS 11

## RESULT 3

US-11-108-135-7  
Sequence 7, Application US/11108135  
Publication No. US20050260213A1  
GENERAL INFORMATION:  
APPLICANT: Koenig, Scott  
APPLICANT: Veri, Maria Conceita  
APPLICANT: Tuallion, Nadine  
APPLICANT: Bonvini, Ezio  
APPLICANT: Stavenhagen, Jeffrey  
TITLE OF INVENTION: PC-gamma-RITB-specific antibodies and methods of use thereof  
FILE REFERENCE: 11183-014-999  
CURRENT APPLICATION NUMBER: US/11/108,135  
CURRENT FILING DATE: 2005-04-15  
PRIOR APPLICATION NUMBER: US 60/562,804  
PRIOR FILING DATE: 2004-04-16  
PRIOR APPLICATION NUMBER: US 60/582,044  
PRIOR FILING DATE: 2004-06-21  
PRIOR APPLICATION NUMBER: US 60/582,045  
PRIOR FILING DATE: 2004-06-21  
PRIOR APPLICATION NUMBER: US 60/654,713  
PRIOR FILING DATE: 2005-02-18  
NUMBER OF SEQ ID NOS: 58  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Framework sequence from human germline VH1-18 and JH6 - FR4  
US-11-108-135-7

Query Match 100.0%; Score 59; DB 7; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0001;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVSS 11  
Db 1 WGGGTTTVSS 11

RESULT 4  
US-11-040-159-4  
Sequence 4, Application US/11040159  
Publication No. US2005025552A1  
GENERAL INFORMATION:  
APPLICANT: Flynn, Peter  
APPLICANT: Luehrs, Kenneth  
APPLICANT: Balint, Robert F.  
APPLICANT: Her, Jeng-Horng  
APPLICANT: Bebbington, Christopher R.  
APPLICANT: Yarranton, Geoffrey T.  
APPLICANT: Kalobilos, Inc.  
TITLE OF INVENTION: Antibody Specificity Transfer Using Minimal Essential  
FILE REFERENCE: 021167-001730US  
CURRENT APPLICATION NUMBER: US/11/040,159  
CURRENT FILING DATE: 2005-01-20  
PRIOR APPLICATION NUMBER: US 60/537,364  
PRIOR FILING DATE: 2004-01-20  
PRIOR APPLICATION NUMBER: US 60/546,216  
PRIOR FILING DATE: 2004-02-23  
NUMBER OF SEQ ID NOS: 133  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 4  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: JH6  
US-11-040-159-4

Query Match 100.0%; Score 59; DB 7; Length 20;



Best Local Similarity 100.0%; Pred. No. 0.00018;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WGGGTTTVSS 11  
|||||  
Db 10 WGGGTTTVSS 20

## RESULT 5

US-11-054-669-107  
; Sequence 107, Application US/11054669  
; Publication No. US20050261480A1  
; GENERAL INFORMATION:  
; APPLICANT: Foote, Jefferson  
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES  
; FILE REFERENCE: 30219/US/3  
; CURRENT APPLICATION NUMBER: US/11/054,669  
; CURRENT FILING DATE: 2005-02-08  
; PRIOR APPLICATION NUMBER: US 10/194,975  
; PRIOR FILING DATE: 2002-07-12  
; PRIOR APPLICATION NUMBER: US 60/305,111  
; PRIOR FILING DATE: 2001-07-12  
; NUMBER OF SEQ ID NOS: 124  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 107  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-054-669-107

Query Match 100.0%; Score 59; DB 7; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.00018;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WGGGTTTVSS 11  
|||||  
Db 10 WGGGTTTVSS 20

## RESULT 6

US-11-144-248-20  
; Sequence 20, Application US/11144248  
; Publication No. US20050244408A1  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Bruce D.  
; APPLICANT: Beebe, Jean  
; APPLICANT: Miller, Penelope E.  
; APPLICANT: Moyer, James D.  
; APPLICANT: Corvalan, Jose R.  
; APPLICANT: Gallo, Michael  
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR  
; FILE REFERENCE: ABX-PF2  
; CURRENT APPLICATION NUMBER: US/11/144,248  
; CURRENT FILING DATE: 2005-06-02  
; PRIOR APPLICATION NUMBER: US/10/038,591  
; PRIOR FILING DATE: 2002-01-04  
; PRIOR APPLICATION NUMBER: 60/259,927  
; PRIOR FILING DATE: 2001-01-05  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 113  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-144-248-20

Query Match 100.0%; Score 59; DB 7; Length 113;  
Best Local Similarity 100.0%; Pred. No. 0.00086;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WGGGTTTVSS 11  
|||||  
Db 103 WGGGTTTVSS 113

RESULT 7  
US-11-174-186-20  
; Sequence 20, Application US/11174186  
; Publication No. US20050244418A1  
; GENERAL INFORMATION:  
; APPLICANT: Gillies, Stephen  
; APPLICANT: Lo, Kin-Ming  
; APPLICANT: Qian, Xingyi  
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof  
; FILE REFERENCE: LEX-019  
; CURRENT APPLICATION NUMBER: US/11/174,186  
; CURRENT FILING DATE: 2005-07-01  
; PRIOR APPLICATION NUMBER: US 60/288,564  
; PRIOR FILING DATE: 2001-05-03  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 20  
; LENGTH: 116  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: KS VH veneered  
US-11-174-186-20

Query Match 100.0%; Score 59; DB 7; Length 116;  
Best Local Similarity 100.0%; Pred. No. 0.00088;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WGGGTTTVSS 11  
|||||  
Db 106 WGGGTTTVSS 116

## RESULT 8

US-11-174-186-21  
; Sequence 21, Application US/11174186  
; Publication No. US20050244418A1  
; GENERAL INFORMATION:  
; APPLICANT: Gillies, Stephen  
; APPLICANT: Lo, Kin-Ming  
; APPLICANT: Qian, Xingyi  
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof  
; FILE REFERENCE: LEX-019  
; CURRENT APPLICATION NUMBER: US/11/174,186  
; CURRENT FILING DATE: 2005-07-01  
; PRIOR APPLICATION NUMBER: US 60/288,564  
; PRIOR FILING DATE: 2001-05-03  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 21  
; LENGTH: 116  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: KS de-immunized VH1  
US-11-174-186-21

Query Match 100.0%; Score 59; DB 7; Length 116;  
Best Local Similarity 100.0%; Pred. No. 0.00088;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WGGGTTTVSS 11  
|||||  
Db 106 WGGGTTTVSS 116

## RESULT 9

US-11-174-186-22  
; Sequence 22, Application US/11174186  
; Publication No. US20050244418A1  
; GENERAL INFORMATION:

APPLICANT: Gillies, Stephen  
APPLICANT: Lo, Kin-Ming  
APPLICANT: Qian, Xingui  
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof  
FILE REFERENCE: LEX-019  
CURRENT APPLICATION NUMBER: US/11/174,186  
CURRENT FILING DATE: 2005-07-01  
PRIOR APPLICATION NUMBER: US 60/288,564  
PRIOR FILING DATE: 2001-05-03  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 22  
LENGTH: 116  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: KS de-immunized VH2  
US-11-174-186-22

Query Match 100.0%; Score 59; DB 7; Length 116;  
Best Local Similarity 100.0%; Pred. No. 0.00088;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGTTVTVSS 11  
|||||  
Db 106 WGGTTVTVSS 116

RESULT 10  
US-11-174-186-23  
Sequence 23, Application US/11/174,186  
Publication No. US20050244418A1  
GENERAL INFORMATION:  
APPLICANT: Gillies, Stephen  
APPLICANT: Lo, Kin-Ming  
APPLICANT: Qian, Xingui  
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof  
FILE REFERENCE: LEX-019  
CURRENT APPLICATION NUMBER: US/11/174,186  
CURRENT FILING DATE: 2005-07-01  
PRIOR APPLICATION NUMBER: US 60/288,564  
PRIOR FILING DATE: 2001-05-03  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 23  
LENGTH: 116  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: KS de-immunized VH3  
US-11-174-186-23

Query Match 100.0%; Score 59; DB 7; Length 116;  
Best Local Similarity 100.0%; Pred. No. 0.00088;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGTTVTVSS 11  
|||||  
Db 106 WGGTTVTVSS 116

RESULT 11  
US-11-174-186-24  
Sequence 24, Application US/11/174,186  
Publication No. US20050244418A1  
GENERAL INFORMATION:  
APPLICANT: Gillies, Stephen  
APPLICANT: Lo, Kin-Ming  
APPLICANT: Qian, Xingui  
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof  
FILE REFERENCE: LEX-019  
CURRENT APPLICATION NUMBER: US/11/174,186  
CURRENT FILING DATE: 2005-07-01

PRIOR APPLICATION NUMBER: US 60/288,564  
PRIOR FILING DATE: 2001-05-03  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 24  
LENGTH: 116  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: KS de-immunized VH4  
US-11-174-186-24

Query Match 100.0%; Score 59; DB 7; Length 116;  
Best Local Similarity 100.0%; Pred. No. 0.00088;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGTTVTVSS 11  
|||||  
Db 106 WGGTTVTVSS 116

RESULT 12  
US-11-174-186-25  
Sequence 25, Application US/11/174,186  
Publication No. US20050244418A1  
GENERAL INFORMATION:  
APPLICANT: Gillies, Stephen  
APPLICANT: Lo, Kin-Ming  
APPLICANT: Qian, Xingui  
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof  
FILE REFERENCE: LEX-019  
CURRENT APPLICATION NUMBER: US/11/174,186  
CURRENT FILING DATE: 2005-07-01  
PRIOR APPLICATION NUMBER: US 60/288,564  
PRIOR FILING DATE: 2001-05-03  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 25  
LENGTH: 116  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: KS de-immunized VH5  
US-11-174-186-25

Query Match 100.0%; Score 59; DB 7; Length 116;  
Best Local Similarity 100.0%; Pred. No. 0.00088;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGTTVTVSS 11  
|||||  
Db 106 WGGTTVTVSS 116

RESULT 13  
US-10-839-799-132  
Sequence 132, Application US/10839799  
Publication No. US20050249726A1  
GENERAL INFORMATION:  
APPLICANT: OKTOMO, Toshitoko  
SATO, Koh  
TSUCHIYA, Masayuki  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
MEDULLOBLASTOMA CELLS  
NUMBER OF SEQUENCES: 132  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/839,799  
FILING DATE: 06-May-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,265  
FILING DATE: 09-SEP-1996  
APPLICATION NUMBER: WO PCT/JP94/01763  
FILING DATE: 19-OCT-1994  
APPLICATION NUMBER: JP 5-291078  
FILING DATE: 19-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/184  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 132:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 117 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 132:  
US-10-839-799-132

Query Match 100.0%; Score 59; DB 6; Length 117;  
Best Local Similarity 100.0%; Pred. No. 0.00089;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WGGGTTTVSS 11  
|||  
Db 107 WGGGTTTVSS 117

RESULT 14  
US-11-054-669-120  
Sequence 120, Application US/11054669  
Publication No. US20050261480A1  
GENERAL INFORMATION:  
APPLICANT: Foote, Jefferson  
TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES  
FILE REFERENCE: 30219/US/3  
CURRENT APPLICATION NUMBER: US/11/054,669  
CURRENT FILING DATE: 2005-02-08  
PRIOR APPLICATION NUMBER: US 10/194,975  
PRIOR FILING DATE: 2002-07-12  
PRIOR APPLICATION NUMBER: US 60/305,111  
PRIOR FILING DATE: 2001-07-12  
NUMBER OF SEQ ID NOS: 124  
SOFTWARE: Patent version 3.3  
SEQ ID NO 120  
LENGTH: 117  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-054-669-120

Query Match 100.0%; Score 59; DB 7; Length 117;  
Best Local Similarity 100.0%; Pred. No. 0.00089;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WGGGTTTVSS 11  
|||  
Db 107 WGGGTTTVSS 117

RESULT 15

US-10-932-334-75  
Sequence 75, Application US/10932334  
Publication No. US20050249728A1  
GENERAL INFORMATION:  
APPLICANT: Immunogen, Inc.  
TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY  
FILE REFERENCE: A8689  
CURRENT APPLICATION NUMBER: US/10/932,334  
CURRENT FILING DATE: 2004-09-02  
PRIOR APPLICATION NUMBER: US/10/729,441  
PRIOR FILING DATE: 2003-12-08  
PRIOR APPLICATION NUMBER: 10/170,390  
PRIOR FILING DATE: 2002-06-14  
NUMBER OF SEQ ID NOS: 96  
SOFTWARE: Patent version 3.2  
SEQ ID NO 75  
LENGTH: 118  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic antibody structure  
US-10-932-334-75

Query Match 100.0%; Score 59; DB 6; Length 118;  
Best Local Similarity 100.0%; Pred. No. 0.0009;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WGGGTTTVSS 11  
|||  
Db 108 WGGGTTTVSS 118

Search completed: December 4, 2005, 04:37:50  
Job time : 3.20833 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:07:28 ; Search time 78.8333 Seconds  
(without alignments)  
58.302 Million cell updates/sec

Title: US-10-632-706-198  
Perfect score: 59  
Sequence: 1 WGQGTVTWSS 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA\_Main:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	100.0	11	3	US-09-253-794-40 Sequence 40, App1
2	59	100.0	11	3	US-09-828-708-78 Sequence 78, App1
3	59	100.0	11	3	US-09-749-873-114 Sequence 114, App1
4	59	100.0	11	3	US-09-748-873-129 Sequence 129, App1
5	59	100.0	11	3	US-09-268-921-137 Sequence 137, App1
6	59	100.0	11	3	US-09-563-222-157 Sequence 157, App1
7	59	100.0	11	3	US-09-563-222-165 Sequence 165, App1
8	59	100.0	11	3	US-09-563-222-181 Sequence 181, App1
9	59	100.0	11	3	US-09-563-222-197 Sequence 197, App1
10	59	100.0	11	3	US-09-508-098-179 Sequence 179, App1
11	59	100.0	11	4	US-10-218-253-137 Sequence 137, App1
12	59	100.0	11	4	US-10-169-351-4 Sequence 4, App11
13	59	100.0	11	4	US-10-160-506-40 Sequence 40, App11
14	59	100.0	11	4	US-10-310-113-26 Sequence 26, App1
15	59	100.0	11	4	US-10-310-113-147 Sequence 147, App1
16	59	100.0	11	4	US-10-310-113-148 Sequence 148, App1
17	59	100.0	11	4	US-10-310-113-149 Sequence 149, App1
18	59	100.0	11	4	US-10-310-113-150 Sequence 150, App1
19	59	100.0	11	4	US-10-310-113-151 Sequence 151, App1
20	59	100.0	11	4	US-10-310-113-152 Sequence 152, App1
21	59	100.0	11	4	US-10-310-113-153 Sequence 153, App1
22	59	100.0	11	4	US-10-310-113-154 Sequence 154, App1
23	59	100.0	11	4	US-10-310-113-155 Sequence 155, App1
24	59	100.0	11	4	US-10-310-113-156 Sequence 156, App1
25	59	100.0	11	4	US-10-310-113-157 Sequence 157, App1
26	59	100.0	11	4	US-10-310-113-158 Sequence 158, App1
27	59	100.0	11	4	US-10-310-113-159 Sequence 159, App1

28	59	100.0	11	4	US-10-412-703A-135 Sequence 135, App1
29	59	100.0	11	4	US-10-443-466A-69 Sequence 69, App1
30	59	100.0	11	4	US-10-443-466A-120 Sequence 120, App1
31	59	100.0	11	4	US-10-449-379-40 Sequence 40, App1
32	59	100.0	11	4	US-10-688-015-40 Sequence 40, App1
33	59	100.0	11	4	US-10-632-706-195 Sequence 195, App1
34	59	100.0	11	4	US-10-632-706-198 Sequence 198, App1
35	59	100.0	11	4	US-10-632-706-201 Sequence 201, App1
36	59	100.0	11	4	US-10-632-706-204 Sequence 204, App1
37	59	100.0	11	4	US-10-783-950-146 Sequence 146, App1
38	59	100.0	11	4	US-10-783-950-169 Sequence 169, App1
39	59	100.0	11	4	US-10-160-505-40 Sequence 40, App1
40	59	100.0	11	5	US-10-751-826-120 Sequence 120, App1
41	59	100.0	11	5	US-10-923-068-113 Sequence 113, App1
42	59	100.0	11	5	US-10-630-009-78 Sequence 78, App1
43	59	100.0	11	5	US-10-785-382-40 Sequence 40, App1
44	59	100.0	11	5	US-10-984-960A-9 Sequence 9, App11
45	59	100.0	11	5	US-10-984-960A-45 Sequence 45, App1

ALIGNMENTS

RESULT 1  
US-09-253-794-40  
Sequence 40, Application US/09253794  
Patent No. US20020018750A1  
GENERAL INFORMATION:  
APPLICANT: HANSEN, Hans J.  
ARMOUR, Kathryn L.  
TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED MOUSE MONOCLONAL ANTIBODIES  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
City: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/253,794  
FILING DATE: 22-Feb-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/318,157  
FILING DATE: 05-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: SAXE, Bernhard D.  
REGISTRATION NUMBER: 28,665  
REFERENCE/DOCKET NUMBER: 18733/464  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 40:  
US-09-253-794-40  
Query Match 100.0%; Score 59; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.01;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTVVSS 11  
|||  
Db 1 WGGGTTVVSS 11

RESULT 2  
US-09-828-708-78  
Sequence 78, Application US/09828708  
Patent No. US20020146753A1  
GENERAL INFORMATION:  
APPLICANT: Ditzel, H.  
APPLICANT: Burton, D.  
APPLICANT: Schaller, M.  
TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partic  
FILE REFERENCE: 1361.005US1  
CURRENT APPLICATION NUMBER: US/09/828,708  
CURRENT FILING DATE: 2001-09-24  
NUMBER OF SEQ ID NOS: 123  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 78  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-828-708-78

Query Match 100.0%; Score 59; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.01; Mismatches 0; Indels 0; Gaps 0;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTVVSS 11  
|||  
Db 1 WGGGTTVVSS 11

RESULT 3  
US-09-749-873-114  
Sequence 114, Application US/09749873  
Publication No. US20030023045A1  
GENERAL INFORMATION:  
APPLICANT: OHTOMO, Toshihiko  
SATO, Koh  
TSUCHIYA, Masayuki  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
MEDULLOBLASTOMA CELLS  
NUMBER OF SEQUENCES: 132  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/749,873  
FILING DATE: 29-Dec-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/646,265  
FILING DATE: 1996-09-09  
APPLICATION NUMBER: JP 5-291078  
FILING DATE: 19-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/184  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
INFORMATION FOR SEQ ID NO: 114:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 114:  
US-09-749-873-114

Qy 1 WGGGTTVVSS 11  
|||  
Db 1 WGGGTTVVSS 11

Query Match 100.0%; Score 59; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.01; Mismatches 0; Indels 0; Gaps 0;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4  
US-09-749-873-129  
Sequence 129, Application US/09749873  
Publication No. US20030023045A1  
GENERAL INFORMATION:  
APPLICANT: OHTOMO, Toshihiko  
SATO, Koh  
TSUCHIYA, Masayuki  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
MEDULLOBLASTOMA CELLS  
NUMBER OF SEQUENCES: 132  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/749,873  
FILING DATE: 29-Dec-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/646,265  
FILING DATE: 1996-09-09  
APPLICATION NUMBER: JP 5-291078  
FILING DATE: 19-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/184  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
INFORMATION FOR SEQ ID NO: 129:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 129:  
US-09-749-873-129

Query Match 100.0%; Score 59; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.01; Mismatches 0; Indels 0; Gaps 0;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTVTSS 11  
|||  
Db 1 WGGGTTVTSS 11

## RESULT 5

US-09-269-921-137  
; Sequence 137, Application US/09269921  
; Publication No. US20030045691A1  
; GENERAL INFORMATION:  
; APPLICANT: Ono, Koichiro  
; APPLICANT: Ohtomo, Toshiniko  
; APPLICANT: Tsuchiya, Masayuki  
; APPLICANT: Yoshimura, Yasushi  
; APPLICANT: Koshihara, Yasuo  
; TITLE OF INVENTION: RESHAPED HUMAN ANTI-IFN 1.24 ANTIBODY  
; FILE REFERENCE: 35029-20007.00  
; CURRENT FILING DATE: 1999-04-01  
; EARLIER APPLICATION NUMBER: PCT/JP97/03553  
; EARLIER FILING DATE: 1997-10-03  
; EARLIER APPLICATION NUMBER: JP 8-264756  
; EARLIER FILING DATE: 1996-10-04  
; NUMBER OF SEQ ID NOS: 137  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 137  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: JH6  
; PUBLICATION INFORMATION:  
; AUTHORS: Ravetch, J. et al.  
; JOURNAL: CELL  
; VOLUME: 27  
; PAGES: 583-591  
; DATE: 1981  
US-09-269-921-137

Query Match 100.0%; Score 59; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.01;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTVTSS 11  
|||  
Db 1 WGGGTTVTSS 11

## RESULT 6

US-09-563-222-157  
; Sequence 157, Application US/09563222  
; Publication No. US20030079253A1  
; GENERAL INFORMATION:  
; APPLICANT: Hiatt, Andrew  
; APPLICANT: Hein, Mich B.  
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN  
; FILE REFERENCE: 310098.406  
; CURRENT APPLICATION NUMBER: US/09/563,222  
; CURRENT FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 197  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 157  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-563-222-157

Query Match 100.0%; Score 59; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.01;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTVTSS 11  
|||  
Db 1 WGGGTTVTSS 11

## RESULT 7

US-09-563-222-165  
; Sequence 165, Application US/09563222  
; Publication No. US20030079253A1  
; GENERAL INFORMATION:  
; APPLICANT: Hiatt, Andrew  
; APPLICANT: Hein, Mich B.  
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN  
; FILE REFERENCE: 310098.406  
; CURRENT APPLICATION NUMBER: US/09/563,222  
; CURRENT FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 197  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 165  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-563-222-165

Query Match 100.0%; Score 59; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.01;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTVTSS 11  
|||  
Db 1 WGGGTTVTSS 11

## RESULT 8

US-09-563-222-181  
; Sequence 181, Application US/09563222  
; Publication No. US20030079253A1  
; GENERAL INFORMATION:  
; APPLICANT: Hiatt, Andrew  
; APPLICANT: Hein, Mich B.  
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN  
; FILE REFERENCE: 310098.406  
; CURRENT APPLICATION NUMBER: US/09/563,222  
; CURRENT FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 197  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 181  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-563-222-181

Query Match 100.0%; Score 59; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.01;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTVTSS 11  
|||  
Db 1 WGGGTTVTSS 11

## RESULT 9

US-09-563-222-197  
; Sequence 197, Application US/09563222  
; Publication No. US20030079253A1  
; GENERAL INFORMATION:  
; APPLICANT: Hiatt, Andrew  
; APPLICANT: Hein, Mich B.  
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN  
; FILE REFERENCE: 310098.406

;; CURRENT APPLICATION NUMBER: US/09/563,222  
;; CURRENT FILING DATE: 2000-05-02  
;; NUMBER OF SEQ ID NOS: 197  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 197  
;; LENGTH: 11  
;; TYPE: PRT  
;; ORGANISM: Mus musculus  
US-09-563-222-197

Query Match 100.0%; Score 59; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.01;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVSS 11  
|||  
Db 1 WGGGTTTVSS 11

RESULT 10  
US-09-509-098-179  
;; Sequence 179, Application US/09509098  
;; Publication No. US20030103970A1  
;; GENERAL INFORMATION:  
;; APPLICANT: TSUCHIYA, MASAYUKI  
;; TITLE OF INVENTION: NATURAL HUMANIZED ANTIBODY  
;; FILE REFERENCE: 053466/0274  
;; CURRENT APPLICATION NUMBER: US/09/509,098  
;; PRIOR FILING DATE: 2000-03-22  
;; PRIOR APPLICATION NUMBER: PCT/JP98/04469  
;; PRIOR FILING DATE: 1998-10-02  
;; PRIOR APPLICATION NUMBER: JP 9-271726  
;; PRIOR FILING DATE: 1997-10-03  
;; NUMBER OF SEQ ID NOS: 203  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 179  
;; LENGTH: 11  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Amino acid  
US-09-509-098-179

Query Match 100.0%; Score 59; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.01;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVSS 11  
|||  
Db 1 WGGGTTTVSS 11

RESULT 11  
US-10-218-253-137  
;; Sequence 137, Application US/10218253  
;; Publication No. US20030129185A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Ono, Koichiro  
;; APPLICANT: Ohtomo, Toshiniko  
;; APPLICANT: Tsuchiya, Masayuki  
;; APPLICANT: Yoshimura, Yasushi  
;; APPLICANT: Koshihara, Yasuo  
;; TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY  
;; FILE REFERENCE: 35029-20007.00  
;; CURRENT APPLICATION NUMBER: US/10/218,253  
;; CURRENT FILING DATE: 2002-11-21  
;; PRIOR APPLICATION NUMBER: US/09/269,921  
;; PRIOR FILING DATE: 1999-04-01  
;; PRIOR APPLICATION NUMBER: PCT/JP97/03553  
;; PRIOR FILING DATE: 1997-10-03  
;; PRIOR APPLICATION NUMBER: JP 8-264756  
;; PRIOR FILING DATE: 1996-10-04

;; NUMBER OF SEQ ID NOS: 137  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 137  
;; LENGTH: 11  
;; TYPE: PRT  
;; ORGANISM: Unknown  
;; FEATURE:  
;; OTHER INFORMATION: Description of Unknown Organism: H6  
;; PUBLICATION INFORMATION:  
;; AUTHORS: Ravetch, J. et al.  
;; JOURNAL: CELL  
;; VOLUME: 27  
;; PAGES: 583-591  
;; DATE: 1981  
US-10-218-253-137

Query Match 100.0%; Score 59; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.01;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVSS 11  
|||  
Db 1 WGGGTTTVSS 11

RESULT 12  
US-10-169-351-4  
;; Sequence 4, Application US/10169351  
;; Publication No. US20030157090A1  
;; GENERAL INFORMATION:  
;; APPLICANT: BENVENTO, EUGENIO  
;; APPLICANT: FRANCONI, ROSELLA  
;; APPLICANT: DESIDERIO, ANGIOLA  
;; APPLICANT: TAVLADORAKI, PARASKEVI  
;; TITLE OF INVENTION: STABILIZING PEPTIDES, POLYPEPTIDES AND ANTIBODIES  
;; TITLE OF INVENTION: WHICH INCLUDE THEM  
;; FILE REFERENCE: 4161-4  
;; CURRENT APPLICATION NUMBER: US/10/169,351  
;; CURRENT FILING DATE: 2002-10-29  
;; PRIOR APPLICATION NUMBER: PCT/IT00/00554  
;; PRIOR FILING DATE: 2000-12-29  
;; PRIOR APPLICATION NUMBER: IT RM99A000803  
;; PRIOR FILING DATE: 1999-12-30  
;; NUMBER OF SEQ ID NOS: 118  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 4  
;; LENGTH: 11  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-169-351-4

Query Match 100.0%; Score 59; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.01;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVSS 11  
|||  
Db 1 WGGGTTTVSS 11

RESULT 13  
US-10-160-506-40  
;; Sequence 40, Application US/10160506  
;; Publication No. US20030161832A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Bander, Neil H.  
;; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING  
;; TITLE OF INVENTION: SKIN DISORDERS USING BINDING AGENTS SPECIFIC FOR  
;; TITLE OF INVENTION: PROSTATE SPECIFIC MEMBRANE ANTIGEN  
;; FILE REFERENCE: 10448-162001



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; CURRENT APPLICATION NUMBER: US/10/160,506
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/324,100
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/362,612
; PRIOR FILING DATE: 2002-03-08
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: deimmunized heavy chain J415-4
US-10-160-506-40

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Query Match      100.0%; Score 59; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 WGGGTTTVSS 11
        |||||
Db      1 WGGGTTTVSS 11

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RESULT 14
US-10-310-113-26
; Sequence 26, Application US/10310113
; Publication No. US2003017664A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: WONG, HING C.
; APPLICANT: NIEVES, ESPERANZA LILIANA
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING
; FILE REFERENCE: 58122(71758)
; CURRENT APPLICATION NUMBER: US/10/310,113
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 08/814,806
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-310-113-26

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Query Match      100.0%; Score 59; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 WGGGTTTVSS 11
        |||||
Db      1 WGGGTTTVSS 11

```

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RESULT 15
US-10-310-113-147
; Sequence 147, Application US/10310113
; Publication No. US2003017664A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: WONG, HING C.
; APPLICANT: NIEVES, ESPERANZA LILIANA
; APPLICANT: MOSQUERA, LUIS A.

```

```

; TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING
; FILE REFERENCE: 58122(71758)
; CURRENT APPLICATION NUMBER: US/10/310,113
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 08/814,806
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 147
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: humanized HC-01 FR4 amino acid sequence
US-10-310-113-147

```

```

Query Match      100.0%; Score 59; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 WGGGTTTVSS 11
        |||||
Db      1 WGGGTTTVSS 11

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Job time : 79.8333 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OW protein - protein search, using sw model

Run on: December 4, 2005, 03:59:51 ; Search time 23.6042 Seconds  
(without alignments)  
38.528 Million cell updates/sec

Title: US-10-632-706-198  
Perfect score: 59  
Sequence: 1 WGQGTWTVSS 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/1aa/5 COMB.pep:\*
- 2: /cgn2\_6/ptodata/1/1aa/6 COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/1aa/H\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/1aa/PTTUS\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/1aa/RE\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	100.0	11	1	US-08-471-780C-120 Sequence 120, App
2	59	100.0	11	1	US-08-467-282B-120 Sequence 120, App
3	59	100.0	11	1	US-08-471-282A-120 Sequence 120, App
4	59	100.0	11	1	US-08-318-157B-40 Sequence 40, Appl
5	59	100.0	11	1	US-08-466-710C-120 Sequence 120, App
6	59	100.0	11	2	US-08-468-739C-120 Sequence 120, App
7	59	100.0	11	2	US-08-646-265A-114 Sequence 114, App
8	59	100.0	11	2	US-08-646-265A-129 Sequence 129, App
9	59	100.0	11	2	US-09-253-794-40 Sequence 40, App
10	59	100.0	11	2	US-09-563-222C-146 Sequence 146, App
11	59	100.0	11	2	US-09-563-222C-169 Sequence 169, App
12	59	100.0	11	2	US-09-263-921-137 Sequence 137, App
13	59	100.0	11	2	US-09-293-769A-120 Sequence 120, App
14	59	100.0	13	6	5189147-14 Patent No. 5189147
15	59	100.0	15	6	5189147-179B-8 Patent No. 5189147
16	59	100.0	15	6	5189147-30 Patent No. 5189147
17	59	100.0	16	4	PCT-US91-02942-91 Sequence 91, Appl
18	59	100.0	20	2	US-10-194-975-107 Sequence 107, App
19	59	100.0	22	4	PCT-US91-02942-100 Sequence 100, App
20	59	100.0	29	1	US-08-053-131-73 Sequence 73, Appl
21	59	100.0	29	1	US-08-645-641-73 Sequence 73, Appl
22	59	100.0	29	1	US-07-853-408B-73 Sequence 73, Appl
23	59	100.0	29	1	US-08-096-762-73 Sequence 73, Appl
24	59	100.0	29	1	US-08-308-865-73 Sequence 73, Appl
25	59	100.0	29	2	US-09-042-353-270 Sequence 270, App
26	59	100.0	29	2	US-08-758-417A-118 Sequence 118, App
27	59	100.0	29	4	PCT-US92-10983-73 Sequence 73, Appl

28	59	100.0	31	1	US-08-053-131-83 Sequence 83, Appl
29	59	100.0	31	1	US-08-645-641-83 Sequence 83, Appl
30	59	100.0	31	1	US-07-853-408B-83 Sequence 83, Appl
31	59	100.0	31	1	US-08-096-762-83 Sequence 83, Appl
32	59	100.0	31	1	US-08-308-865-83 Sequence 83, Appl
33	59	100.0	31	2	US-09-042-353-280 Sequence 280, App
34	59	100.0	31	2	US-08-758-417A-128 Sequence 128, App
35	59	100.0	31	4	PCT-US92-10983-83 Sequence 83, Appl
36	59	100.0	32	1	US-08-053-131-92 Sequence 92, Appl
37	59	100.0	32	1	US-08-645-641-92 Sequence 92, Appl
38	59	100.0	32	1	US-07-853-408B-92 Sequence 92, Appl
39	59	100.0	32	1	US-08-096-762-92 Sequence 92, Appl
40	59	100.0	32	1	US-08-308-865-92 Sequence 92, Appl
41	59	100.0	32	2	US-09-042-353-289 Sequence 289, App
42	59	100.0	32	2	US-08-758-417A-137 Sequence 137, App
43	59	100.0	32	4	PCT-US92-10983-92 Sequence 92, Appl
44	59	100.0	33	1	US-08-053-131-89 Sequence 89, Appl
45	59	100.0	33	1	US-08-645-641-89 Sequence 89, Appl

## ALIGNMENTS

RESULT 1  
US-08-471-780C-120  
; Sequence 120, Application US/08471780C  
; Patent No. 5759808  
; GENERAL INFORMATION:  
; APPLICANT: Casterman, Cecile  
; APPLICANT: Hamers, Raymond  
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains  
; NUMBER OF SEQUENCES: 130  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner  
; STREET: 1300 I Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/471,780C  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/106,944  
; FILING DATE: 17-AUG-1993  
; APPLICATION NUMBER: FR 92402326.0  
; FILING DATE: 21-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 93401310.3  
; FILING DATE: 21-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Potter, Jane B.R.  
; REGISTRATION NUMBER: 33,332  
; REFERENCE/DOCKET NUMBER: 04958.0008-00000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 120:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-471-780C-120  
; Query Match 100.0%; Score 59; DB 1; Length 11;  
; Best Local Similarity 100.0%; Pred. No. 0.0017;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVSS 11  
| | | | | | | | | |  
Db 1 WGGGTTTVSS 11

RESULT 2  
US-08-467-282B-120  
; Sequence 120, Application US/08467282B  
; Patent No. 5800988  
; GENERAL INFORMATION:  
; APPLICANT: Caserman, Cecile  
; APPLICANT: Hamers, Raymond  
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains  
; NUMBER OF SEQUENCES: 130  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner  
; STREET: 1300 I Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/467,282B  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/106,944  
; FILING DATE: 17-AUG-1993  
; APPLICATION NUMBER: FR 92402326.0  
; FILING DATE: 21-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 93401310.3  
; FILING DATE: 21-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Potter, Jane E.R.  
; REGISTRATION NUMBER: 33,332  
; REFERENCE/DOCKET NUMBER: 04958-0008-00000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 120:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-467-282B-120

Query Match 100.0%; Score 59; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0017;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVSS 11  
| | | | | | | | | |  
Db 1 WGGGTTTVSS 11

RESULT 3  
US-08-471-282A-120  
; Sequence 120, Application US/08471282A  
; Patent No. 5840853  
; GENERAL INFORMATION:  
; APPLICANT: Caserman, Cecile  
; APPLICANT: Hamers, Raymond  
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains  
; NUMBER OF SEQUENCES: 130

; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner  
; STREET: 1300 I Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/471,282A  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/106,944  
; FILING DATE: 17-AUG-1993  
; APPLICATION NUMBER: FR 92402326.0  
; FILING DATE: 21-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 93401310.3  
; FILING DATE: 21-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Potter, Jane E.R.  
; REGISTRATION NUMBER: 33,332  
; REFERENCE/DOCKET NUMBER: 04958-0008-00000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 120:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-471-282A-120

Query Match 100.0%; Score 59; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0017;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVSS 11  
| | | | | | | | | |  
Db 1 WGGGTTTVSS 11

RESULT 4  
US-08-318-157B-40  
; Sequence 40, Application US/08318157B  
; Patent No. 5874540  
; GENERAL INFORMATION:  
; APPLICANT: HANSEN, Hans J.  
; APPLICANT: ARMOIR, Kathryn L.  
; TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/318,157B  
; FILING DATE: 05-OCT-1994

CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: SAXE, Bernhard D.  
REGISTRATION NUMBER: 28,665  
REFERENCE/DOCKET NUMBER: 18733/464  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-318-157B-40

Query Match 100.0%; Score 59; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0017;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVSS 11  
Db 1 WGGGTTTVSS 11

RESULT 5  
US-08-466-710C-120  
Sequence 120, Application US/08466710C  
Patent No. 5874541  
GENERAL INFORMATION:  
APPLICANT: Casterman, Cecile  
APPLICANT: Hamers, Raymond  
TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains  
NUMBER OF SEQUENCES: 130  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,710C  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/106,944  
FILING DATE: 17-AUG-1993  
APPLICATION NUMBER: FR 92402326.0  
FILING DATE: 21-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 93401310.3  
FILING DATE: 21-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Potter, Jane E.R.  
REGISTRATION NUMBER: 33,332  
REFERENCE/DOCKET NUMBER: 04958-0008-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 120:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

US-08-466-710C-120

Query Match 100.0%; Score 59; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0017;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVSS 11  
Db 1 WGGGTTTVSS 11

RESULT 6  
US-08-468-739C-120  
Sequence 120, Application US/08468739C  
Patent No. 6015695  
GENERAL INFORMATION:  
APPLICANT: Casterman, Cecile  
APPLICANT: Hamers, Raymond  
TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains  
NUMBER OF SEQUENCES: 130  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,739C  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/106,944  
FILING DATE: 17-AUG-1993  
APPLICATION NUMBER: FR 92402326.0  
FILING DATE: 21-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 93401310.3  
FILING DATE: 21-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Potter, Jane E.R.  
REGISTRATION NUMBER: 33,332  
REFERENCE/DOCKET NUMBER: 04958-0008-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 120:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-468-739C-120

Query Match 100.0%; Score 59; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0017;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVSS 11  
Db 1 WGGGTTTVSS 11

RESULT 7  
US-08-646-265A-114  
Sequence 114, Application US/08646265A  
Patent No. 6214973  
GENERAL INFORMATION:

APPLICANT: OHTOMO, Toshiniko  
APPLICANT: SATO, Koh  
APPLICANT: TSUCHIYA, Masayuki  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
TITLE OF INVENTION: MEDULLOBLASTOMA CELLS  
NUMBER OF SEQUENCES: 132  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,265A  
FILING DATE: 09-SEP-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/JP94/01763  
FILING DATE: 19-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-291078  
FILING DATE: 19-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/184  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 114:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-646-265A-114

Query Match 100.0%; Score 59; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0017;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11  
|||  
Db 1 WGGGTTTVSS 11

RESULT 8  
US-08-646-265A-129  
Sequence 129, Application US/08646265A  
Patent No. 6214973  
GENERAL INFORMATION:  
APPLICANT: OHTOMO, Toshiniko  
APPLICANT: SATO, Koh  
APPLICANT: TSUCHIYA, Masayuki  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
TITLE OF INVENTION: MEDULLOBLASTOMA CELLS  
NUMBER OF SEQUENCES: 132  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,265A  
FILING DATE: 09-SEP-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/JP94/01763  
FILING DATE: 19-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-291078  
FILING DATE: 19-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/184  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 129:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-646-265A-129

Query Match 100.0%; Score 59; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0017;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11  
|||  
Db 1 WGGGTTTVSS 11

RESULT 9  
US-09-253-794-40  
Sequence 40, Application US/09253794  
Patent No. 6676324  
GENERAL INFORMATION:  
APPLICANT: HANSEN, Hans J.  
ARMOUR, Kathryn L.  
TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED  
MOUSE MONOCLONAL ANTIBODIES  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/253,794  
FILING DATE: 22-Feb-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/318,157  
FILING DATE: 05-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Saxe, Bernhard D.  
REGISTRATION NUMBER: 28,665  
REFERENCE/DOCKET NUMBER: 18733/464  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: 1linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 40:  
US-09-253-794-40

Query Match 100.0%; Score 59; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0017;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11  
|||  
Db 1 WGGGTTTVSS 11

RESULT 10  
US-09-563-222C-146  
Sequence 146, Application US/09563222C  
Patent No. 6696620  
GENERAL INFORMATION:  
APPLICANT: EPICYTE PHARMACEUTICALS, INC.  
APPLICANT: HIATT, ANDREW C.  
TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS  
FILE REFERENCE: 068904-0501  
CURRENT APPLICATION NUMBER: US/09/563,222C  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: PCT/US01/14349  
PRIOR FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 09/563,222  
NUMBER OF SEQ ID NOS: 182  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 146  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-563-222C-146

Query Match 100.0%; Score 59; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0017;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11  
|||  
Db 1 WGGGTTTVSS 11

RESULT 11  
US-09-563-222C-169  
Sequence 169, Application US/09563222C  
Patent No. 6696620  
GENERAL INFORMATION:  
APPLICANT: EPICYTE PHARMACEUTICALS, INC.  
APPLICANT: HIATT, ANDREW C.  
TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS  
FILE REFERENCE: 068904-0501  
CURRENT APPLICATION NUMBER: US/09/563,222C  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: PCT/US01/14349  
PRIOR FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 09/563,222  
NUMBER OF SEQ ID NOS: 182  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 169

LENGTH: 11  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-563-222C-169

Query Match 100.0%; Score 59; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0017;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11  
|||  
Db 1 WGGGTTTVSS 11

RESULT 12  
US-09-269-921-137  
Sequence 137, Application US/09269921  
Patent No. 6699974  
GENERAL INFORMATION:  
APPLICANT: Ono, Koichiro  
APPLICANT: Ohtomo, Toshiko  
APPLICANT: Tsuchiya, Masayuki  
APPLICANT: Yoshimura, Yasuo  
TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY  
FILE REFERENCE: 35029-20007.00  
CURRENT APPLICATION NUMBER: US/09/269,921  
CURRENT FILING DATE: 1999-04-01  
EARLIER APPLICATION NUMBER: PCT/JP97/03553  
EARLIER FILING DATE: 1997-10-03  
EARLIER APPLICATION NUMBER: JP 8-264756  
NUMBER OF SEQ ID NOS: 137  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 137  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Description of Unknown Organism: JH6  
PUBLICATION INFORMATION:  
AUTHORS: Ravetch, J. et al.  
JOURNAL: CELL  
VOLUME: 27  
PAGES: 583-591  
DATE: 1981  
US-09-269-921-137

Query Match 100.0%; Score 59; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0017;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11  
|||  
Db 1 WGGGTTTVSS 11

RESULT 13  
US-09-293-769A-120  
Sequence 120, Application US/09293769A  
Patent No. 6765087  
GENERAL INFORMATION:  
APPLICANT: CASTERMAN, CECILE  
APPLICANT: HAMERS, RAYMOND  
TITLE OF INVENTION: IMMUNOGLOBULINS DEVOID OF LIGHT CHAINS  
FILE REFERENCE: 04958.0008-07000  
CURRENT APPLICATION NUMBER: US/09/293,769A  
CURRENT FILING DATE: 1999-04-19  
PRIOR APPLICATION NUMBER: 08/471,284  
PRIOR FILING DATE: 1995-06-06  
PRIOR APPLICATION NUMBER: 07/106,944  
PRIOR FILING DATE: 1987-10-15  
PRIOR APPLICATION NUMBER: EPO 92402326.0

;; PRIOR FILING DATE: 1992-08-21  
;; PRIOR APPLICATION NUMBER: EPO 93401310.3  
;; PRIOR FILING DATE: 1993-05-21  
;; NUMBER OF SEQ ID NOS: 130  
;; SOFTWARE: Patentn Ver. 2.1  
;; SEQ ID NO: 120  
;; LENGTH: 11  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-293-769A-120

Query Match 100.0%; Score 59; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0017;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WGGGTTTVSS 11  
Db 1 WGGGTTTVSS 11

RESULT 14  
5189147-14  
; Patent No. 5189147  
; APPLICANT: SAITO, HARUO; KRANZ, DAVID M.; EISEN, HERMAN N.;  
; TONEGAWA, SUSUMU  
; TITLE OF INVENTION: METERODIMERIC T LYMPHOCYTE RECEPTOR  
; ANTI BODY  
; NUMBER OF SEQUENCES: 21  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/271,216  
; FILING DATE: 14-NOV-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 666,988  
; FILING DATE: 31-OCT-1984  
; APPLICATION NUMBER: 620,122  
; FILING DATE: 13-JUN-1984  
; SEQ ID NO: 14  
; LENGTH: 13  
5189147-14

Query Match 100.0%; Score 59; DB 6; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.002;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WGGGTTTVSS 11  
Db 3 WGGGTTTVSS 13

RESULT 15  
US-08-765-179B-8  
; Sequence 8, Application US/08765179B  
; Patent No. 5854027  
; GENERAL INFORMATION:  
; APPLICANT: STEINBE, Boris  
; APPLICANT: STEINBACHER, Stefan  
; TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY  
; TITLE OF INVENTION: OF ANTIBODIES  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP  
; STREET: 655 Fifteenth Street N.W. Suite 330  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005-5701  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/765,179B

;; FILING DATE: 14-JAN-1997  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/EP95/02626  
;; FILING DATE: 06-JUL-1995  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: DE P 44 25 115.7  
;; FILING DATE: 15-JUL-1994  
;; INFORMATION FOR SEQ ID NO: 8:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 15 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-765-179B-8

Query Match 100.0%; Score 59; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.0023;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WGGGTTTVSS 11  
Db 5 WGGGTTTVSS 15

Search completed: December 4, 2005, 04:09:45  
Job time : 24.6042 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:09:54 ; Search time 95.5625 Seconds  
(without alignments)  
50.576 Million cell updates/sec

Title: US-10-632-706-127  
Perfect score: 60  
Sequence: 1 LATYYFGLDV 11

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues  
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_21:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*  
9: Geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	100.0	11	8	ADR38724 Mouse hea
2	60	100.0	11	8	ADR38725 Mouse hea
3	48	80.0	122	9	AEBA5960 Human mon
4	47	78.3	114	7	ADD28082 Lymphoma
5	47	78.3	129	7	ADD28323 Human het
6	47	78.3	134	7	ADD28237 Human het
7	47	78.3	134	9	ADV86824 Bacillus
8	47	78.3	244	8	ADR28082 NPB polyp
9	47	78.3	468	9	AEBA5891 Human mon
10	47	78.3	469	9	AEBA5853 Human mon
11	46	76.7	11	8	ADR38712 Mouse hea
12	46	76.7	21	9	ADM04816 PAP-A im
13	46	76.7	126	9	AD241994 Ig H chai
14	46	76.7	140	9	ADM04810 PAP-A im
15	45	75.0	16	9	ADM04952 PAP-A im
16	45	75.0	21	5	ABP47057 Human Bly
17	45	75.0	21	7	ADG97884 scfV VHCD
18	45	75.0	117	9	ADG97826 Human pla
19	45	75.0	117	9	AEBO1019 Human hea
20	45	75.0	135	9	ADM04846 PAP-A im
21	45	75.0	256	7	ADP45589 Human Bly
22	45	75.0	256	7	ADG96416 Single ch
23	44	73.3	13	4	AAU02710 CDR regio
24	44	73.3	14	9	ADY70216 Human Mab

25	44	73.3	16	5	ABP46118 Human Bly
26	44	73.3	16	7	ADG96945 scfV VHCD
27	44	73.3	17	5	ABP46865 Human Bly
28	44	73.3	17	7	ADG97692 scfV VHCD
29	44	73.3	18	9	AEBA21444 Human ant
30	44	73.3	109	8	AD105782 Human mon
31	44	73.3	117	7	ADK18782 Anti-huma
32	44	73.3	122	4	AAU02589 Anti-adip
33	44	73.3	123	7	ADP03879 Murine-ex
34	44	73.3	123	7	ADP03878 Murine-ex
35	44	73.3	123	9	ADY70198 Human mon
36	44	73.3	127	5	ADG76565 HCV E1 an
37	44	73.3	127	7	ADK18819 Anti-huma
38	44	73.3	127	7	ADK18901 Anti-huma
39	44	73.3	127	7	ADK18607 Anti-huma
40	44	73.3	127	8	ADL25432 Human mAb
41	44	73.3	127	9	AEBA21438 Human ant
42	44	73.3	129	7	ADDE28407 Human ant
43	44	73.3	134	7	ADD28238 Human het
44	44	73.3	134	7	ADD28332 Human het
45	44	73.3	134	7	ADD28331 Human het

## ALIGNMENTS

RESULT 1	ADR38724	standard; peptide; 11 AA.
ID	ADR38724	
AC	ADR38724;	
XX		
DT	02-DEC-2004	(first entry)
XX		
DE	Mouse heavy chain variable region CDR3 seqid 126.	
XX		
KW	antibacterial; antibody; botulinum neurotoxin type A; BONT/A;	
KW	BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;	
KW	toxin neutralisation; botulinum neurotoxin poisoning; mouse;	
KW	heavy chain variable region; complementarily determining region; CDR3.	
XX		
OS	Mus sp.	
XX		
PN	US2004175385-A1.	
XX		
PD	09-SEP-2004.	
XX		
PF	01-AUG-2003; 2003US-00632706.	
XX		
PR	31-AUG-1998; 98US-00144886.	
PR	01-AUG-2002; 2002US-0400721P.	
XX		
PA	(REGC ) UNIV CALIFORNIA.	
XX		
PI	Marks JD, Amersdorfer P;	
XX		
DR	WPI: 2004-652009/63.	
XX		
PT	New isolated antibody that neutralizes botulinum neurotoxin type A,	
PT	useful for diagnosing botulism or for treating pathologies associated	
XX	with botulinum neurotoxin poisoning.	
XX		
PS	Example 3; SEQ ID NO 126; 110pp; English.	
XX		
CC	The invention describes an isolated antibody (I) that specifically binds	
CC	to an epitope specifically bound by an antibody expressed by a specific	
CC	clone where (I) binds to and neutralises botulinum neurotoxin type A	
CC	(BONT/A). An isolated antibody (I) that specifically binds to an epitope	
CC	specifically bound by an antibody expressed by a clone chosen from clone	
CC	S25, C25, C35, 1C6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1,	
CC	3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum	
CC	neurotoxin type A (BONT/A). Also described are: a polypeptide (II)	
CC	comprising BONT/A neutralising epitope having an epitope that is	

CC specifically bound by an antibody expressed by clones as mentioned in (1)  
 CC ; producing (1) ; and a composition (iii) comprising several anti-  
 CC botulinum neurotoxin antibodies, where each antibody is specific for a  
 CC different epitope of a botulinum neurotoxin and the combination of  
 CC antibodies shows greater toxin neutralisation than the single antibodies  
 CC in surplus. The following are disclosed: a pharmaceutical composition  
 CC comprising (i) ; and a kit comprising (i) . (i) is useful for neutralising  
 CC BONT/A antibody and for neutralising a botulinum neurotoxin which  
 CC involves contacting neurotoxin with (1) in surplus, where each of (1) is  
 CC specific for a different epitope of the botulinum neurotoxin and the  
 CC combination of antibodies shows greater toxin neutralisation than the  
 CC single antibodies in surplus. (1) is useful for diagnosing the botulism  
 CC or for treating pathologies associated with botulinum neurotoxin  
 CC poisoning. (1) exhibits specificity and affinity towards BONT/A. (1)  
 CC enables rapid detection or diagnosis of botulism. This is the amino acid  
 CC sequence of mouse heavy chain variable region complementarily determining  
 CC region 3 (CDR3) from anti-botulinum neurotoxin antibodies.

XX  
 SQ Sequence 11 AA;

Query Match 100.0%; Score 60; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.0017;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LATYYFGLDV 11  
 |||||  
 Db 1 LATYYFGLDV 11

RESULT 2  
 ADR38725

ID ADR38725 standard; peptide; 11 AA.

AC ADR38725;

DT 02-DEC-2004 (first entry)

XX Mouse heavy chain variable region CDR3 seqid 127.

DS antibacterial; antibody; botulinum neurotoxin type A; BONT/A;

KM BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;

KM toxin neutralisation; botulinum neurotoxin poisoning; mouse;

XX heavy chain variable region; complementarity determining region; CDR3.

OS Mus sp.

XX US2004175385-A1.

XX 09-SEP-2004.

PF 01-AUG-2003; 2003US-00632706.

XX 31-AUG-1998; 98US-00144886.

PR 01-AUG-2002; 2002US-0400721P.

XX (REGC ) UNIV CALIFORNIA.

PA Marks JD, Amersdorfer P;

XX WPI; 2004-652009/63.

DR WPI; 2004-652009/63.

XX New isolated antibody that neutralizes botulinum neurotoxin type A,

PT useful for diagnosing botulism or for treating pathologies associated

PT with botulinum neurotoxin poisoning.

XX Example 3, SEQ ID NO 127; 110pp; English.

XX The invention describes an isolated antibody (1) that specifically binds

CC to an epitope specifically bound by an antibody expressed by a specific

CC clone where (1) binds to and neutralises botulinum neurotoxin type A

CC (BONT/A). An isolated antibody (1) that specifically binds to an epitope

CC specifically bound by an antibody expressed by a clone chosen from clone

CC S25, C35, C39, 1C6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WRI(V), WRI(T), 3-1,

CC 3-8, 3-10 and INGI, where (1) binds to and neutralizes botulinum  
 CC neurotoxin type A (BONT/A). Also described are: a polypeptide (ii)  
 CC comprising BONT/A neutralising epitope having an epitope that is  
 CC specifically bound by an antibody expressed by clones as mentioned in (1)  
 CC ; producing (1) ; and a composition (iii) comprising several anti-  
 CC botulinum neurotoxin antibodies, where each antibody is specific for a  
 CC different epitope of a botulinum neurotoxin and the combination of  
 CC antibodies shows greater toxin neutralisation than the single antibodies  
 CC in surplus. The following are disclosed: a pharmaceutical composition  
 CC comprising (i) ; and a kit comprising (i) . (i) is useful for neutralising  
 CC BONT/A antibody and for neutralising a botulinum neurotoxin which  
 CC involves contacting neurotoxin with (1) in surplus, where each of (1) is  
 CC specific for a different epitope of the botulinum neurotoxin and the  
 CC combination of antibodies shows greater toxin neutralisation than the  
 CC single antibodies in surplus. (1) is useful for diagnosing the botulism  
 CC or for treating pathologies associated with botulinum neurotoxin  
 CC poisoning. (1) exhibits specificity and affinity towards BONT/A. (1)  
 CC enables rapid detection or diagnosis of botulism. This is the amino acid  
 CC sequence of mouse heavy chain variable region complementarily determining  
 CC region 3 (CDR3) from anti-botulinum neurotoxin antibodies.

XX  
 SQ Sequence 11 AA;

Query Match 100.0%; Score 60; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.0017;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LATYYFGLDV 11  
 |||||  
 Db 1 LATYYFGLDV 11

RESULT 3  
 ABB45960

ID ABB45960 standard; protein; 122 AA.

AC ABB45960;

DT 06-OCT-2005 (first entry)

XX Human monoclonal anti-MADCAM antibody related protein #4.

XX Monoclonal antibody; mucosal addressin cell adhesion molecule; MADCAM;

KM inflammation; inflammatory bowel disease; Crohn's disease;

KM ulcerative colitis; diverticular disease; gastritis; liver disease;

KM primary biliary cirrhosis; primary sclerosing cholangitis;

KM insulin dependent diabetes; graft versus host disease; antiinflammatory;

KM gastrointestinal-gen.; antidiabetic;

XX immunosuppressive; antibody.

XX Homo sapiens.

XX WO2005067620-A2.

XX 28-JUL-2005.

PF 07-JAN-2005; 2005WO-US000370.

XX 09-JAN-2004; 2004US-0535490P.

XX (PRIZ ) PRIZER INC.

PA (ABGE-) ABGENIX INC.

XX (PRIZ ) PRIZER LTD.

PI Pullen N, Molloy E, Kellermann S, Green LL, Haak-Frendscho M;

XX WPI; 2005-554958/56.

DR New antibody to Mucosal Addressin Cell Adhesion Molecule, useful for

PT diagnosing and treating an inflammatory disease, e.g. inflammatory bowel

PT disease, ulcerative colitis, gastritis, insulin-dependent diabetes or

PT graft versus host disease.

XX

PS Example 5; Fig 1; 167pp; English.

CC The invention relates to a human monoclonal antibody or its antigen-  
CC binding portion that specifically binds to mucosa addressin cell  
CC adhesion molecule (MAdCAM). The invention also relates to a hybridoma  
CC cell line that produces the human monoclonal antibody, a pharmaceutical  
CC composition comprising an amount of the monoclonal antibody or its  
CC antigen-binding portion and a pharmaceutical carrier, a method of  
CC treating inflammatory disease in a subject, an isolated cell line that  
CC produces the monoclonal antibody or its antigen-binding portion or the  
CC heavy chain or light chain of the antibody or of its portion, an isolated  
CC nucleic acid molecule comprising a nucleotide sequence encoding the heavy  
CC chain or its antigen-binding portion or the light chain or its antigen-  
CC binding portion of an antibody described above, a vector comprising the  
CC nucleic acid molecule, where the vector optionally comprises an  
CC expression control sequence operably linked to the nucleic acid molecule,  
CC a host cell comprising the vector or the nucleic acid molecule above, a  
CC method of producing a human monoclonal antibody or its antigen-binding  
CC portion that specifically binds MAdCAM, a method of isolating an antibody  
CC or its antigen-binding portion that specifically binds to MAdCAM, a  
CC method of treating a subject in need of a human antibody or its antigen-  
CC binding portion that specifically binds to MAdCAM and inhibits binding to  
CC alpha4beta7, a method of inhibiting alpha4beta7 binding to cells  
CC expressing human MAdCAM, a method of inhibiting MAdCAM-mediated leukocyte  
CC -endothelial cell adhesion, migration and infiltration into tissues, a  
CC method of inhibiting alpha4beta7/MAdCAM-dependent cellular adhesion,  
CC inhibiting the MAdCAM-mediated recruitment of lymphocytes to  
CC gastrointestinal lymphoid tissue, a method of diagnosing a disorder  
CC characterized by circulating soluble human MAdCAM and detecting  
CC inflammation in a subject. The antibody, composition and methods are  
CC useful for diagnosing and treating inflammatory disease, e.g.  
CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,  
CC diverticular disease, gastritis, liver disease, primary biliary  
CC cirrhosis, primary sclerosing cholangitis, insulin dependent diabetes and  
CC graft versus host disease. This sequence represents a human monoclonal  
CC anti-MAdCAM antibody related protein of the invention.

SO Sequence 122 AA;

Query Match 80.0%; Score 48; DB 9; Length 122;  
Best Local Similarity 63.6%; Pred. No. 2.5;  
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 LATYYFGLDV 11  
: |||:|:|

DB 100 VVITYYGMVDV 110

RESULT 4  
ADD28082  
ID ADD28082 standard; protein, 114 AA.

AC ADD28082;

DT 15-JAN-2004 (first entry)

DE Lymphoma related immunoglobulin variable region.

XX B-cell; malignant; immunoglobulin; immunoglobulin variable region;  
XX Ig variable region; glycosylation site; lymphoma; B cell receptor;  
XX cytoskeletal; gene therapy; glycosylation inhibitor;  
XX non-Hodgkin's lymphoma.

OS Synthetic.

OS Homo sapiens.

PN WO2003074059-A2.

PD 12-SEP-2003.

PR 24-FEB-2003; 2003WO-GB000783.

PR 07-MAR-2002; 2002GB-0005395.

XX (CAN-C) CANCER RES TECHNOLOGY LTD.

XX Zhu D, Stevenson F;

XX WPI; 2003-902720/82.

PT Classifying a B-cell as malignant or normal by isolating a sequence  
PT representing an Ig variable region from the B cell, detecting the  
PT presence of a glycosylation site and classifying the cell as malignant or  
PT normal.

PS Disclosure; Fig 3; 61pp; English.

CC The present invention describes a method for classifying a B-cell as  
CC malignant or normal comprising: (a) isolating a sequence representing an  
CC immunoglobulin (Ig) variable region from the B cell; (b) detecting the  
CC presence of a glycosylation site; and (c) classifying the cell as  
CC malignant or normal on the basis of the presence or absence of a  
CC glycosylation site. Also described: (1) treating a patient suffering from  
CC or at risk of having lymphoma; (2) screening for substances capable of  
CC inhibiting glycosylation of the Ig variable region of the B cell receptor  
CC; and (3) screening for substances (S) capable of inhibiting the  
CC interaction between lectins of the type found in the germinal centre and  
CC N-glycans found on the surface of Ig of lymphoma cells. (S) has  
CC cytostatic activity, and can be used in gene therapy, and as a  
CC glycosylation inhibitor. The method is useful in classifying a B-cell as  
CC malignant or normal. The glycosylation inhibitor is useful in preparing a  
CC medicament for treating non-Hodgkin's lymphoma. The present sequence  
CC represents an Ig variable region sequence which is used in the  
CC exemplification of the present invention.

SO Sequence 114 AA;

Query Match 78.3%; Score 47; DB 7; Length 114;  
Best Local Similarity 77.8%; Pred. No. 3.4;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 TTYTFFGLDV 11  
|||:|:|

DB 106 TTYTFFGMVDV 114

RESULT 5  
ADD28323  
ID ADD28323 standard; protein, 129 AA.

AC ADD28323;

DT 15-JAN-2004 (first entry)

DE Human heterodimeric antibody heavy chain variable region SEQ ID NO:101.

XX human heterodimeric antibody; human; antibody; binding affinity;  
XX protective antigen; Bacillus anthracis; anthrax infection; cell receptor;  
XX edema factor; lethal factor; virulence; antibacterial; immunotherapy;  
XX anti-toxin; anti-infective; anthrax; botulinum; smallpox;  
XX Venezuelan equine encephalomyelitis virus; VEEV; West Nile virus; WNV.

OS Synthetic.

OS Homo sapiens.

PN WO2003076568-A2.

PD 18-SEP-2003.

PR 11-FEB-2003; 2003WO-US004206.

PR 11-FEB-2002; 2002US-0356086P.

PR 29-APR-2002; 2002US-0376408P.

PR 27-SEP-2002; 2002US-0414053P.

PR 25-NOV-2002; 2002US-0428807P.

PA (ALEX-) ALEXION PHARM INC.  
XX Bowdish KS, Wild MA;  
XX WPI; 2003-722327/68.  
XX  
XX New human heterodimeric antibodies or their antibody fragments, useful as  
PT anti-toxins or anti-infectives with respect to infective agents, e.g.  
PT anthrax, botulinum, smallpox, Venezuelan equine encephalomyelitis or West  
PT Nile virus.  
XX  
XX Claim 11; SEQ ID NO 101; 67pp; English.  
XX  
XX The present invention describes a human heterodimeric antibody (I)  
CC (fragment) having a binding affinity of at least 1x10<sup>-8</sup> M to the  
CC protective antigen of Bacillus anthracis or a molecule involved in  
CC anthrax infection that blocks binding of the antigen or molecule to cell  
CC receptors, edema factor and lethal factor. (I) has virucide and  
CC antibacterial activities, and can be used in immunotherapy. The  
CC antibodies (I) are useful as anti-toxins or anti-infectives with respect  
CC to infective agents, such as anthrax, botulinum, smallpox, Venezuelan  
CC equine encephalomyelitis virus (VEEV), or West Nile virus (WNV). The  
CC present sequence represents a human heterodimeric antibody heavy chain  
CC variable region amino acid sequence, which is used in the exemplification  
CC of the present invention.  
XX  
SQ Sequence 129 AA;  
Query Match 78.3%; Score 47; DB 7; Length 129;  
Best Local Similarity 77.8%; Pred. No. 3.9;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
OY 3 TYYYFGLDV 11  
Db 105 TYYYGMDV 113  
RESULT 6  
ADD28237  
ID ADD28237 standard; protein; 134 AA.  
XX  
XX ADD28237;  
AC  
XX 15-JAN-2004 (first entry)  
DT  
XX Human heterodimeric antibody heavy chain variable region SEQ ID NO:15.  
DE  
XX human heterodimeric antibody; human; antibody; binding affinity;  
XX protective antigen; Bacillus anthracis; anthrax infection; cell receptor;  
XX edema factor; lethal factor; virucide; antibacterial; immunotherapy;  
XX anti-toxin; anti-infective; anthrax; botulinum; smallpox;  
XX Venezuelan equine encephalomyelitis virus; VEEV; West Nile virus; WNV.  
XX  
XX Synthetic.  
OS  
XX Homo sapiens.  
PA  
XX WO2003076568-A2.  
PN  
XX 18-SEP-2003.  
PD  
XX 11-FEB-2003; 2003WO-US004206.  
PF  
XX 11-FEB-2002; 2002US-0356086P.  
PR 29-APR-2002; 2002US-0376408P.  
PR 27-SEP-2002; 2002US-0414053P.  
PR 25-NOV-2002; 2002US-0428807P.  
XX  
XX (ALEX-) ALEXION PHARM INC.  
PA  
XX Bowdish KS, Wild MA;  
PI  
XX WPI; 2003-722327/68.  
DR  
XX

PT New human heterodimeric antibodies or their antibody fragments, useful as  
PT anti-toxins or anti-infectives with respect to infective agents, e.g.  
PT anthrax, botulinum, smallpox, Venezuelan equine encephalomyelitis or West  
PT Nile virus.  
XX  
XX Claim 6; SEQ ID NO 15; 67pp; English.  
XX  
XX The present invention describes a human heterodimeric antibody (I)  
CC (fragment) having a binding affinity of at least 1x10<sup>-8</sup> M to the  
CC protective antigen of Bacillus anthracis or a molecule involved in  
CC anthrax infection that blocks binding of the antigen or molecule to cell  
CC receptors, edema factor and lethal factor. (I) has virucide and  
CC antibacterial activities, and can be used in immunotherapy. The  
CC antibodies (I) are useful as anti-toxins or anti-infectives with respect  
CC to infective agents, such as anthrax, botulinum, smallpox, Venezuelan  
CC equine encephalomyelitis virus (VEEV), or West Nile virus (WNV). The  
CC present sequence represents a human heterodimeric antibody heavy chain  
CC variable region amino acid sequence, which is used in the exemplification  
CC of the present invention.  
XX  
SQ Sequence 134 AA;  
Query Match 78.3%; Score 47; DB 7; Length 134;  
Best Local Similarity 77.8%; Pred. No. 4;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
OY 3 TYYYFGLDV 11  
Db 110 TYYYGMDV 118  
RESULT 7  
ADV86824  
ID ADV86824 standard; protein; 134 AA.  
XX  
XX ADV86824;  
AC  
XX 10-MAR-2005 (first entry)  
DT  
XX Bacillus anthracis toxin Fab 9 K 2e G pro heavy chain variable region.  
DE  
XX  
XX Bioterrorism; Bacillus anthracis infection; vaccine; diagnosis;  
XX antibacterial; antibody; heavy chain variable region.  
XX  
XX Homo sapiens.  
OS  
XX WO2004110362-A2.  
PN  
XX 23-DEC-2004.  
PD  
XX 26-MAY-2004; 2004WO-US016557.  
PF  
XX 02-JUN-2003; 2003US-00452593.  
PR  
XX  
XX (ALEX-) ALEXION PHARM INC.  
PA  
XX Bowdish KS, Frederickson S, Wild MA, Maruyama T, Nolan MJ;  
PI  
XX WPI; 2005-057715/06.  
PD  
XX  
XX Treating an animal with anthrax infection by administering an antibody to  
PT the protective antigen of Bacillus anthracis, and blocking binding to  
PT cell receptors, edema factor or lethal factor.  
XX  
XX Claim 7; SEQ ID NO 15; 87pp; English.  
XX  
XX A claimed method for treating an animal infected with Bacillus anthracis  
CC comprises administering an antibody or antibody fragment that binds to a  
CC molecule involved in anthrax infection and which has the ability to block  
CC the binding of the molecule to at least one of a cell receptor, PA63,  
CC PA63 heptamer, PA83, edema factor and lethal factor. A claimed method for  
CC determining exposure to B. anthracis comprises assaying a sample for the  
CC presence of a molecule selected from cell receptors, PA63, PA63 heptamer,

PA63, edema factor or lethal factor with an antibody that has binding affinity for the molecule, where the presence of elevated levels of the antibody correlates with the presence of a disease associated with B. anthracis. Alternatively, the method involves assaying for the presence of an antibody to a cell receptor, PA63, PA63 heptamer, PA83, edema factor or lethal factor with a secondary antibody having binding affinity for the antibody, where the presence of elevated levels of the secondary antibody correlates with the presence of B. anthracis in a subject. In all cases, the antibody (full-length or functional fragment) may comprise a heavy chain variable region selected from a group of sequences ADV6810-ADV6827, a light chain kappa region selected from a group of sequences ADV6828-ADV6835, and a light chain lambda region selected from a group of sequences ADV6836-ADV6847. Diagnostic kits are provided. A claimed vaccine comprises a multimer of anthrax toxin PA63. The methods and compositions of the present invention are also useful for producing anti-toxins or anti-infectives to infective agents such as anthrax, botulinum, smallpox, Venezuelan equine encephalomyelitis and West Nile virus. The present sequence is that of the heavy chain variable region of a human Fab (designated 9 K 2e G pro) with positive reactivity to anthrax proteins PA63 and PA83. Phage libraries were developed from mRNA isolated from blood and bone marrow samples of donors who had been vaccinated against anthrax. The libraries were panned against PA83 and PA63, and sequence analysis was performed on positive responders. Neutralization of anthrax toxin activity by purified Fabs was demonstrated.

SQ Sequence 134 AA;

Query Match 78.3%; Score 47; DB 9; Length 134;  
Best Local Similarity 77.8%; Pred. No. 4;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TYYYFGLDV 11  
|||:|:|  
Db 110 TYYYGMDV 118

RESULT 8  
ADR28082  
ID ADR28082 standard; protein; 244 AA.

XX ADR28082;

DT 07-OCT-2004 (first entry)

XX NPB polypeptide scFv27, seq id 29.

XX Cytostatic; metastasis inhibitor; neuropilin binder; NPB, scFv;  
KW single chain antibody; neuropilin-1; NP-1; angiogenesis; tumour; cancer.

XX Mus gp.  
OS Synthetic.

XX Key Location/Qualifiers  
FH Region 87..103  
FT /note="complementary determining region claimed under  
FT claim 5"

XX WO2004056874-A2.

XX 08-JUL-2004.

XX 22-DEC-2003; 2003WO-BP014756.

XX 20-DEC-2002; 2002US-0435893P.

XX 15-JAN-2003; 2003EP-00000615.

XX (XERI-) XERION PHARM AG.

XX (TUPF) UNIV TUPF.

XX Unger CM, Beate G, Zehetmeier C, Iain B, Torella C, Niswöhner J;  
PI Jay DG, Eustace BK, Knauer R, Jensen KH;  
XX WPI, 2004-507700/48.

DR N-PSDB; ADR28116.

XX Novel neuropilin binder which is scFv, antibody fragment or bioconjugate,  
PT that modulates neuropilin-1 function or inhibits NP-1 dependent  
PT angiogenesis of endothelial cells and/or invasion of tumor cells useful  
PT for treating cancer.

XX Claim 3; SEQ ID NO 29; 120pp; English.

XX The invention relates to a neuropilin binder (NPB) (I) which is a  
CC polypeptide, antibody, scFv, antibody fragment or bioconjugate, that  
CC modulates neuropilin-1 (NP-1) function or inhibits NP-1 dependent  
CC angiogenesis of endothelial cells and/or invasion of tumor cells,  
CC whereby the NPB binds to NP-1 and modulates NP-1 function. Further  
CC disclosed is an ex vivo method of determining the dependency of the  
CC invasiveness of a naturally occurring invasive cancer cell on the  
CC functionality of NP-1. The NPB of the invention is an inhibitor of  
CC metastasis of NP-1 mediated invasion and/or adhesion and an inhibitor of  
CC tumour-associated NP-1 dependent angiogenesis. The NPB of the invention  
CC is useful for detecting NP-1 expression, modulation of NP-1 function,  
CC particularly modulation or inhibition of NP-dependent invasion or  
CC adhesion of cells, preferably tumour cells. It is useful in the  
CC manufacture of medicament for the treatment or prevention of NP-dependent  
CC angiogenesis and non-physiological blood vessel growth, particularly  
CC correlated with a tumour. It is also useful for treatment or prevention  
CC of cancer and/or metastasis of tumour cells. The current sequence  
CC represents a single chain antibody neuropilin binder (NPB) polypeptide.

SQ Sequence 244 AA;

Query Match 78.3%; Score 47; DB 8; Length 244;  
Best Local Similarity 77.8%; Pred. No. 7.7;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TYYYFGLDV 11  
|||:|:|  
Db 95 TYYYGMDV 103

RESULT 9  
AEB45891  
ID AEB45891 standard; protein; 468 AA.

XX AEB45891;

DT 06-OCT-2005 (first entry)

XX Human monoclonal anti-MAdCAM antibody #27.

XX Monoclonal antibody; mucosal addressin cell adhesion molecule; MAdCAM;  
KW inflammation; inflammatory bowel disease; Crohn's disease;  
KW ulcerative colitis; diverticular disease; gastritis; liver disease;  
KW primary biliary cirrhosis; primary sclerosing cholangitis;  
KW insulin dependent diabetes; graft versus host disease; antiinflammatory;  
KW gastrointestinal-gen.; antitumor; hepatotropic; antidiabetic;  
KW immunosuppressive; antibody.

XX Homo sapiens.

XX WO2005067620-A2.

XX 28-JUL-2005.

XX 07-JAN-2005; 2005WO-US000370.

XX 09-JAN-2004; 2004US-0535490P.

XX (PRIZ) PRIZ INC.

XX (ABGE-) ABGENIX INC.

XX (PRIZ) PRIZ LTD.

XX Pullen N, Molloy E, Kellermann S, Green LT, Haak-Frendocho M;  
XX



RESULT 11  
 ADR38712  
 ID ADR38712 standard; peptide; 13 AA.  
 AC ADR38712;  
 DT 02-DEC-2004 (first entry)  
 XX  
 XX Mouse heavy chain variable region CDR3 seqid 114.  
 DE  
 KM antibacterial; antibody; botulinum neurotoxin type A; BONT/A;  
 KM BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
 KM toxin neutralisation; botulinum neurotoxin poisoning; mouse;  
 KM heavy chain variable region; complementarity determining region; CDR3.  
 XX  
 OS Mus sp.  
 XX  
 PN US2004175385-A1.  
 XX  
 PD 09-SEP-2004.  
 XX  
 PF 01-AUG-2003; 2003US-00632706.  
 XX  
 PR 31-AUG-1998; 98US-00144886.  
 PR 01-AUG-2002; 2002US-0400721P.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 XX  
 P1 Marks JD, Amersdorfer P;  
 P1 WPI; 2004-652009/63.  
 DR  
 XX  
 PT New isolated antibody that neutralizes botulinum neurotoxin type A,  
 PT useful for diagnosing botulism or for treating pathologies associated  
 PT with botulinum neurotoxin poisoning.  
 XX  
 PS Example 3; SEQ ID NO 114; 110pp; English.  
 XX  
 CC The invention describes an isolated antibody (I) that specifically binds  
 CC to an epitope specifically bound by an antibody expressed by a specific  
 CC clone where (I) binds to and neutralises botulinum neurotoxin type A  
 CC (BONT/A). An isolated antibody (I) that specifically binds to an epitope  
 CC specifically bound by an antibody expressed by a clone chosen from clone  
 CC S25, C25, C39, 1G6, 3D12, B4, 1P3, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1,  
 CC 3-8, 3-10 and 1NK1, where (I) binds to and neutralizes botulinum  
 CC neurotoxin type A (BONT/A). Also described are: a polypeptide (II)  
 CC comprising BONT/A neutralising epitope having an epitope that is  
 CC specifically bound by an antibody expressed by clones as mentioned in (I)  
 CC ; producing (I); and a composition (III) comprising several anti-  
 CC botulinum neurotoxin antibodies, where each antibody is specific for a  
 CC different epitope of a botulinum neurotoxin and the combination of  
 CC antibodies shows greater toxin neutralisation than the single antibodies  
 CC in surplus. The following are disclosed: a pharmaceutical composition  
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising  
 CC BONT/A antibody and for neutralising a botulinum neurotoxin which  
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is  
 CC specific for a different epitope of the botulinum neurotoxin and the  
 CC combination of antibodies shows greater toxin neutralisation than the  
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism  
 CC or for treating pathologies associated with botulinum neurotoxin  
 CC poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)  
 CC enables rapid detection or diagnosis of botulism. This is the amino acid  
 CC sequence of mouse heavy chain variable region complementarity determining  
 CC region 3 (CDR3) from anti-botulinum neurotoxin antibodies.  
 CC  
 XX  
 SQ Sequence 13 AA;

Query Match 76.7%; Score 46; DB 8; Length 13;  
 Best Local Similarity 70.0%; Pred. No. 0.5;  
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

2 ATYYFGGLDV 11  
 | |||:|:|

Db 4 ANYYYGMGV 13  
 RESULT 12  
 ADW04816  
 ID ADW04816 standard; peptide; 21 AA.  
 AC ADW04816;  
 DT 07-APR-2005 (first entry)  
 XX  
 XX PAPP-A immunoglobulin variable domain AB b03 heavy chain CDR3 SEQ ID 141.  
 DE  
 KM Cysteatic; Vasotrophic; heavy chain variable domain;  
 KM proliferative disorder; restenosis; glioblastoma; osteosarcoma.  
 XX  
 OS Unidentified.  
 XX  
 PN US2005009136-A1.  
 XX  
 PD 13-JAN-2005.  
 XX  
 PF 19-FEB-2004; 2004US-00783311.  
 XX  
 PR 19-FEB-2003; 2003US-0448515P.  
 XX  
 PA (DYAX-) DYAX CORP.  
 XX  
 P1 Nixon A, Hogan S;  
 P1 WPI; 2005-080519/09.  
 DR  
 XX  
 PT New pregnancy-associated plasma protein-A (PAPP-A) binding proteins  
 PT comprising immunoglobulin variable domain sequences, useful for  
 PT diagnosing, preventing or treating diseases such as cancer.  
 XX  
 PS Example; SEQ ID NO 141; 168pp; English.  
 XX  
 CC The present invention relates to novel proteins (I) that bind to  
 CC pregnancy-associated plasma protein A (PAPP-A ADW04676). (I) comprises a  
 CC first and second immunoglobulin variable domain sequence which binds to  
 CC PAPP-A. Also claimed are proteins (II) which comprise light chain (LC)  
 CC and heavy chain immunoglobulin variable domain sequences which binds to  
 CC PAPP-A. The proteins are useful for diagnosing, preventing or treating  
 CC proliferative diseases such as glioblastoma, osteosarcoma and overgrowth  
 CC of vascular smooth muscle cells following e.g., balloon angioplasty  
 CC (which may cause restenosis). The proteins are especially useful for  
 CC useful for treating diseases involving IGF regulated growth. The present  
 CC sequence is one such immunoglobulin variable domain sequence.  
 CC  
 XX  
 SQ Sequence 21 AA;

Query Match 76.7%; Score 46; DB 9; Length 21;  
 Best Local Similarity 63.6%; Pred. No. 0.83;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

1 LATTYFGGLDV 11  
 | |||:|:|

11 LGNYYYGMGV 21

RESULT 13  
 ADZ41994  
 ID ADZ41994 standard; peptide; 126 AA.  
 AC ADZ41994;  
 DT 30-JUN-2005 (first entry)  
 XX  
 XX Ig H chain variable region, B-CLL set II peptide #4.  
 DE  
 XX Antibody; antibody engineering; antibody therapy;  
 KM light chain variable region; heavy chain variable region;



KM chronic lymphocytic leukemia; cytostatic; Hodgkins disease; lymphoma;  
 KM Burkitts lymphoma; multiple myeloma; systemic lupus erythematosus;  
 KM antinflammatory; dermatologic; immunosuppressive; myasthenia gravis;  
 KM muscular-gen.; neuroprotective; Graves disease; antithyroid;  
 KM insulin dependent diabetes; diabetes mellitus; antidiabetic;  
 KM autoimmune hemolytic anemia; antineoplastic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO2005034733-A2.  
 XX  
 XX 21-APR-2005.  
 PD  
 XX 08-OCT-2004; 2004WO-US033176.  
 XX  
 XX 08-OCT-2003; 2003US-0509473P.  
 PR  
 XX (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.  
 PA  
 PI Mesamer BT, Chiorazzi N, Albesiano E;  
 XX  
 XX WPI, 2005-306220/31.  
 DR  
 XX  
 PT New isolated and purified preparation of light chain and heavy chain  
 PT antibody genes, useful for diagnosing, preventing or treating B cell  
 PT chronic lymphocytic leukemia, or in screening for agents that may treat  
 PT such disease.  
 XX  
 PS Disclosure; Fig 2; 58pp; English.  
 XX  
 XX The new invention relates to combinations of light chain antibody genes  
 CC and heavy chain antibody genes, useful for treating B cell chronic  
 CC lymphocytic leukemia (B-CLL). B-CLL is a disease of slowly proliferating  
 CC CD5+ B lymphocytes. These cells express low levels of surface membrane Ig  
 CC that serves as the receptor for antigen (BCR). Analysis of V region gene  
 CC cassette usage has shown that distribution of variable region gene  
 CC cassettes used by B-CLL clones differs from that in normal cells, with an  
 CC increased frequency of VH3-07, VH4-34, and VH1-69 genes. This implies  
 CC that the structure of the antibody molecule, and antigen specificity,  
 CC play a role in the leukemic transformation of particular B cells. The  
 CC present invention discloses that a significant proportion of B-CLL  
 CC patients with aggressive disease share the same classes of VH, D, JH, VL  
 CC and JH antibody genes, forming sets of patients with highly homologous B  
 CC cell receptors. Alternatively, the patients have a disorder selected from  
 CC Hodgkin's disease, non-Hodgkin's lymphoma, Burkitt's lymphoma, myeloma or  
 CC systemic lupus erythematosus, myasthenia gravis, Grave's disease, type I  
 CC diabetes mellitus, autoimmune peripheral neuropathy, and autoimmune  
 CC hemolytic anemia. The new members of the antibody genes are: VH4-39/D6-  
 CC 13/JH5/VLkappa012/2/JLkappa1/kappa2 (Set I); VH4-34/D5-  
 CC 5/JH6/VLkappa012/2/JLkappa1/kappa2 (Set II); VH3-  
 CC 21/JH6/VLlambda03/JLlambda3 (Set III); VH1-69/D3-  
 CC 16/JH3/VLkappa027/JLkappa1/kappa4 (Set IV); VH1-69/D3-  
 CC 10/JH6/VLlambda03/JLlambda1 (Set V); VH1-02/D6-  
 CC 19/JH4/VLkappa012/2/JLkappa1/kappa2 (Set VIa); VH1-03/D6-  
 CC 19/JH4/VLkappa012/2/JLkappa1/kappa2 (Set VIb); VH1-18/D6-  
 CC 51/D6-19/JH4/VLkappa012/2/JLkappa1 (Set VIC); VH1-46/D6-19/JH4 (Set VID); VH5-  
 CC 3/JH4/VLkappa012/2/JLkappa2 (Set VIE); VH1-69/D3-  
 CC 2/JH6/VLkappa019/JLkappa4 (Set VII); VH1-69/D2-  
 CC 2/JH6/VLkappa067/JLkappa3 (Set VIII). Treating a patient having B-CLL  
 CC with the above genes comprises administering an agent that binds to the  
 CC antigen-binding region of an antibody encoded by the antibody genes. The  
 CC agent is an anti-idiotypic antibody, a peptide antigen, or an aptamer. The  
 CC present sequence is an Ig H chain variable region, B-CLL set II peptide.  
 CC  
 XX  
 SQ Sequence 126 AA;  
 Query Match 76.7%; Score 46; DB 9; Length 126;  
 Best Local Similarity 72.7%; Pred. No. 5.6;  
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

RESULT 14  
 ADM04810  
 ID ADM04810 standard, protein, 140 AA.  
 XX  
 AC ADM04810;  
 XX  
 DT 07-APR-2005 (first entry)  
 XX  
 DE PAPP-A immunoglobulin variable domain AB b03 heavy chain SEQ ID 135.  
 XX  
 KM Cytostatic; Vasoactive; heavy chain variable domain;  
 KM proliferative disorder; restenosis; glioblastoma; osteosarcoma.  
 XX  
 OS unidentified.  
 XX  
 PN US2005009136-A1.  
 XX  
 PD 13-JAN-2005.  
 PF 19-FEB-2004; 2004US-00783311.  
 PR 19-FEB-2003; 2003US-0448515P.  
 PA (DYAX-) DYAX CORP.  
 XX  
 PI Nixon A, Hogan S;  
 XX  
 XX WPI, 2005-080519/09.  
 DR  
 PT New pregnancy-associated plasma protein-A (PAPP-A) binding proteins  
 PT comprising immunoglobulin variable domain sequences, useful for  
 PT diagnosing, preventing or treating diseases such as cancer.  
 XX  
 PS Example; SEQ ID NO 135; 168pp; English.  
 XX  
 XX The present invention relates to novel proteins (I) that bind to  
 CC pregnancy-associated plasma protein A (PAPP-A ADM04810). (I) comprises a  
 CC first and second immunoglobulin variable domain sequence which binds to  
 CC PAPP-A. Also claimed are proteins (II) which comprise light chain (LC)  
 CC and heavy chain immunoglobulin variable domain sequences which binds to  
 CC PAPP-A. The proteins are useful for diagnosing, preventing or treating  
 CC proliferative diseases such as glioblastoma, osteosarcoma and overgrowth  
 CC of vascular smooth muscle cells following e.g., balloon angioplasty  
 CC (which may cause restenosis). The proteins are especially useful for  
 CC useful for treating diseases involving IGF regulated growth. The present  
 CC sequence is one such immunoglobulin variable domain sequence.  
 CC  
 XX  
 SQ Sequence 140 AA;  
 Query Match 76.7%; Score 46; DB 9; Length 140;  
 Best Local Similarity 63.6%; Pred. No. 6.3;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LATYYFGADV 11  
 | | | | | | | | | |  
 DB 109 LGNYYYGMADV 119  
 | | | | | | | | | |

RESULT 15  
 ADM04952  
 ID ADM04952 standard, peptide, 16 AA.  
 XX  
 AC ADM04952;  
 XX  
 DT 07-APR-2005 (first entry)  
 XX  
 DE PAPP-A immunoglobulin variable domain AB f03 heavy chain CDR3 SEQ ID 277.  
 XX  
 KM Cytostatic; Vasoactive; heavy chain variable domain;  
 KM proliferative disorder; restenosis; glioblastoma; osteosarcoma.



OS Unidentified.

XX US2005009136-A1.

XX 13-JAN-2005.

XX 19-FEB-2004; 2004US-00783311.

XX 19-FEB-2003; 2003US-0448515P.

XX (DYAX-) DYAX CORP.

XX Nixon A, Hogan S;

XX WPI, 2005-080519/09.

PT New pregnancy-associated plasma protein-A (PAPP-A) binding proteins  
PT comprising immunoglobulin variable domain sequences, useful for  
PT diagnosing, preventing or treating diseases such as cancer.

PS Example; SEQ ID NO 277; 168bp; English.

CC The present invention relates to novel proteins (I) that bind to  
CC pregnancy-associated plasma protein A (PAPP-A ADW04676). (I) comprises a  
CC first and second immunoglobulin variable domain sequence which binds to  
CC PAPP-A. Also claimed are proteins (II) which comprise light chain (LC)  
CC and heavy chain immunoglobulin variable domain sequences which binds to  
CC PAPP-A. The proteins are useful for diagnosing, preventing or treating  
CC proliferative diseases such as glioblastoma, osteosarcoma and overgrowth  
CC of vascular smooth muscle cells following e.g., balloon angioplasty  
CC (which may cause restenosis). The proteins are especially useful for  
CC useful for treating diseases involving IGF regulated growth. The present  
CC sequence is one such immunoglobulin variable domain sequence.

XX Sequence 16 AA;

Query Match 75.0%; Score 45; DB 9; Length 16;

Best Local Similarity 63.6%; Pred. No. 0.92;

Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 LATYYFGLDV 11

Db 6 VAGYYYYGMDV 16

Search completed: December 4, 2005, 04:44:54  
Job time : 98.5625 secs

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GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: December 4, 2005, 04:31:45 / Search time 15.5833 Seconds  
(without alignments)  
67.918 Million cell updates/sec

Title: US-10-632-706-127  
Perfect score: 60  
Sequence: 1 LATYYFGLDV 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query length	ID	Description
1	43	71.7	19	PH1307	Ig heavy chain DJ
2	43	71.7	23	PH1361	Ig heavy chain DJ
3	43	71.7	29	PH1328	Ig heavy chain DJ
4	43	71.7	160	D70189	conserved hypotetic
5	43	71.7	160	S05271	Ig heavy chain pre
6	43	71.7	408	E70380	Na+/H+-exchanging
7	42	70.0	19	PH1304	Ig heavy chain DJ
8	42	70.0	19	S43960	Ig mu chain V regi
9	42	70.0	23	PH1364	Ig heavy chain DJ
10	42	70.0	24	PT0258	Ig heavy chain CDR
11	42	70.0	27	PH1371	Ig heavy chain DJ
12	42	70.0	27	PH1355	Ig heavy chain DJ
13	42	70.0	74	S25793	Ig heavy chain V r
14	42	70.0	118	PH1666	Ig heavy chain V r
15	42	70.0	119	PH0961	Ig heavy chain V r
16	42	70.0	120	PH1650	Ig heavy chain V r
17	42	70.0	125	S24686	Ig heavy chain V6
18	42	70.0	128	S48797	Ig heavy chain V r
19	42	70.0	132	PH0954	Ig heavy chain V r
20	42	70.0	133	C33548	Ig heavy chain V-1
21	42	70.0	136	A49047	Ig heavy chain V-1
22	42	70.0	147	I37780	Ig variable region
23	42	70.0	627	S14683	Ig mu chain precu
24	40	66.7	22	PH1325	Ig heavy chain DJ
25	39.5	65.8	581	E03729	adenine deaminase
26	39	65.0	126	S44107	Ig heavy chain V-D
27	39	65.0	375	A83788	spore germination
28	38	63.3	22	PH1359	Ig heavy chain DJ
29	38	63.3	45	PL0094	Ig heavy chain V r

30	38	63.3	287	2	T27056	hypothetical prote
31	38	63.3	473	2	H86240	hypothetical prote
32	38	63.3	979	2	A39792	transcription acti
33	37	61.7	14	2	PH1601	Ig H chain V-D-J r
34	37	61.7	126	1	MHHU0U	Ig heavy chain V-I
35	37	61.7	276	2	S16892	probable transpos
36	37	61.7	447	2	T09809	NADH2 dehydrogen
37	37	61.7	448	2	T12006	glycerol-3-phosph
38	37	61.7	527	2	C70130	conditioned mediu
39	37	61.7	571	2	A42138	conditoned mediu
40	37	61.7	571	2	S24482	se1-1 protein - Ca
41	37	61.7	685	2	T22223	Ig heavy chain V r
42	36.5	60.8	120	2	E49590	hypothetical prote
43	36.5	60.8	316	2	C75205	Ig heavy chain DJ
44	36	60.0	18	2	PH1368	30S ribosomal prot
45	36	60.0	145	2	H97707	

## ALIGNMENTS

## RESULT 1

PH1307  
Ig heavy chain DJ region (clone C96-119) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C:Accession: PH1307  
R:Masserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
J. Exp. Med. 176, 1577-1581, 1992  
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph  
A:Reference number: PH1302; MUID:93094761; PMID:1460419  
A:Accession: PH1307  
A:Molecule type: DNA  
A:Residues: 1-19 <MAS>  
A:Cross-references: UNIPARC:UPI0000176935  
A:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

Query Match 71.7%; Score 43; DB 2; Length 19;  
Best Local Similarity 66.7%; Pred. No. 0.23;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 3 TYYFGLDV 11  
Db 6 SYTYGMDV 14

## RESULT 2

PH1361  
Ig heavy chain DJ region (clone C178-122B) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C:Accession: PH1361  
R:Masserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
J. Exp. Med. 176, 1577-1581, 1992  
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph  
A:Reference number: PH1302; MUID:93094761; PMID:1460419  
A:Accession: PH1361  
A:Molecule type: DNA  
A:Residues: 1-23 <MAS>  
A:Cross-references: UNIPARC:UPI0000176948  
A:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

Query Match 71.7%; Score 43; DB 2; Length 23;  
Best Local Similarity 63.6%; Pred. No. 0.28;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1 LATYYFGLDV 11  
Db 8 LFPYYGMDV 18

```
RESULT 3
PH1328
I: heavy chain Df region (clone C113-148) - human (fragment)
A:Residues: 1-144 <K1S2>
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PH1328
R:Masserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A:Reference number: PH1302; MUID:93094761; PMID:1460419
A:Accession: PH1328
A:Molecule type: DNA
A:Residues: 1-29 <WAS>
A:Cross-references: UNIPARC:UPI0000176939
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match
Best Local Similarity 71.7%; Score 43; DB 2; Length 29;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYTGGLDV 11
DB 16 SYTYGMDV 24

RESULT 4
D70189
conserved hypothetical integral membrane protein B80717 - Lyme disease spirochete
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C:Accession: D70189
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
son, D.; Peterson, J.; Kexlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 350, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A:Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.
A:Reference number: A70100; MUID:98065943; PMID:9403685
A:Accession: D70189
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-160 <KLB>
A:Cross-references: UNIPROT:O51659; UNIPARC:UPI00000575B2; GB:AE001171; GB:AE000783; NID
A:Experimental source: strain B31

Query Match
Best Local Similarity 71.7%; Score 43; DB 2; Length 160;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATYYFGLDV 11
DB 23 ATYYFSTDI 32

RESULT 5
S05271
I: heavy chain precursor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 31-Dec-2004
C:Accession: S05271; S04602
R:Kishimoto, T.
submitted to the EMBL Data Library, March 1989
A:Reference number: S05270
A:Accession: S05271
A:Molecule type: mRNA
A:Residues: 1-160 <K1S1>
A:Cross-references: UNIPROT:Q96B99; UNIPARC:UPI0000176B50; EMBL:X14584
R:Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.
Nucleic Acids Res. 17, 4385, 1989
A:Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of
A:Reference number: S04601; MUID:89296497; PMID:250664
A:Accession: S04602
```

```
A:Molecule type: mRNA
A:Residues: 1-144 <K1S2>
A:Cross-references: UNIPARC:UPI0000176B51; EMBL:X14584
C:Superfamily: immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F1-19/Domain: signal sequence #status predicted <SIG>
F120-160/Product: Ig heavy chain (fragment) #status predicted <MAT>
F134-117/Domain: immunoglobulin homology <IMW>

Query Match
Best Local Similarity 71.7%; Score 43; DB 2; Length 160;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYTGGLDV 11
DB 125 SYTYGMDV 133

RESULT 6
E70380
Na+/H+-exchanging protein - Aquifex aeolicus
N:Alternate names: Na+/H+ antiporter
C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C:Accession: E70380
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
V.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:99196666; PMID:9537320
A:Accession: E70380
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-408 <AOP>
A:Cross-references: UNIPROT:O67072; UNIPARC:UPI00000564AB; GB:AE000714; NID:G2983446; PI
A:Experimental source: strain VF5
A:Genetics:
A:Gene: napA2
C:Superfamily: Aquifex aeolicus Na+/H+-exchanging protein napA1

Query Match
Best Local Similarity 71.7%; Score 43; DB 2; Length 408;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 LATYYFGLDV 11
DB 116 IVSYTFFGLDL 126

RESULT 7
PH1304
I: heavy chain Df region (clone C439-111) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PH1304
R:Masserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A:Reference number: PH1302; MUID:93094761; PMID:1460419
A:Accession: PH1304
A:Molecule type: DNA
A:Residues: 1-19 <WAS>
A:Cross-references: UNIPARC:UPI0000176934
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match
Best Local Similarity 70.0%; Score 42; DB 2; Length 19;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11
DB 7 YYYGMDV 14
```

## RESULT 8

S43960  
 Ig mu chain V region (clone 18) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 20-Oct-1994 #sequence\_revision 26-Jul-1996 #text\_change 17-Mar-1999  
 C:Accession: S43960  
 R:Wagner, S.D.; Williams, G.T.; Larson, T.; Neuburger, M.S.; Kitamura, D.; Rajewsky, K.;  
 Nucleic Acids Res. 22, 1389-1393, 1994  
 A:Title: Antibodies generated from human immunoglobulin miniloci in transgenic mice.  
 A:Reference number: S43956; MUID:94248036; PMID:8190629  
 A:Accession: S43960  
 A:Molecule type: DNA  
 A:Residues: 1-19 <WAS>  
 A:Cross-references: UNIPARC:UPI000017690D  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: immunoglobulin

Query Match 70.0%; Score 42; DB 2; Length 19;  
 Best Local Similarity 75.0%; Pred. No. 0.35;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11  
 |||:|:|  
 Db 10 YYYGMDV 17

## RESULT 9

PH1364  
 Ig heavy chain DJ region (clone C178-136A) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
 C:Accession: PH1364  
 R:Masserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
 J. Exp. Med. 176, 1577-1581, 1992  
 A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph  
 A:Reference number: PH1302; MUID:93094761; PMID:1460419  
 A:Accession: PH1364  
 A:Molecule type: DNA  
 A:Residues: 1-23 <WAS>  
 A:Cross-references: UNIPARC:UPI0000176949  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin

Query Match 70.0%; Score 42; DB 2; Length 23;  
 Best Local Similarity 75.0%; Pred. No. 0.42;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11  
 |||:|:|  
 Db 11 YYYGMDV 18

## RESULT 10

PT0258  
 Ig heavy chain CDR3 region (clone 2-118B) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 30-May-1997  
 C:Accession: PT0258  
 R:Yamada, M.; Masserman, R.; Reichard, B.A.; Shane, S.; Cacon, A.J.; Rovera, G.  
 J. Exp. Med. 173, 395-407, 1991  
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J  
 A:Reference number: PT0222; MUID:91108337; PMID:1899102  
 A:Accession: PT0258  
 A:Molecule type: DNA  
 A:Residues: 1-24 <YAM>  
 A:Cross-references: UNIPARC:UPI0000176940  
 A:Experimental source: B lymphocyte  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin

Query Match 70.0%; Score 42; DB 2; Length 24;

Best Local Similarity 75.0%; Pred. No. 0.44;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11  
 |||:|:|  
 Db 12 YYYGMDV 19

## RESULT 11

PH1371  
 Ig heavy chain DJ region (clone C111-145) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
 C:Accession: PH1371  
 R:Masserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
 J. Exp. Med. 176, 1577-1581, 1992  
 A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph  
 A:Reference number: PH1302; MUID:93094761; PMID:1460419  
 A:Accession: PH1371  
 A:Molecule type: DNA  
 A:Residues: 1-27 <WAS>  
 A:Cross-references: UNIPARC:UPI000017694B  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin

Query Match 70.0%; Score 42; DB 2; Length 27;  
 Best Local Similarity 75.0%; Pred. No. 0.5;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11  
 |||:|:|  
 Db 15 YYYGMDV 22

## RESULT 12

PH1355  
 Ig heavy chain DJ region (clone C100-136) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
 C:Accession: PH1355  
 R:Masserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
 J. Exp. Med. 176, 1577-1581, 1992  
 A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph  
 A:Reference number: PH1302; MUID:93094761; PMID:1460419  
 A:Accession: PH1355  
 A:Molecule type: DNA  
 A:Residues: 1-27 <WAS>  
 A:Cross-references: UNIPARC:UPI0000176945  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin

Query Match 70.0%; Score 42; DB 2; Length 27;  
 Best Local Similarity 75.0%; Pred. No. 0.5;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11  
 |||:|:|  
 Db 15 YYYGMDV 22

## RESULT 13

S26793  
 Ig heavy chain V region - human  
 C:Species: Homo sapiens (man)  
 C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Jun-2000  
 C:Accession: S26793  
 R:Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.  
 Eur. J. Immunol. 22, 241-245, 1992  
 A:Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene fami  
 A:Reference number: S26786; MUID:92111632; PMID:1730251  
 A:Accession: S26793  
 A:Status: preliminary  
 A:Molecule type: mRNA

A:Residues: 1-74 <MOR>  
 A:Cross-references: UNIPARC:UPI0000115FCA; EMBL:X61019; MID:932787; PIDN:CAA43353.1; PII  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin

Query Match 70.0%; Score 42; DB 2; Length 74;  
 Best Local Similarity 75.0%; Pred. No. 1.4;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYFGLDV 11  
 |||:|:|  
 DB 56 YYYGMDV 63

## RESULT 14

PH1666  
 Ig heavy chain V region (clone 6C9) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 16-Aug-1996  
 C:Accession: PH1666  
 R:Hillson, J.L.; Karr, N.S.; Opliger, I.R.; Mannik, M.; Sasso, E.H.  
 J. Exp. Med. 178, 331-336, 1993  
 A>Title: The structural basis of germ-line-encoded VH3 immunoglobulin binding to staphylo  
 A:Reference number: PH1642; MUID:93301610; PMID:8315388  
 A:Accession: PH1666  
 A:Molecule type: mRNA  
 A:Residues: 1-118 <HIL>  
 A:Cross-references: UNIPARC:UPI0000176BE7  
 A:Experimental source: B cell  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 70.0%; Score 42; DB 2; Length 118;  
 Best Local Similarity 75.0%; Pred. No. 2.2;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYFGLDV 11  
 |||:|:|  
 DB 100 YYYGMDV 107

## RESULT 15

PH0961  
 Ig heavy chain V region (G6+ T-L33) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996  
 C:Accession: PH0961  
 R:Martin, T.; Duffly, S.F.; Carson, D.A.; Kipps, T.J.  
 J. Exp. Med. 175, 983-991, 1992  
 A>Title: Evidence for somatic selection of natural autoantibodies.  
 A:Reference number: PH0952; MUID:92202880; PMID:1552291  
 A:Accession: PH0961  
 A>Status: nucleic acid sequence not shown  
 A:Molecule type: DNA  
 A:Residues: 1-119 <MAR>  
 A:Cross-references: UNIPARC:UPI0000176CES  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:1-30/Region: framework 1  
 F:15-98/Domain: immunoglobulin homology <IMM>  
 F:31-35/Region: complementarity-determining 1  
 F:36-50/Region: framework 2  
 F:51-67/Region: complementarity-determining 2  
 F:68-98/Region: framework 3  
 F:99-107/Region: complementarity-determining 3

Query Match 70.0%; Score 42; DB 2; Length 119;  
 Best Local Similarity 75.0%; Pred. No. 2.2;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYFGLDV 11  
 |||:|:|

DB 101 YYYGMDV 108

Search completed: December 4, 2005, 04:53:32  
 Job time : 17.5833 secs

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: December 4, 2005, 04:31:36 ; Search time 100.375 Seconds  
(without alignments)  
77.318 Million cell updates/sec

Title: US-10-632-706-127  
Perfect score: 60  
Sequence: 1 LATYYFGLDV 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_05.80: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
44	73.3	1348	Q4N9V2_THEPA	Q4N9V2 theileria p
44	73.3	2262	Q4N9V2_THEPA	Q4N9V2 theileria p
43	71.7	160	Q516S3_BORBU	Q516S3 borrelia bu
43	71.7	160	Q660FE_BORGA	Q660FE borrelia ga
5	71.7	408	Q67072_AQUAE	Q67072 aquifex aeo
6	70.0	364	Q7VY71_BORPE	Q7VY71 borrelia
7	70.0	364	Q7W926_BORPA	Q7W926 borrelia
8	70.0	364	Q7W926_BORPA	Q7W926 borrelia
9	70.0	378	Q4QAL0_LEIMA	Q4QAL0 leishmania
10	70.0	382	Q89NT9_BRAJA	Q89NT9 bradyrhizob
11	70.0	594	Q7AN07_NANEO	Q7AN07 nanarchaeu
12	70.0	606	Q6GMY2_HUMAN	Q6GMY2 homo sapien
13	70.0	1062	Q96X97_SUITO	Q96X97 sulfolobus
14	70.0	3212	Q4FWX4_LEIMA	Q4FWX4 leishmania
15	68.3	716	Q6HQZ1_DESPS	Q6HQZ1 desulfofatale
16	66.7	288	Q6F6N6_ACTIAD	Q6F6N6 actinobact
17	66.7	291	Q4ZUB1_PESY	Q4ZUB1 pseudomonas
18	66.7	293	Q6D0Z3_ERMCT	Q6D0Z3 erwinia car
19	66.7	447	Q8EU78_OCEIH	Q8EU78 oceanobacil
20	66.7	702	Q8C3X8_MOUSE	Q8C3X8 mus musculu
21	66.7	978	Q8ANVE_CANAL	Q8ANVE candida alb
22	66.7	1113	Q6WED5_ARALY	Q6WED5 arabidopsis
23	66.7	3964	Q4Q8V4_LEIMA	Q4Q8V4 leishmania
24	65.8	581	Y637_BACHD	Q9F649 bacillus ha
25	65.0	188	Q5G3J1_MAGGR	Q5G3J1 magnaporthe
26	65.0	215	Q5YXQ2_NOCFA	Q5YXQ2 nocardia fa
27	65.0	317	Q97BK3_THREVO	Q97BK3 thermoplasma
28	65.0	319	Q9KDV6_BACHD	Q9KDV6 bacillus ha
29	65.0	419	Q82700_MEDTR	Q82700 medicago tr
30	65.0	423	Q9STAS_MEDTR	Q9STAS medicago tr
31	65.0	434	Q6GBX7_ORYSA	Q6GBX7 oryza sativ

32	39	65.0	451	2	Q6ZBX6_ORYSA	Q6ZBX6 oryza sativ
33	39	65.0	478	2	Q6PI81_HUMAN	Q6PI81 homo sapien
34	39	65.0	662	2	Q88T15_LACBL	Q88T15 lactobacill
35	39	65.0	701	1	LSP2_DROME	Q24388 drosophila
36	39	65.0	779	2	Q6S5Z1_MANSB	Q6S5Z1 mannefina
37	39	65.0	780	2	Q7VOH6_CANBF	Q7VQH6 candidatus
38	38	63.3	116	2	Q723V6_HUMAN	Q723V6 homo sapien
39	38	63.3	148	2	Q5TXK6_ANOGA	Q5TXK6 anopheles g
40	38	63.3	159	2	Q96QSO_HUMAN	Q96QSO homo sapien
41	38	63.3	239	2	Q5XOG3_LEGGL	Q5XOG3 legionella
42	38	63.3	243	2	Q5Z2F4_LEGPH	Q5Z2F4 legionella
43	38	63.3	307	2	Q6NSD3_RHOPA	Q6NSD3 rhodospheudo
44	38	63.3	350	2	Q8TVT5_METRA	Q8TVT5 methanopyru
45	38	63.3	366	2	Q9XTT1_CAEEL	Q9XTT1 caenorhabdi

## ALIGNMENTS

RESULT 1	Q4N9V2_THEPA	PRELIMINARY;	PRT;	1348 AA.
ID	Q4N9V2;			
AC	Q4N9V2;			
DT	13-SEP-2005 (TREMBLrel. 31, Created)			
DT	13-SEP-2005 (TREMBLrel. 31, Last sequence update)			
DT	13-SEP-2005 (TREMBLrel. 31, Last annotation update)			
DE	Hypothetical protein.			
GN	ORFNames=TP01_0021;			
OS	Theileria parva.			
OC	Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;			
OC	Theileria.			
OX	NCBI_TaxID=5675;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=Muguga;			
RA	Gardner M.J., Bishop R., Shah T., de Villiers E.P., Carlson J.M.,			
RA	Hall N., Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M.,			
RA	Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J.,			
RA	Uiang L., Lynn J., Weaver B., Shoalbi A., Waaswo D., Crabtree J.,			
RA	Wortman J.R., Haas B., Angiuoli S.V., Creasy T.H., Lu C., Suh B.,			
RA	Silva J.C., Utecherack T.R., Feldblyum T.V., Petrea M., Allen J.,			
RA	Taracha E.L.N., Salzberg S.L., White O.R., Fitzhugh H.A., Morzaria S.,			
RA	Venter J.C., Fraser C.M., Nene V.;			
RT	"Genome sequence of Theileria parva, a bovine pathogen that transforms			
RT	lymphocytes."			
RL	Science 309:134-137(2005).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=Muguga;			
RA	Gardner M., Bishop R., Shah T., de Villiers E., Carlson J.M., Hall N.,			
RA	Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,			
RA	Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J., Uiang L.,			
RA	Lynn J., Weaver B., Shoalbi A., Waaswo D., Crabtree J., Wortman J.R.,			
RA	Haas B., Angiuoli S., Creasy T.H., Lu C., Suh B., Silva J.C.,			
RA	Utecherack T., Feldblyum T., Petrea M., Allen J., Taracha E.L.,			
RA	Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C.,			
RA	Fraser C.M., Nene V.;			
RL	Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.			
CC	-i- CAUTION: The sequence shown here is derived from an			
CC	EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is			
CC	preliminary data.			
CC	EMBL: AAGK0100001; EMBL33265.1; -; Genomic_DNA.			
KM	HYPOTHETICAL protein.			
DR	SEQUENCE 1348 AA; 155635 MW; 474C3A40C23B8C5F CRC64;			
SO	SEQUENCE			
Query Match	73.3%; Score 44; DB 2; Length 1348;			
Best Local Similarity	87.5%; Pred. No. 60;			
Matches	7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;			
Oy	3 TYTYFGLD 10			
Db	386 SYTYFGLD 393			

```
RESULT 2
Q4UFY8_THEAN
ID Q4UFY8_THEAN PRELIMINARY; PRT; 2262 AA.
AC Q4UFY8;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DE Hypothetical protein.
GN ORFNames=TA19710;
OS Theileria annulata.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
OC Theileria.
OX NCBI_TaxID=5874;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ankara isolate clone C9;
RA Pain A., Renauld H., Murphy L., Harris D.A., Quail M.A., Berriman M.,
RA Hall N., Barrall B.G.;
RT "The chromosome 1 sequence of Theileria annulata."
RL Submitted (Apr-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR940347; CAI74001.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ
SEQUENCE 2262 AA; 26206 MW; FD9B8915243BF512 CRC64;
Match
Best Local Similarity 73.3%; Score 44; DB 2; Length 2262;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYTFFGLD 10
Db 1244 STTYFGLD 1251

RESULT 3
OS1659_BORBU PRELIMINARY; PRT; 160 AA.
ID OS1659_BORBU PRELIMINARY; PRT; 160 AA.
AC OS1659;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DE Conserved hypothetical integral membrane protein.
GN OrderedLocustNames=BB0717;
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia;
OC Borrelia burgdorferi group.
OX NCBI_TaxID=139;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 35210 / B31;
RX MEDLINE=98065943; PubMed=9403685; DOI=10.1038/371551;
RA Frazer C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Latifga R., White O., Ketchum K.A., Dodson R.J., Hickey E.K.,
RA Gwinn M.L., Dougherty B.A., Tomb J.-F., Fleischmann R.D.,
RA Richardson D.L., Peterson J.D., Kerlavage A.R., Quackenbush J.,
RA Salzberg S.L., Hanson M., van Vugt R., Palmer N., Adams M.D.,
RA Gocayne J.D., Weidman J.F., Utterback T.R., Matthey L., McDonald L.A.,
RA Artach P., Bowman C., Garland S.A., Fujii C., Cotton M.D., Horst K.,
RA Roberts K.M., Hatch B., Smith H.O., Venter J.C.;
RT "Genomic sequence of a Lyme disease spirochete, Borrelia
burgdorferi."
RL Nature 390:580-586 (1997).
DR EMBL; AB001171; AAC67057.1; -; Genomic_DNA.
DR PIR; D70189; D70189.
DR TIGR; BB0717; -.
KW Complete proteome; Hypothetical protein.
SQ
SEQUENCE 160 AA; 19300 MW; 9DE28A497C0F5737 CRC64;

Query Match
Best Local Similarity 71.7%; Score 43; DB 2; Length 160;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATTYTFFGLDV 11
```

```
Db 23 ATTYFFSIDI 32

RESULT 4
O660F6_BORGA
ID O660F6_BORGA PRELIMINARY; PRT; 160 AA.
AC O660F6;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DE Conserved hypothetical integral membrane protein.
GN OrderedLocustNames=BB0739;
OS Borrelia garinii.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia;
OC Borrelia burgdorferi group.
OX NCBI_TaxID=29519;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PB1;
RA Gloeckner G., Lehmann R., Romualdi A., Pradella S.,
RA Schulte-Spechtel U., Wilske B., Suenkel J., Platzer M.;
RT "Comparative analysis of the Borrelia garinii genome."
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000013; AAU07555.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ
SEQUENCE 160 AA; 19293 MW; B65B15C5197BF89 CRC64;

Query Match
Best Local Similarity 71.7%; Score 43; DB 2; Length 160;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATTYTFFGLDV 11
Db 23 ATTYFFSIDI 32

RESULT 5
O67072_AQUAE
ID O67072_AQUAE PRELIMINARY; PRT; 408 AA.
AC O67072;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DE Na(+)/H(+) antiporter.
GN Name=napA2; OrderedLocustNames=AQ_929;
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320; DOI=10.1038/32831;
RA Decker G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Aulay M., Huber R.,
RA Feldman R.A., Short J.M., Olsen G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
aeolicus."
RL Nature 392:353-358 (1998).
DR EMBL; AF000714; AAC07034.1; -; Genomic_DNA.
DR PIR; E70380; E70380.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006153; Na_Hporter.
DR Pfam; PF00999; Na_H_Exchange; 1.
KW Complete proteome; Transmembrane; Transport.
SQ
SEQUENCE 408 AA; 43582 MW; 7B05B4B367A6C506 CRC64;

Query Match
Best Local Similarity 71.7%; Score 43; DB 2; Length 408;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
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```
Qy 1 LATYFFGLDV 11
   :|||||:
Db 116 IVSYFFFLDL 126

RESULT 6
Q7VY71 BORPE PRELIMINARY; PRT; 364 AA.
ID Q7VY71 BORPE PRELIMINARY; PRT; 364 AA.
AC Q7VY71 BORPE PRELIMINARY; PRT; 364 AA.
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Putative periplasmic solute-binding protein.
GN Name=smow; OrderedLocustNames=BP1487;
OS Bordetella pertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcalligenaceae; Bordetella.
OX NCBI_TaxID=520;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebailia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Cherevach I.,
RA Achtman M., Atkin R., Baker S., Cronin A., Davis P., Doggett J.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holtroyd S., Jagsels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrett B.G., Maskell D.J.,
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica."
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640415; CAB317248.1; -; Genomic DNA.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006311; Tat.
DR InterPro; IPR004682; TRAP_transpdcct.
DR Pfam; PF03480; SBP_bac_7; 1.
DR TIGRFAMs; TIGR01409; TAT_signal_seq; 1.
KW Complete proteome.
SQ SEQUENCE 364 AA; 40021 MW; 03F1C2B6F51D502 CRC64;

Query Match 70.0%; Score 42; DB 2; Length 364;
Best Local Similarity 77.8%; Pred. No. 38;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ATYYFFGLD 10
   :|||||:
Db 98 ASYYFFGLD 106

RESULT 7
Q7W926 BORPA PRELIMINARY; PRT; 364 AA.
ID Q7W926 BORPA PRELIMINARY; PRT; 364 AA.
AC Q7W926 BORPA PRELIMINARY; PRT; 364 AA.
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Putative periplasmic solute-binding protein.
GN Name=smow; OrderedLocustNames=BP1948;
OS Bordetella parapertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcalligenaceae; Bordetella.
OX NCBI_TaxID=519;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=12822 / ATCC BAA-587;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebailia M., Preston A., Murphy L.D., Thomson N.R.,
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RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holtroyd S., Jagsels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrett B.G., Maskell D.J.,
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica."
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640428; CAB37248.1; -; Genomic DNA.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006311; Tat.
DR InterPro; IPR004682; TRAP_transpdcct.
DR Pfam; PF03480; SBP_bac_7; 1.
DR TIGRFAMs; TIGR01409; TAT_signal_seq; 1.
KW Complete proteome.
SQ SEQUENCE 364 AA; 39967 MW; 9700BC4608CF1D88 CRC64;

Query Match 70.0%; Score 42; DB 2; Length 364;
Best Local Similarity 77.8%; Pred. No. 38;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ATYYFFGLD 10
   :|||||:
Db 98 ASYYFFGLD 106

RESULT 8
Q7WKH1 BORBR PRELIMINARY; PRT; 364 AA.
ID Q7WKH1 BORBR PRELIMINARY; PRT; 364 AA.
AC Q7WKH1 BORBR PRELIMINARY; PRT; 364 AA.
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Putative periplasmic solute-binding protein.
GN Name=smow; OrderedLocustNames=BB2136;
OS Bordetella bronchiseptica (Alcalligenes bronchisepticus).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcalligenaceae; Bordetella.
OX NCBI_TaxID=518;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=RB50 / ATCC BAA-588;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebailia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Cherevach I.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holtroyd S., Jagsels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrett B.G., Maskell D.J.,
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica."
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640443; CAB32632.1; -; Genomic DNA.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006311; Tat.
DR InterPro; IPR004682; TRAP_transpdcct.
DR Pfam; PF03480; SBP_bac_7; 1.
DR TIGRFAMs; TIGR01409; TAT_signal_seq; 1.
KW Complete proteome.
SQ SEQUENCE 364 AA; 39997 MW; 8AB6672BA3BF09AD CRC64;

Query Match 70.0%; Score 42; DB 2; Length 364;
Best Local Similarity 77.8%; Pred. No. 38;
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Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 Qy 2 ATYYFGKD 10  
 DB 98 ASYYFGKD 106

# RESULT 9 Q4QA10 LEIMA

ID Q4QA10 LEIMA PRELIMINARY; PRT; 378 AA.  
 AC Q4QA10;  
 DT 13-SEP-2005 (TRENBLrel. 31, Created)  
 DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)  
 DE Hypothetical protein.  
 GN ORFNames=LmjF25\_0840;  
 OS Leishmania major.  
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.  
 NC NCB1\_TaxID=5664;  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=Friledlin;  
 RA Peacock C.S., Murphy L., Ivens A.C., Berriman M., Blackwell J.,  
 RA Smith D., Collins M., Foster N., Harris D., Oliver K., O'Neill S.,  
 RA Saunders D., Seeger K., Warren T., Rajandream M., and Barrell B.G.;  
 RA Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; CTO05264; CAJ04989.1; -; Genomic\_DNA.  
 KW Hypothetical protein.  
 SQ SEQUENCE 378 AA; 41605 MW; 983B87C7C1F04839 CRC64;

Query Match 70.0%; Score 42; DB 2; Length 378;  
 Best Local Similarity 100.0%; Pred. No. 40;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTYTFFGL 9  
 DB 112 TTYTFFGL 118

## RESULT 10

ID 089NT9 BRAJA PRELIMINARY; PRT; 362 AA.  
 AC 089NT9;  
 DT 01-JUN-2003 (TRENBLrel. 24, Created)  
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE Periplasmic mannitol-binding protein.  
 GN OrderedLocustNames=blc3745;  
 OS Bradyrhizobium japonicum.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Bradyrhizobiaceae; Bradyrhizobium.  
 NC NCB1\_TaxID=375;  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=USDA 110;  
 RC MEDLINE=2248498; PubMed=12597275;  
 RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,  
 RA Sasamoto S., Watanabe A., Ideasa K., Iriyuchi M., Kawashima K.,  
 RA Kohara M., Matsunoto M., Shimo S., Teunouka H., Wada T., Yamada M.,  
 RA Tabata S.;  
 RA "Complete genomic sequence of nitrogen-fixing symbiotic bacterium  
 RT Bradyrhizobium japonicum USDA110."  
 RL DNA Res. 9:189-197(2002).  
 DR EMBL; BA000040; BAC49010.1; -; Genomic DNA.  
 DR GO; GO:0030288; C:periplasmic space (Genus Gram-negative Bact. .; IBA.  
 DR GO; GO:0006810; P:transport; IBA.  
 DR InterPro; IPR006311; Tat.  
 DR InterPro; IPR004682; TRAP\_transpctcP.  
 DR Pfam; PF03480; SBP\_bac\_7; 1.  
 DR TIGRfam; TIGR01405; TAT\_signal\_seq; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 362 AA; 42090 MW; 23C64980A9F98BD CRC64;

Query Match 70.0%; Score 42; DB 2; Length 382;  
 Best Local Similarity 77.8%; Pred. No. 40;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 Qy 2 ATYYFGKD 10  
 DB 117 ASYYFGKD 125

# RESULT 11

ID 07AN07 NANEQ PRELIMINARY; PRT; 594 AA.  
 AC 07AN07;  
 DT 05-JUL-2004 (TRENBLrel. 27, Created)  
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)  
 DE NEQ353.  
 GN OrderedLocustNames=NEQ353;  
 OS Nanoarchaeum equitans.  
 OC Archaea; Nanoarchaeota; Nanoarchaeum.  
 NC NCB1\_TaxID=160232;  
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RP STRAIN=K14-M.  
 RC PubMed=14566062; DOI=10.1073/pnas.1735403100;  
 RX Waters E., Hohn M.U., Abel I., Graham D.E., Adams M.D., Barnstead M.,  
 RA Beeson K.Y., Bibbs L., Bolanos R., Keller M., Kretz K., Lin X.,  
 RA Machur E., Ni J., Podar K., Richardson T., Sutton G.G., Simon M.,  
 RA Soell D., Stetter K.O., Short J.M., Noordermeer M.;  
 RA "The genome of Nanoarchaeum equitans: insights into early archaeal  
 RT evolution and derived parasitism."  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:12984-12988(2003).  
 DR EMBL; AE017199; AAR39202.1; -; Genomic\_DNA.  
 KW Complete proteome.  
 SQ SEQUENCE 594 AA; 69673 MW; F2B60ACF00CD9F4 CRC64;

Query Match 70.0%; Score 42; DB 2; Length 594;  
 Best Local Similarity 54.5%; Pred. No. 62;  
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LATYYFGADV 11  
 DB 569 LSRHYFQVDI 579

## RESULT 12

ID 06GMV2 HUMAN PRELIMINARY; PRT; 606 AA.  
 AC 06GMV2;  
 DT 05-JUL-2004 (TRENBLrel. 27, Created)  
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)  
 DE IGHM protein.  
 GN Name=IGHM.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
 OC Homo.  
 NC NCB1\_TaxID=9606;  
 RN NUCLEOTIDE SEQUENCE.  
 RP TISSUE=Primary B-Cells;  
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Boeck S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,

```
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.W.,
RA Rutherford Y.S.N., Krzywinski M.I., Skalska U., Smallus D.B.,
RA Schercher A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RU
RN
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC073758; AAH73758.1; -, mRNA.
DR SMK, Q6GM12; 20-256.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; CI-bee; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN.3.
SO SEQUENCE 606 AA; 66185 MW; B6B3B85114E4C55 CRC64;

Query Match 70.0%; Score 42; DB 2; Length 606;
Best Local Similarity 75.0%; Pred. No. 63;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 4 YYYFGLDV 11
Db 135 YYYFGMDV 142

RESULT 13
O96X97_SULTO PRELIMINARY; PRT; 1062 AA.
AC O96X97;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 1062aa long hypothetical thermopain.
GN OrderedLocustNames=ST2615;
OS Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=111955;
RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JCM 10545 / ?;
RX MEDLINE=21456155; PubMed=11572479;
RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Anka A., Kosugi H., Hosoymama A., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Kato Y.,
RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagita M., Nishimura M., Yamagishi A.,
RA Oshima T., Kikuchi H.;
RT "Complete genome sequence of an aerobic thermophilic
RT Crenarchaeon, Sulfolobus tokodaii strain?";
RL DNA Res. 8:123-140(2001).
DR EMBL, BA000023; BAB67731.1; -, Genomic_DNA.
DR InterPro; IPR007981; Peptidase_A5.
DR Pfam; PF05317; Thermopain; 1.
KV Complete proteome; Hypothetical protein.
SQ SEQUENCE 1062 AA; 118024 MW; 16674ED60A040B4 CRC64;

Query Match 70.0%; Score 42; DB 2; Length 1062;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 TYYFGL 9
Db 623 TYYFGL 629

RESULT 14
O4FWX4_LEIMA PRELIMINARY; PRT; 3212 AA.
AC O4FWX4;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=LMJ_1075;
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Friedlin;
RX PubMed=16020728; DOI=10.1126/science.1112680;
RA Ivens A.C., Peacock C.S., Worthey E.A., Murphy L., Aggarwal G.,
RA Berriman M., Siak E., Rajandream M.A., Adlem E., Aert R., Anupama A.,
RA Apostolou Z., Attipoe P., Baason N., Bauser C., Beck A., Beverley S.M.,
RA Bianchetti G., Borzym K., Bothe G., Brusch C.V., Collins M.,
RA Cadag E., Clarioti L., Clayton C., Coulson R.M., Cronin A., Cruz A.K.,
RA Davies R.M., De Gaudenzi J., Dobson D.E., Duesterhoeft A.,
RA Fazelina G., Foster N., Frasch A.C., Fraser A., Fuchs M., Gabel C.,
RA Goble A., Goffeau A., Harris D., Hertz-Fowler C., Hilbert H., Horn D.,
RA Huang Y., Klages S., Knights A., Kube M., Larke N., Livyin L.,
RA Lord A., Louie T., Marra M., Masny D., Matthews K., Michael S.,
RA Mortam J.C., Miller-Aner S., Munden H., Nelson S., Norbertczak H.,
RA Oliver K., O'Neil S., Pencony M., Pohl T.M., Price C., Furnelle B.,
RA Quail M.A., Rabinowitsch E., Reinhardt R., Rieger M., Rinta J.,
RA Robben J., Robertson L., Ruiz J.C., Rutter S., Saunders D.,
RA Schaefer M., Schein J., Schwartz D.C., Seeger K., Seyler A., Sharp S.,
RA Shin H., Sivam D., Squares R., Squares S., Tosato V., Vogt C.,
RA Voicakeert G., Wambut R., Warren T., Wedler H., Woodward J., Zhou S.,
RA Zimmermann W., Smith D.F., Blackwell J.M., Stuart K.D., Barrell B.,
RA Myler P.J.;
RT "The genome of the Kinetoplastid Parasite, Leishmania major.";
RL Science 309:436-442(2005).
DR EMBL, CP000081; AA214369.1; -, Genomic_DNA.
KV Hypothetical protein.
SQ SEQUENCE 3212 AA; 342958 MW; E26EA125060F8A6B CRC64;

Query Match 70.0%; Score 42; DB 2; Length 3212;
Best Local Similarity 70.0%; Pred. No. 3.3e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 LATYYFGLD 10
Db 164 LAGYYFGVE 173

RESULT 15
O6A021_DESPS PRELIMINARY; PRT; 716 AA.
AC O6A021;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Related to mercuric reductase.
GN OrderedLocustNames=DP0504;
OS Desulfocala psychrophila.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacterales;
OC Desulfobacterales; Desulfocala.
OX NCBI_TaxID=84980;
RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=LSv54 / DSM 12343;
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RX PubMed15305914, DOI:10.1111/j.1462-2920.2004.00665.x;
RA Rabus R., Ruepp A., Frickey T., Rattei T., Partmann B., Stark M.,
RA Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K.,
RA Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R.,
RA Klank H.-P.;
RT "The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium
RT from permanently cold Arctic sediments."
RL Environ. Microbiol. 6:887-902(2004).
DR EMBL/CRS22870; CAG35233.1; -; Genomic_DNA.
DR GO:GO:0005737; C:cytoplasm; IEA.
DR GO:GO:0015036; F:disulfide oxidoreductase activity; IEA.
DR GO:GO:0050660; F:FAD binding; IEA.
DR GO:GO:0006118; P:electron transport; IEA.
DR InterPro:IPR001327; FAD_pyr_redox.
DR InterPro:IPR000815; Hg_reductase.
DR InterPro:IPR006162; Ppatne.S.
DR InterPro:IPR001100; Pyr_redox.
DR InterPro:IPR004099; Pyr_redox_dim.
DR Pfam:PF00070; Pyr_redox; 2.
DR Pfam:PF02852; Pyr_redox_dim; 1.
DR PRINTS; PR00368; FADPNR.
DR PRINTS; PR00945; HGRDTASE.
DR PRINTS; PR00411; PNDRDTASEI.
DR PRODOM; PD000139; FAD_pyr_redox; 1.
DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN_1.
DR PROSITE; PS00076; PYRIDINE_REDOX_1; 1.
KW Complete proteome.
SQ SEQUENCE 716 AA; 78725 MW; 68EFC0600DE44094 CRC64;

Query Match          68.3%; Score 41; DB 2; Length 716;
Best Local Similarity 60.0%; Pred.No. 1.1e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
OY 1 LATYYFGSD 10
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DB 14 VSATYFGSD 23

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 Job time : 104.375 secs

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OM protein - protein search, using sw model

Run on: December 4, 2005, 03:59:51 ; Search time 23.6042 Seconds  
(without alignments)  
38.528 Million cell. updates/sec

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Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfill1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	71.7	33	1 US-08-053-131-78	Sequence 78, App1
2	43	71.7	33	1 US-08-645-641-78	Sequence 78, App1
3	43	71.7	33	1 US-07-853-408B-78	Sequence 78, App1
4	43	71.7	33	1 US-08-096-762-78	Sequence 78, App1
5	43	71.7	33	1 US-08-308-865-78	Sequence 78, App1
6	43	71.7	33	1 US-09-042-353-275	Sequence 275, App
7	43	71.7	33	2 US-08-758-417A-123	Sequence 123, App1
8	43	71.7	33	4 PCT-US92-10983-78	Sequence 78, App1
9	43	71.7	125	2 US-09-840-459-84	Sequence 84, App1
10	43	71.7	125	2 US-09-497-625A-84	Sequence 84, App1
11	42	70.0	29	1 US-08-053-131-73	Sequence 73, App1
12	42	70.0	29	1 US-08-645-641-73	Sequence 73, App1
13	42	70.0	29	1 US-07-853-408B-73	Sequence 73, App1
14	42	70.0	29	1 US-08-096-762-73	Sequence 73, App1
15	42	70.0	29	1 US-08-308-865-73	Sequence 73, App1
16	42	70.0	29	2 US-09-042-353-270	Sequence 270, App
17	42	70.0	29	2 US-08-758-417A-118	Sequence 118, App
18	42	70.0	29	4 PCT-US92-10983-73	Sequence 73, App1
19	42	70.0	31	1 US-08-053-131-83	Sequence 83, App1
20	42	70.0	31	1 US-08-645-641-83	Sequence 83, App1
21	42	70.0	31	1 US-07-853-408B-83	Sequence 83, App1
22	42	70.0	31	1 US-08-096-762-83	Sequence 83, App1
23	42	70.0	31	1 US-08-308-865-83	Sequence 83, App1
24	42	70.0	31	1 US-09-042-353-280	Sequence 280, App
25	42	70.0	31	2 US-08-758-417A-128	Sequence 128, App
26	42	70.0	31	4 PCT-US92-10983-83	Sequence 83, App1
27	42	70.0	36	1 US-08-053-131-84	Sequence 84, App1

28	42	70.0	36	1 US-08-645-641-84	Sequence 84, App1
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30	42	70.0	36	1 US-08-096-762-84	Sequence 84, App1
31	42	70.0	36	1 US-08-308-865-84	Sequence 84, App1
32	42	70.0	36	2 US-09-042-353-281	Sequence 281, App
33	42	70.0	36	2 US-08-758-417A-129	Sequence 129, App
34	42	70.0	36	4 PCT-US92-10983-84	Sequence 84, App1
35	42	70.0	119	2 US-09-840-459-88	Sequence 88, App1
36	42	70.0	119	2 US-09-497-625A-88	Sequence 88, App1
37	42	70.0	128	2 US-09-840-459-77	Sequence 77, App1
38	42	70.0	128	2 US-09-840-459-79	Sequence 79, App1
39	42	70.0	128	2 US-09-497-625A-77	Sequence 77, App1
40	42	70.0	128	2 US-09-497-625A-79	Sequence 79, App1
41	42	70.0	167	2 US-09-472-087-80	Sequence 80, App1
42	42	70.0	236	2 US-09-456-090A-64	Sequence 64, App1
43	42	70.0	236	2 US-09-456-090A-104	Sequence 104, App
44	42	70.0	236	2 US-09-453-234-64	Sequence 64, App1
45	42	70.0	236	2 US-09-453-234-104	Sequence 104, App

#### ALIGNMENTS

RESULT 1  
US-08-053-131-78  
; Sequence 78, Application US/08053131  
; Patent No. 5661016  
; GENERAL INFORMATION:  
; APPLICANT: Lomborg, Nila  
; APPLICANT: Kay, Robert M.  
; TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for  
; TITLE OF INVENTION: Producing Heterologous Antibodies  
; NUMBER OF SEQUENCES: 197  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: One Market Plaza, Stewart Tower, Suite 200  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/053,131  
; FILING DATE: 26-Apr-1993  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/990,860  
; FILING DATE: 16-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/810,279  
; FILING DATE: 17-DEC-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/853,408  
; FILING DATE: 18-MAR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 14643-9-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 78:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 33 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-053-131-78

Query Match 71.7% Score 43; DB 1; Length 33;  
Best Local Similarity 66.7%; Pred. No. 1.6;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTYFGLDV 11  
:||||:|  
Db 10 SYYYGMDV 18

## RESULT 2

US-08-645-641-78  
; Sequence 78, Application US/08645641  
; Patent No. 5719032  
; GENERAL INFORMATION:  
; APPLICANT: Lomborg, Nils  
; APPLICANT: Kay, Robert M.  
; TITLE OF INVENTION: Transgenic No. 5719032-Human Animals for  
; TITLE OF INVENTION: Producing Heterologous Antibodies  
; NUMBER OF SEQUENCES: 150  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: William M. Smith  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/645,641  
; FILING DATE: 20-MAY-1996  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/904,068  
; FILING DATE: 23-JUN-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 14643-000913  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 78:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 33 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-645-641-78

Query Match 71.7% Score 43; DB 1; Length 33;  
Best Local Similarity 66.7%; Pred. No. 1.6;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTYFGLDV 11  
:||||:|  
Db 10 SYYYGMDV 18

## RESULT 3

US-07-853-408B-78  
; Sequence 78, Application US/07853408B  
; Patent No. 5789650  
; GENERAL INFORMATION:  
; APPLICANT: Lomborg, Nils  
; APPLICANT: Kay, Robert M.  
; TITLE OF INVENTION: Transgenic No. 5789650-Human Animals for  
; TITLE OF INVENTION: Producing Heterologous Antibodies

NUMBER OF SEQUENCES: 150  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: William M. Smith  
; STREET: One Market Plaza, Stewart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/853,408B  
; FILING DATE: 19920318  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 14643-9  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 78:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 33 amino acids  
; TYPE: AMINO ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-07-853-408B-78

Query Match 71.7% Score 43; DB 1; Length 33;  
Best Local Similarity 66.7%; Pred. No. 1.6;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTYFGLDV 11  
:||||:|  
Db 10 SYYYGMDV 18

## RESULT 4

US-08-096-762-78  
; Sequence 78, Application US/08096762  
; Patent No. 5814318  
; GENERAL INFORMATION:  
; APPLICANT: Lomborg, Nils  
; APPLICANT: Kay, Robert M.  
; TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for  
; TITLE OF INVENTION: Producing Heterologous Antibodies  
; NUMBER OF SEQUENCES: 210  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Townsend and Townsend Kourile and Crew  
; STREET: One Market Plaza, Stewart Tower, Suite 200  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/096,762  
; FILING DATE: 22-JUL-1993  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/053,131  
; FILING DATE: 26-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/990,860

FILED DATE: 16-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/904,068  
FILING DATE: 23-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/853,408  
FILING DATE: 18-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/810,279  
FILING DATE: 17-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 14643-9-4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 78:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-096-762-78

Query Match 71.7%; Score 43; DB 1; Length 33;  
Best Local Similarity 66.7%; Pred. No. 1.6;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTYTFFGLDV 11  
:||||:|  
Db 10 SYTYGMDV 18

RESULT 5  
US-08-308-865-78  
Sequence 78, Application US/08308865  
Patent No. 5877397  
GENERAL INFORMATION:  
APPLICANT: Lomborg, Nils  
TITLE OF INVENTION: Transgenic No. 5877397-Human Animals for  
TITLE OF INVENTION: Producing Heterologous Antibodies  
NUMBER OF SEQUENCES: 150  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: William M. Smith  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/308,865  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/145,707  
FILING DATE:  
APPLICATION NUMBER: US 07/904,068  
FILING DATE: 23-JUN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 14643-9-1-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 78:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-308-865-78

Query Match 71.7%; Score 43; DB 1; Length 33;  
Best Local Similarity 66.7%; Pred. No. 1.6;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTYTFFGLDV 11  
:||||:|  
Db 10 SYTYGMDV 18

RESULT 6  
US-09-042-353-275  
Sequence 275, Application US/09042353  
Patent No. 6255458  
GENERAL INFORMATION:  
APPLICANT: Lomborg, Nils  
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for  
TITLE OF INVENTION: Producing Heterologous Antibodies  
NUMBER OF SEQUENCES: 421  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/042,353  
FILING DATE: 13-MAR-1998  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/810,279  
FILING DATE: 17-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/853,408  
FILING DATE: 18-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/904,068  
FILING DATE: 23-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/990,860  
FILING DATE: 16-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/053,131  
FILING DATE: 26-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/096,762  
FILING DATE: 22-JUL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/155,301  
FILING DATE: 18-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/161,739  
FILING DATE: 03-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/165,699  
FILING DATE: 10-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/209,741

FILED DATE: 09-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/352,322  
FILING DATE: 07-DEC-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/544,404  
FILING DATE: 10-OCT-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/728,463  
FILING DATE: 10-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: MO PCT/US96/16433  
FILING DATE: 10-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/758,417  
FILING DATE: 02-DEC-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: MO PCT/US97/21803  
FILING DATE: 01-DEC-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 014643-009040US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 275:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-042-353-275

Query Match 71.7%; Score 43; DB 2; Length 33;  
Best Local Similarity 66.7%; Pred. No. 1.6;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 3 TTYVFGLDV 11  
:||||:|  
DB 10 SYYYGMDV 18

RESULT 7  
US-08-758-417A-123  
Sequence 123, Application US/08758417A  
GENERAL INFORMATION:  
APPLICANT: Lomborg, Nils  
Kay, Robert M.  
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for  
Producing Heterologous Antibodies  
NUMBER OF SEQUENCES: 417  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/758,417A  
FILING DATE: 02-DEC-1996  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/728,463  
FILING DATE: 10-OCT-1996

APPLICATION NUMBER: US 08/544,404  
FILING DATE: 10-OCT-1995  
APPLICATION NUMBER: US 08/352,322  
FILING DATE: 07-DEC-1994  
APPLICATION NUMBER: US 08/209,741  
FILING DATE: 09-MAR-1994  
APPLICATION NUMBER: US 08/165,699  
FILING DATE: 10-DEC-1993  
APPLICATION NUMBER: US 08/161,739  
FILING DATE: 03-DEC-1993  
APPLICATION NUMBER: US 08/155,301  
FILING DATE: 18-NOV-1993  
APPLICATION NUMBER: US 08/096,762  
FILING DATE: 22-JUL-1993  
APPLICATION NUMBER: US 08/053,131  
FILING DATE: 26-APR-1993  
APPLICATION NUMBER: US 07/990,860  
FILING DATE: 16-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Seratini, Andrew T.  
REGISTRATION NUMBER: 41,303  
REFERENCE/DOCKET NUMBER: 014643-009030US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 123:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 123:  
US-08-758-417A-123

Query Match 71.7%; Score 43; DB 2; Length 33;  
Best Local Similarity 66.7%; Pred. No. 1.6;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 3 TTYVFGLDV 11  
:||||:|  
DB 10 SYYYGMDV 18

RESULT 8  
PCT-US92-10983-78  
Sequence 78, Application PC/TVS9210983  
GENERAL INFORMATION:  
APPLICANT: Lomborg, Nils  
Kay, Robert M.  
TITLE OF INVENTION: Transgenic Non-Human Animals for  
Producing Heterologous Antibodies  
NUMBER OF SEQUENCES: 152  
CORRESPONDENCE ADDRESS:  
ADDRESSER: William M. Smith  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10983  
FILING DATE: 19921217  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 14643-9-2



TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 78:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US92-10983-78

Query Match 71.7%; Score 43; DB 4; Length 33;  
Best Local Similarity 66.7%; Pred. No. 1.6;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTYTGGDV 11  
Db 10 SYYYGMDV 18

RESULT 9  
US-09-840-459-84  
Sequence 84, Application US/09840459  
Patent No. 6696550  
GENERAL INFORMATION:  
APPLICANT: Larosa, Gregory J.  
APPLICANT: Horvath, Christopher  
APPLICANT: Newman, Walter  
APPLICANT: Jones, S. Tarran  
APPLICANT: O'Brien, Siobhan H.  
APPLICANT: O'Keefe, Theresa  
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
TITLE OF INVENTION: METHODS OF USE THEREFOR  
FILE REFERENCE: 1855.1052-012  
CURRENT APPLICATION NUMBER: US/09/840,459  
PRIOR FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: PCT/US01/03537  
PRIOR FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: 09/497,625  
PRIOR FILING DATE: 2000-02-03  
PRIOR APPLICATION NUMBER: 09/359,193  
PRIOR FILING DATE: 1999-07-22  
PRIOR APPLICATION NUMBER: 09/121,781  
PRIOR FILING DATE: 1998-07-23  
NUMBER OF SEQ ID NOS: 107  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 84  
LENGTH: 125  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-840-459-84

Query Match 71.7%; Score 43; DB 2; Length 125;  
Best Local Similarity 66.7%; Pred. No. 6.4;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTYTGGDV 11  
Db 106 SYYYGMDV 114

RESULT 10  
US-09-497-625A-84  
Sequence 84, Application US/09497625A  
Patent No. 6727349  
GENERAL INFORMATION:  
APPLICANT: Larosa, Gregory J.  
APPLICANT: Horvath, Christopher  
APPLICANT: Newman, Walter  
APPLICANT: Jones, S. Tarran  
APPLICANT: O'Brien, Siobhan H.  
APPLICANT: O'Keefe, Theresa

TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
TITLE OF INVENTION: METHODS OF USE THEREFOR  
FILE REFERENCE: 1855.1052-004  
CURRENT APPLICATION NUMBER: US/09/497,625A  
CURRENT FILING DATE: 2000-02-03  
PRIOR APPLICATION NUMBER: 09/359,193  
PRIOR FILING DATE: 1999-07-22  
PRIOR APPLICATION NUMBER: 09/121,781  
PRIOR FILING DATE: 1998-07-23  
NUMBER OF SEQ ID NOS: 106  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 84  
LENGTH: 125  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-497-625A-84

Query Match 71.7%; Score 43; DB 2; Length 125;  
Best Local Similarity 66.7%; Pred. No. 6.4;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTYTGGDV 11  
Db 106 SYYYGMDV 114

RESULT 11  
US-08-053-131-73  
Sequence 73, Application US/08053131  
Patent No. 5661016  
GENERAL INFORMATION:  
APPLICANT: Lomborg, Nils  
APPLICANT: Kay, Robert M.  
TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for  
TITLE OF INVENTION: Producing Heterologous Antibodies  
NUMBER OF SEQUENCES: 197  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Stewart Tower, Suite 200  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/053,131  
FILING DATE: 26-APR-1993  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/990,860  
FILING DATE: 16-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/810,279  
FILING DATE: 17-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/853,408  
FILING DATE: 18-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 14643-9-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 73:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 29 amino acids  
TYPE: amino acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-053-131-73

Query Match 70.0%; Score 42; DB 1; Length 29;  
Best Local Similarity 75.0%; Pred. No. 2.1;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11  
|||:|:  
DB 7 YYYGMDV 14

RESULT 12  
US-08-645-641-73  
Sequence 73, Application US/08645641  
Patent No. 5719032  
GENERAL INFORMATION:  
APPLICANT: Lonberg, Nils  
APPLICANT: Kay, Robert M.  
TITLE OF INVENTION: Transgenic No. 5719032-Human Animals for  
TITLE OF INVENTION: Producing Heterologous Antibodies  
NUMBER OF SEQUENCES: 150  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: William M. Smith  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/645,641  
FILING DATE: 20-May-1996  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/904,068  
FILING DATE: 23-JUN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 14643-000913  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 73:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 29 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-645-641-73

Query Match 70.0%; Score 42; DB 1; Length 29;  
Best Local Similarity 75.0%; Pred. No. 2.1;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11  
|||:|:  
DB 7 YYYGMDV 14

RESULT 13  
US-07-853-408B-73  
Sequence 73, Application US/07853408B  
Patent No. 5789650  
GENERAL INFORMATION:  
APPLICANT: Lonberg, Nils

APPLICANT: Kay, Robert M.  
TITLE OF INVENTION: Transgenic No. 5789650-Human Animals for  
TITLE OF INVENTION: Producing Heterologous Antibodies  
NUMBER OF SEQUENCES: 150  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: William M. Smith  
STREET: One Market Plaza, Stewart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/853,408B  
FILING DATE: 19920318  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 14643-9  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 73:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 29 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-853-408B-73

Query Match 70.0%; Score 42; DB 1; Length 29;  
Best Local Similarity 75.0%; Pred. No. 2.1;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11  
|||:|:  
DB 7 YYYGMDV 14

RESULT 14  
US-08-096-762-73  
Sequence 73, Application US/08096762  
Patent No. 5814318  
GENERAL INFORMATION:  
APPLICANT: Lonberg, Nils  
APPLICANT: Kay, Robert M.  
TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for  
TITLE OF INVENTION: Producing Heterologous Antibodies  
NUMBER OF SEQUENCES: 210  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourile and Crew  
STREET: One Market Plaza, Stewart Tower, Suite 200  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/096,762  
FILING DATE: 22-JUL-1993  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/053,131

FILED DATE: 26-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/990,860  
FILING DATE: 16-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/904,068  
FILING DATE: 23-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/853,408  
FILING DATE: 18-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/810,279  
FILING DATE: 17-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 14643-9-4  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 73:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 29 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-096-762-73

Query Match 70.0%; Score 42; DB 1; Length 29;  
Best Local Similarity 75.0%; Pred. No. 2.1;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYFGLDV 11  
|||:|:  
Db 7 YYYGMDV 14

RESULT 15  
US-08-308-865-73  
Sequence 73, Application US/08308865  
Patent No. 5877397  
GENERAL INFORMATION:  
APPLICANT: Lonberg, Nils  
TITLE OF INVENTION: Transgenic No. 5877397-Human Animals for  
TITLE OF INVENTION: Producing Heterologous Antibodies  
NUMBER OF SEQUENCES: 150  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: William M. Smith  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/308,865  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/145,707  
FILING DATE:  
APPLICATION NUMBER: US 07/904,068  
FILING DATE: 23-JUN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 14643-9-1-1

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 73:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 29 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-308-865-73

Query Match 70.0%; Score 42; DB 1; Length 29;  
Best Local Similarity 75.0%; Pred. No. 2.1;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYFGLDV 11  
|||:|:  
Db 7 YYYGMDV 14

Search completed: December 4, 2005, 04:09:43  
Job time: 24.6042 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:07:28 ; Search time 78.833 Seconds  
(without alignments)  
58.302 Million cell updates/sec

Title: US-10-632-706-127  
Perfect score: 60  
Sequence: 1 LATYFFGLDV 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA Main:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	100.0	11	4	US-10-632-706-126 Sequence 126, App
2	60	100.0	11	4	US-10-632-706-127 Sequence 127, App
3	48	80.0	122	6	US-11-031-485-116 Sequence 116, App
4	47	78.3	129	4	US-10-364-743-101 Sequence 101, App
5	47	78.3	129	5	US-10-452-593-101 Sequence 101, App
6	47	78.3	134	4	US-10-364-743-15 Sequence 15, App1
7	47	78.3	134	5	US-10-452-593-15 Sequence 15, App1
8	47	78.3	468	6	US-11-031-485-56 Sequence 56, App1
9	47	78.3	469	6	US-11-031-485-18 Sequence 18, App1
10	46	76.7	13	4	US-10-632-706-114 Sequence 114, App
11	46	76.7	21	5	US-10-783-311-141 Sequence 141, App
12	46	76.7	140	5	US-10-783-311-115 Sequence 135, App
13	45	75.0	16	5	US-10-783-311-277 Sequence 135, App
14	45	75.0	21	4	US-09-880-748-3068 Sequence 3068, App
15	45	75.0	21	4	US-10-293-418-3068 Sequence 3068, App
16	45	75.0	117	6	US-11-009-731-47 Sequence 47, App1
17	45	75.0	135	5	US-10-783-311-271 Sequence 271, App
18	45	75.0	256	5	US-09-880-748-1600 Sequence 1600, App
19	45	75.0	256	4	US-10-293-418-1600 Sequence 1600, App
20	44	73.3	16	3	US-09-880-748-2129 Sequence 2129, App
21	44	73.3	16	4	US-10-293-418-2129 Sequence 2129, App
22	44	73.3	17	3	US-09-880-748-2876 Sequence 2876, App
23	44	73.3	17	4	US-10-293-418-2876 Sequence 2876, App
24	44	73.3	18	5	US-10-984-960A-8 Sequence 8, App1
25	44	73.3	117	4	US-10-041-860-206 Sequence 206, App
26	44	73.3	123	4	US-10-309-762-18 Sequence 18, App1
27	44	73.3	123	4	US-10-309-762-19 Sequence 19, App1

28	44	73.3	124	4	US-10-292-088-106 Sequence 106, App
29	44	73.3	127	4	US-10-041-860-31 Sequence 31, App1
30	44	73.3	127	4	US-10-041-860-243 Sequence 243, App
31	44	73.3	127	4	US-10-041-860-325 Sequence 325, App
32	44	73.3	127	4	US-10-665-383-92 Sequence 42, App1
33	44	73.3	127	4	US-10-466-242-53 Sequence 53, App1
34	44	73.3	127	5	US-10-984-960A-2 Sequence 2, App1
35	44	73.3	129	4	US-10-292-088-10 Sequence 10, App1
36	44	73.3	134	4	US-10-364-743-16 Sequence 109, App
37	44	73.3	134	4	US-10-364-743-109 Sequence 109, App
38	44	73.3	134	4	US-10-364-743-110 Sequence 110, App
39	44	73.3	134	5	US-10-452-593-16 Sequence 16, App1
40	44	73.3	134	5	US-10-452-593-109 Sequence 109, App
41	44	73.3	134	5	US-10-452-593-110 Sequence 110, App
42	44	73.3	145	5	US-10-644-377-146 Sequence 146, App
43	44	73.3	157	5	US-10-473-287-34 Sequence 34, App1
44	44	73.3	157	5	US-10-473-287-63 Sequence 63, App1
45	44	73.3	249	5	US-10-935-290-61 Sequence 61, App1

## ALIGNMENTS

```
RESULT 1
US-10-632-706-126
; Sequence 126, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: AMERSORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 126
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-126
Query Match 100.0%; Score 60; DB 4; Length 11,
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 LATYFFGLDV 11
Db 1 LATYFFGLDV 11
RESULT 2
US-10-632-706-127
; Sequence 127, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; APPLICANT: AMERSORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
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; PRIOR FILING DATE: 1998-08-31  
 ; NUMBER OF SEQ ID NOS: 278  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 127  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Artificial  
 ; FEATURE:  
 ; OTHER INFORMATION: single chain antibody fragment  
 US-10-632-706-127

Query Match 100.0%; Score 60; DB 4; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.0027;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LATYFFGLDV 11  
 |||||  
 DB 1 LATYFFGLDV 11

RESULT 3  
 US-11-031-485-116  
 ; Sequence 116, Application US/11031485  
 ; Publication No. US20050232917A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: PULLEN, NICHOLAS  
 ; APPLICANT: MOLLOY, ELIZABETH  
 ; APPLICANT: KELLERMAN, SIRID-AIMEE  
 ; APPLICANT: GREEN, LARRY L.  
 ; APPLICANT: HAAK-FRENSCH, MARY  
 ; TITLE OF INVENTION: ANTIBODIES TO MADCAM  
 ; FILE REFERENCE: ABX-PF6  
 ; CURRENT APPLICATION NUMBER: US/11/031,485  
 ; PRIOR FILING DATE: 2005-01-07  
 ; PRIOR APPLICATION NUMBER: 60/535,490  
 ; PRIOR FILING DATE: 2004-01-09  
 ; NUMBER OF SEQ ID NOS: 147  
 ; SOFTWARE: PatentIn Ver. 3.3  
 ; SEQ ID NO 116  
 ; LENGTH: 122  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-11-031-485-116

Query Match 80.0%; Score 48; DB 6; Length 122;  
 Best Local Similarity 63.6%; Pred. No. 2.8;  
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LATYFFGLDV 11  
 :|||:|  
 DB 100 VVTTYGGMDV 110

RESULT 4  
 US-10-364-743-101  
 ; Sequence 101, Application US/10364743  
 ; Publication No. US20040009178A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bowdish, Katherine S.  
 ; APPLICANT: Frederickson, Shana  
 ; APPLICANT: Wild, Martha A.  
 ; APPLICANT: Maruyama, Yoshiaki  
 ; APPLICANT: No. US20040009178A1an, Mary Jean  
 ; TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE  
 ; FILE REFERENCE: 84 (1087-73)  
 ; CURRENT APPLICATION NUMBER: US/10/364,743  
 ; PRIOR FILING DATE: 2003-02-11  
 ; PRIOR APPLICATION NUMBER: US 60/428,807  
 ; PRIOR FILING DATE: 2002-11-25  
 ; NUMBER OF SEQ ID NOS: 118  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 101  
 ; LENGTH: 129

; TYPE: PRT  
 ; ORGANISM: human  
 US-10-364-743-101

Query Match 78.3%; Score 47; DB 4; Length 129;  
 Best Local Similarity 77.8%; Pred. No. 4.4;  
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYFFGLDV 11  
 ||||:|  
 DB 105 TTYTGGMDV 113

RESULT 5  
 US-10-452-593-101  
 ; Sequence 101, Application US/10452593  
 ; Publication No. US20040258699A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bowdish, Katherine S.  
 ; APPLICANT: Frederickson, Shana  
 ; APPLICANT: Maruyama, Yoshiaki  
 ; APPLICANT: Nolan, Mary Jean  
 ; TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE  
 ; FILE REFERENCE: 98 CIP (1087-73 CIP)  
 ; CURRENT APPLICATION NUMBER: US/10/452,593  
 ; PRIOR FILING DATE: 2003-06-02  
 ; PRIOR APPLICATION NUMBER: US 10/364,743  
 ; PRIOR FILING DATE: 2003-02-11  
 ; PRIOR APPLICATION NUMBER: US 60/356,086  
 ; PRIOR FILING DATE: 2002-02-11  
 ; PRIOR APPLICATION NUMBER: US 60/376,408  
 ; PRIOR FILING DATE: 2002-04-29  
 ; PRIOR APPLICATION NUMBER: US 60/428,807  
 ; PRIOR FILING DATE: 2002-11-25  
 ; NUMBER OF SEQ ID NOS: 118  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 101  
 ; LENGTH: 129  
 ; TYPE: PRT  
 ; ORGANISM: human  
 US-10-452-593-101

Query Match 78.3%; Score 47; DB 5; Length 129;  
 Best Local Similarity 77.8%; Pred. No. 4.4;  
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYFFGLDV 11  
 ||||:|  
 DB 105 TTYTGGMDV 113

RESULT 6  
 US-10-364-743-15  
 ; Sequence 15, Application US/10364743  
 ; Publication No. US20040009178A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bowdish, Katherine S.  
 ; APPLICANT: Frederickson, Shana  
 ; APPLICANT: Wild, Martha A.  
 ; APPLICANT: Maruyama, Yoshiaki  
 ; APPLICANT: No. US20040009178A1an, Mary Jean  
 ; TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE  
 ; FILE REFERENCE: 84 (1087-73)  
 ; CURRENT APPLICATION NUMBER: US/10/364,743  
 ; PRIOR FILING DATE: 2003-02-11  
 ; PRIOR APPLICATION NUMBER: US 60/428,807  
 ; PRIOR FILING DATE: 2002-11-25  
 ; NUMBER OF SEQ ID NOS: 118  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 15  
 ; LENGTH: 134  
 ; TYPE: PRT

ORGANISM: human  
US-10-364-743-15

Query Match 78.3%; Score 47; DB 4; Length 134;  
Best Local Similarity 77.8%; Pred. No. 4.5;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYTFFGLDV 11  
Db 110 TTYTFFGMDV 118

## RESULT 7

US-10-452-593-15  
Sequence 15, Application US/10452593  
Publication No. US20040258699A1  
GENERAL INFORMATION:  
APPLICANT: Bowdish, Katherine S.  
APPLICANT: Frederickson, Shana  
APPLICANT: Wild, Martha A.  
APPLICANT: Maruyama, Toshiaki  
APPLICANT: Nolan, Mary Jean  
TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE  
FILE REFERENCE: 98 CIP (1087-73 CIP)  
CURRENT APPLICATION NUMBER: US/10/452,593  
CURRENT FILING DATE: 2003-06-02  
PRIOR APPLICATION NUMBER: US 10/364,743  
PRIOR FILING DATE: 2003-02-11  
PRIOR APPLICATION NUMBER: US 60/356,086  
PRIOR FILING DATE: 2002-02-11  
PRIOR APPLICATION NUMBER: US 60/376,408  
PRIOR FILING DATE: 2002-04-29  
PRIOR APPLICATION NUMBER: US 60/428,807  
PRIOR FILING DATE: 2002-11-25  
NUMBER OF SEQ ID NOS: 118  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 15  
LENGTH: 134  
TYPE: PRT  
ORGANISM: human  
US-10-452-593-15

Query Match 78.3%; Score 47; DB 5; Length 134;  
Best Local Similarity 77.8%; Pred. No. 4.5;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYTFFGLDV 11  
Db 110 TTYTFFGMDV 118

## RESULT 8

US-11-031-485-56  
Sequence 56, Application US/11031485  
Publication No. US20050232917A1  
GENERAL INFORMATION:  
APPLICANT: PULLEN, NICHOLAS  
APPLICANT: MOLLOY, ELIZABETH  
APPLICANT: KELLERMANN, SIRID-AIMEE  
APPLICANT: GREEN, LARRY L.  
APPLICANT: HAAK-FREDSCHO, MARY  
TITLE OF INVENTION: ANTIBODIES TO MADCAM  
FILE REFERENCE: ABX-PF6  
CURRENT APPLICATION NUMBER: US/11/031,485  
CURRENT FILING DATE: 2005-01-07  
PRIOR APPLICATION NUMBER: 60/535,490  
PRIOR FILING DATE: 2004-01-09  
NUMBER OF SEQ ID NOS: 147  
SOFTWARE: PatentIn Ver. 3.3  
SEQ ID NO 56  
LENGTH: 468  
TYPE: PRT  
ORGANISM: Homo sapiens

US-11-031-485-56

Query Match 78.3%; Score 47; DB 6; Length 468;  
Best Local Similarity 77.8%; Pred. No. 16;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYTFFGLDV 11  
Db 123 TTYTFFGMDV 131

## RESULT 9

US-11-031-485-18  
Sequence 18, Application US/11031485  
Publication No. US20050232917A1  
GENERAL INFORMATION:  
APPLICANT: PULLEN, NICHOLAS  
APPLICANT: MOLLOY, ELIZABETH  
APPLICANT: KELLERMANN, SIRID-AIMEE  
APPLICANT: GREEN, LARRY L.  
APPLICANT: HAAK-FREDSCHO, MARY  
TITLE OF INVENTION: ANTIBODIES TO MADCAM  
FILE REFERENCE: ABX-PF6  
CURRENT APPLICATION NUMBER: US/11/031,485  
CURRENT FILING DATE: 2005-01-07  
PRIOR APPLICATION NUMBER: 60/535,490  
PRIOR FILING DATE: 2004-01-09  
NUMBER OF SEQ ID NOS: 147  
SOFTWARE: PatentIn Ver. 3.3  
SEQ ID NO 18  
LENGTH: 469  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-031-485-18

Query Match 78.3%; Score 47; DB 6; Length 469;  
Best Local Similarity 77.8%; Pred. No. 16;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYTFFGLDV 11  
Db 123 TTYTFFGMDV 131

## RESULT 10

US-10-632-706-114  
Sequence 114, Application US/10632706  
Publication No. US20040175385A1  
GENERAL INFORMATION:  
APPLICANT: MARKS, JAMES D.  
APPLICANT: AMERSDORFER, PETER  
TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM  
FILE REFERENCE: 407T-895120US  
CURRENT APPLICATION NUMBER: US/10/632,706  
CURRENT FILING DATE: 2003-08-01  
PRIOR APPLICATION NUMBER: US 60/400,721  
PRIOR FILING DATE: 2002-08-01  
PRIOR APPLICATION NUMBER: US 09/144,806  
PRIOR FILING DATE: 1998-08-31  
NUMBER OF SEQ ID NOS: 278  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 114  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Artificial  
FEATURES:  
OTHER INFORMATION: single chain antibody fragment  
US-10-632-706-114

Query Match 76.7%; Score 46; DB 4; Length 13;  
Best Local Similarity 70.0%; Pred. No. 0.64;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy      2 ATYYFGLDV 11
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Db      4 ANYYYGMDV 13

RESULT 11
US-10-783-311-141
; Sequence 141, Application US/10783311
; Publication No. US20050009136A1
; GENERAL INFORMATION:
; APPLICANT: Nixon, Andrew
; APPLICANT: Hogan, Shannon
; TITLE OF INVENTION: PAPP-A LIGANDS
; FILE REFERENCE: 10280-059001
; CURRENT APPLICATION NUMBER: US/10/783,311
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/448,515
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 394
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 141
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy Chain amino acid sequence
US-10-783-311-141

Query Match      76.7%; Score 46; DB 5; Length 21;
Best Local Similarity 63.6%; Pred. No. 1;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 LATYYFGLDV 11
      |||:|:|
Db      11 LGNTYYGMDV 21

RESULT 12
US-10-783-311-135
; Sequence 135, Application US/10783311
; Publication No. US20050009136A1
; GENERAL INFORMATION:
; APPLICANT: Nixon, Andrew
; APPLICANT: Hogan, Shannon
; TITLE OF INVENTION: PAPP-A LIGANDS
; FILE REFERENCE: 10280-059001
; CURRENT APPLICATION NUMBER: US/10/783,311
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/448,515
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 394
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 135
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy Chain amino acid sequence
US-10-783-311-135

Query Match      76.7%; Score 46; DB 5; Length 140;
Best Local Similarity 63.6%; Pred. No. 6.9;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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; Publication No. US20050009136A1
; GENERAL INFORMATION:
; APPLICANT: Nixon, Andrew
; APPLICANT: Hogan, Shannon
; TITLE OF INVENTION: PAPP-A LIGANDS
; FILE REFERENCE: 10280-059001
; CURRENT APPLICATION NUMBER: US/10/783,311
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/448,515
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 394
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 277
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy Chain amino acid sequence
US-10-783-311-277

Query Match      75.0%; Score 45; DB 5; Length 16;
Best Local Similarity 63.6%; Pred. No. 1.2;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      1 LATYYFGLDV 11
      |||:|:|
Db      6 VAGYYGMDV 16

RESULT 14
US-09-880-748-3068
; Sequence 3068, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17/276,248
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3068
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-3068

Query Match      75.0%; Score 45; DB 3; Length 21;
Best Local Similarity 70.0%; Pred. No. 1.5;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      2 ATYYFGLDV 11
      |||:|:|
Db      12 APYYGMDV 21

RESULT 15
US-10-293-418-3068
; Sequence 3068, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
```



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; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3068
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-3068

```

```

Query Match 75.0%; Score 45; DB 4; Length 21;
Best Local Similarity 70.0%; Pred. No. 1.5;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 2 ATYYFGADV 11
Db 12 APYYGMDV 21

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Search completed: December 4, 2005, 04:37:28  
 Job time : 80.8333 secs

**This Page Blank (uspo10)**

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:08:08 ; Search time 3.20833 Seconds  
(without alignments)  
16.417 Million cell updates/sec

Title: US-10-632-706-127  
Perfect score: 60  
Sequence: 1 LATYYFGLDV 11

Scoring table: BLASTSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

1: /cgn2\_6/ptodata/1/pubppaa/US09\_NEW\_PUB.pep:\*  
2: /cgn2\_6/ptodata/1/pubppaa/US06\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubppaa/US07\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubppaa/US08\_NEW\_PUB.pep:\*  
5: /cgn2\_6/ptodata/1/pubppaa/PTC\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/1/pubppaa/US10\_NEW\_PUB.pep:\*  
7: /cgn2\_6/ptodata/1/pubppaa/US11\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/1/pubppaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	75.0	21	US-11-054-515-3068	Sequence 3068, Ap
2	45	75.0	256	US-11-054-515-1600	Sequence 1600, Ap
3	44	73.3	16	US-11-054-515-2129	Sequence 2129, Ap
4	44	73.3	17	US-11-054-515-2876	Sequence 2876, Ap
5	44	73.3	252	US-11-054-515-1431	Sequence 1431, Ap
6	44	73.3	254	US-11-054-515-3	Sequence 3, Appl1
7	44	73.3	254	US-11-054-515-838	Sequence 838, App
8	44	73.3	254	US-11-054-515-870	Sequence 870, App
9	44	73.3	254	US-11-054-515-1287	Sequence 1287, App
10	44	73.3	254	US-11-054-515-1288	Sequence 1288, App
11	43	71.7	306	US-11-017-550-47	Sequence 47, Appl
12	42	70.0	13	US-11-054-515-3091	Sequence 3091, Ap
13	42	70.0	17	US-11-054-515-2817	Sequence 2817, Ap
14	42	70.0	19	US-11-054-515-2735	Sequence 2735, Ap
15	42	70.0	19	US-11-054-515-2899	Sequence 2899, Ap
16	42	70.0	19	US-11-054-515-2928	Sequence 2928, Ap
17	42	70.0	19	US-11-054-515-2935	Sequence 2935, Ap
18	42	70.0	19	US-11-054-515-3038	Sequence 3038, Ap
19	42	70.0	19	US-11-054-515-3052	Sequence 3052, Ap
20	42	70.0	19	US-11-054-515-3067	Sequence 3067, Ap
21	42	70.0	19	US-11-054-515-3087	Sequence 3087, Ap
22	42	70.0	19	US-11-054-515-3145	Sequence 3145, Ap
23	42	70.0	20	US-11-040-159-4	Sequence 4, Appl1
24	42	70.0	20	US-11-054-515-2767	Sequence 2767, Ap
25	42	70.0	20	US-11-054-515-3039	Sequence 3039, Ap

26	42	70.0	24	US-11-054-515-2926	Sequence 2926, Ap
27	42	70.0	124	US-11-144-248-8	Sequence 8, Appl1
28	42	70.0	125	US-11-144-248-16	Sequence 16, Appl1
29	42	70.0	174	US-11-144-248-4	Sequence 4, Appl1
30	42	70.0	248	US-11-054-515-1965	Sequence 1965, Ap
31	42	70.0	251	US-11-054-515-1974	Sequence 1974, Ap
32	42	70.0	251	US-11-054-515-1315	Sequence 1315, Ap
33	42	70.0	251	US-11-054-515-1740	Sequence 1740, Ap
34	42	70.0	251	US-11-054-515-1921	Sequence 1921, Ap
35	42	70.0	252	US-11-054-515-1731	Sequence 1731, Ap
36	42	70.0	253	US-11-054-515-934	Sequence 934, App
37	42	70.0	254	US-11-054-515-1001	Sequence 1001, Ap
38	42	70.0	254	US-11-054-515-1259	Sequence 1259, Ap
39	42	70.0	254	US-11-054-515-1334	Sequence 1334, Ap
40	42	70.0	254	US-11-054-515-1701	Sequence 1701, Ap
41	42	70.0	254	US-11-054-515-1735	Sequence 1735, Ap
42	42	70.0	254	US-11-054-515-1739	Sequence 1739, Ap
43	42	70.0	255	US-11-054-515-1271	Sequence 1271, Ap
44	42	70.0	255	US-11-054-515-1284	Sequence 1284, Ap
45	42	70.0	256	US-11-054-515-1209	Sequence 1209, Ap

## ALIGNMENTS

RESULT 1  
US-11-054-515-3068  
Sequence 3068, Application US/11054515  
Publication No. US2005025532A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: Antibodies that Immunoselectively Bind Blys  
FILE REFERENCE: PE523P3  
CURRENT APPLICATION NUMBER: US/11/054,515  
CURRENT FILING DATE: 2005-02-10  
PRIOR APPLICATION NUMBER: 60/543,296  
PRIOR FILING DATE: 2004-02-11  
PRIOR APPLICATION NUMBER: 60/580,347  
PRIOR FILING DATE: 2004-06-18  
PRIOR APPLICATION NUMBER: 10/293,418  
PRIOR FILING DATE: 2002-11-14  
PRIOR APPLICATION NUMBER: 60/331,469  
PRIOR FILING DATE: 2001-11-16  
PRIOR APPLICATION NUMBER: 60/340,817  
PRIOR FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: 09/880,748  
PRIOR FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/293,499  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: 60/277,379  
PRIOR FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/276,248  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/240,816  
PRIOR FILING DATE: 2000-10-17  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 3247  
SEQ ID NO 3068  
LENGTH: 21  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-054-515-3068  
Query Match 75.0%; Score 45; DB 7; Length 21;  
Best Local Similarity 70.0%; Pred. No. 0.017;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
Oy 2 ATYYFGLDV 11  
Db 12 APYYIGMDV 21  
RESULT 2

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US-11-054-515-1600
; Sequence 1600, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1600
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1600

Query Match          75.0%; Score 45; DB 7; Length 256;
Best Local Similarity 70.0%; Pred. No. 0.19;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      2 ATYYFGLDV 11
      |||:|:|
Db      110 APYYTGMDV 119

RESULT 3
US-11-054-515-2129
; Sequence 2129, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2876
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2876

Query Match          73.3%; Score 44; DB 7; Length 17;
Best Local Similarity 63.6%; Pred. No. 0.021;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2129
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2129

Query Match          73.3%; Score 44; DB 7; Length 16;
Best Local Similarity 63.6%; Pred. No. 0.021;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 LATYYFGLDV 11
      |||:|:|
Db      6 LTGYTYGMDV 16

RESULT 4
US-11-054-515-2876
; Sequence 2876, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2876
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2876

Query Match          73.3%; Score 44; DB 7; Length 17;
Best Local Similarity 63.6%; Pred. No. 0.021;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 LATYYFGLDV 11
      |||:|:|
Db      7 LTGYTYGMDV 17

RESULT 5
US-11-054-515-1431
; Sequence 1431, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
```

```
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: PF523P3
;; CURRENT APPLICATION NUMBER: US/11/054,515
;; CURRENT FILING DATE: 2005-02-10
;; PRIOR APPLICATION NUMBER: 60/543,296
;; PRIOR FILING DATE: 2004-02-11
;; PRIOR APPLICATION NUMBER: 60/580,347
;; PRIOR FILING DATE: 2004-06-18
;; PRIOR APPLICATION NUMBER: 10/293,418
;; PRIOR FILING DATE: 2002-11-14
;; PRIOR APPLICATION NUMBER: 60/331,469
;; PRIOR FILING DATE: 2001-11-16
;; PRIOR APPLICATION NUMBER: 60/340,817
;; PRIOR FILING DATE: 2001-12-19
;; PRIOR APPLICATION NUMBER: 09/880,748
;; PRIOR FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 3247
;; SEQ ID NO 1431
;; LENGTH: 252
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-054-515-1431
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Query Match      73.3%  Score 44;  DB 7;  Length 252;
Best Local Similarity 63.6%  Pred. No. 0.28;
Matches 7;  Conservative 2;  Mismatches 2;  Indels 0;  Gaps 0;
```

```
QY      1  LATYYFGLDV 11
Db      105  LTGYYYGMDV 115

RESULT 6
US-11-054-515-3
;; Sequence 3, Application US/11054515
;; Publication No. US20050255532A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: PF523P3
;; CURRENT APPLICATION NUMBER: US/11/054,515
;; CURRENT FILING DATE: 2005-02-10
;; PRIOR APPLICATION NUMBER: 60/543,296
;; PRIOR FILING DATE: 2004-02-11
;; PRIOR APPLICATION NUMBER: 60/580,347
;; PRIOR FILING DATE: 2004-06-18
;; PRIOR APPLICATION NUMBER: 10/293,418
;; PRIOR FILING DATE: 2002-11-14
;; PRIOR APPLICATION NUMBER: 60/331,469
;; PRIOR FILING DATE: 2001-11-16
;; PRIOR APPLICATION NUMBER: 60/340,817
;; PRIOR FILING DATE: 2001-12-19
;; PRIOR APPLICATION NUMBER: 09/880,748
;; PRIOR FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 3247
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;; SEQ ID NO 3
;; LENGTH: 254
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-054-515-3
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Query Match      73.3%  Score 44;  DB 7;  Length 254;
Best Local Similarity 63.6%  Pred. No. 0.28;
Matches 7;  Conservative 2;  Mismatches 2;  Indels 0;  Gaps 0;
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```
QY      1  LATYYFGLDV 11
Db      107  LTGYYYGMDV 117
```

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RESULT 7
US-11-054-515-838
;; Sequence 838, Application US/11054515
;; Publication No. US20050255532A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: PF523P3
;; CURRENT APPLICATION NUMBER: US/11/054,515
;; CURRENT FILING DATE: 2005-02-10
;; PRIOR APPLICATION NUMBER: 60/543,296
;; PRIOR FILING DATE: 2004-02-11
;; PRIOR APPLICATION NUMBER: 60/580,347
;; PRIOR FILING DATE: 2004-06-18
;; PRIOR APPLICATION NUMBER: 10/293,418
;; PRIOR FILING DATE: 2002-11-14
;; PRIOR APPLICATION NUMBER: 60/331,469
;; PRIOR FILING DATE: 2001-11-16
;; PRIOR APPLICATION NUMBER: 60/340,817
;; PRIOR FILING DATE: 2001-12-19
;; PRIOR APPLICATION NUMBER: 09/880,748
;; PRIOR FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 3247
;; SEQ ID NO 838
;; LENGTH: 254
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-054-515-838

Query Match      73.3%  Score 44;  DB 7;  Length 254;
Best Local Similarity 63.6%  Pred. No. 0.28;
Matches 7;  Conservative 2;  Mismatches 2;  Indels 0;  Gaps 0;
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QY      1  LATYYFGLDV 11
Db      107  LTGYYYGMDV 117
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RESULT 8
US-11-054-515-870
;; Sequence 870, Application US/11054515
;; Publication No. US20050255532A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: PF523P3
;; CURRENT APPLICATION NUMBER: US/11/054,515
;; CURRENT FILING DATE: 2005-02-10
;; PRIOR APPLICATION NUMBER: 60/543,296
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PRIOR FILING DATE: 2004-02-11  
PRIOR APPLICATION NUMBER: 60/580,347  
PRIOR FILING DATE: 2004-06-18  
PRIOR APPLICATION NUMBER: 10/293,418  
PRIOR FILING DATE: 2002-11-14  
PRIOR APPLICATION NUMBER: 60/331,469  
PRIOR FILING DATE: 2001-11-16  
PRIOR APPLICATION NUMBER: 60/340,817  
PRIOR FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: 09/880,748  
PRIOR FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/293,499  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: 60/277,379  
PRIOR FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/276,248  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/240,816  
PRIOR FILING DATE: 2000-10-17  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 3247  
SEQ ID NO 870  
LENGTH: 254  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: Site  
LOCATION: (42)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
FEATURE:  
NAME/KEY: Site  
LOCATION: (45)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
FEATURE:  
NAME/KEY: Site  
LOCATION: (51)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
FEATURE:  
NAME/KEY: Site  
LOCATION: (57)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
FEATURE:  
NAME/KEY: Site  
LOCATION: (65)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
FEATURE:  
NAME/KEY: Site  
LOCATION: (67)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
FEATURE:  
NAME/KEY: Site  
LOCATION: (70)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
FEATURE:  
NAME/KEY: Site  
LOCATION: (170)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
FEATURE:  
NAME/KEY: Site  
LOCATION: (176)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
FEATURE:  
NAME/KEY: Site  
LOCATION: (192)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
FEATURE:  
NAME/KEY: Site  
LOCATION: (235)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
FEATURE:  
NAME/KEY: Site  
LOCATION: (239)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

FEATURE:  
NAME/KEY: Site  
LOCATION: (240)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-11-054-515-870  
Query Match 73.3% Score 44; DB 7; Length 254;  
Best Local Similarity 63.6% Pred. No. 0.28;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 1 LATYYFGADV 11  
DB 107 LTGYTYGMDV 117  
RESULT 9  
US-11-054-515-1287  
Sequence 1287, Application US/11054515  
Publication No. US20050255532A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
FILE REFERENCE: PFS23P3  
CURRENT FILING DATE: 2005-02-10  
PRIOR APPLICATION NUMBER: 60/543,296  
PRIOR FILING DATE: 2004-02-11  
PRIOR APPLICATION NUMBER: 60/580,347  
PRIOR FILING DATE: 2004-06-18  
PRIOR APPLICATION NUMBER: 10/293,418  
PRIOR FILING DATE: 2002-11-14  
PRIOR APPLICATION NUMBER: 60/331,469  
PRIOR FILING DATE: 2001-11-16  
PRIOR APPLICATION NUMBER: 60/340,817  
PRIOR FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: 09/880,748  
PRIOR FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/293,499  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: 60/277,379  
PRIOR FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/276,248  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/240,816  
PRIOR FILING DATE: 2000-10-17  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 3247  
SEQ ID NO 1287  
LENGTH: 254  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-054-515-1287  
Query Match 73.3% Score 44; DB 7; Length 254;  
Best Local Similarity 63.6% Pred. No. 0.28;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 1 LATYYFGADV 11  
DB 107 LTGYTYGMDV 117  
RESULT 10  
US-11-054-515-1288  
Sequence 1288, Application US/11054515  
Publication No. US20050255532A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
FILE REFERENCE: PFS23P3  
CURRENT FILING DATE: 2005-02-10  
PRIOR APPLICATION NUMBER: 60/543,296

PRIOR FILING DATE: 2004-02-11  
PRIOR APPLICATION NUMBER: 60/580,347  
PRIOR FILING DATE: 2004-06-18  
PRIOR APPLICATION NUMBER: 10/293,418  
PRIOR FILING DATE: 2002-11-14  
PRIOR APPLICATION NUMBER: 60/331,469  
PRIOR FILING DATE: 2001-11-16  
PRIOR APPLICATION NUMBER: 60/340,817  
PRIOR FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: 09/880,748  
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PRIOR FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/276,248  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/240,816  
PRIOR FILING DATE: 2000-10-17  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 3247  
SEQ ID NO 1288  
LENGTH: 254  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-054-515-1288

Query Match 73.3%; Score 44; DB 7; Length 254;  
Best Local Similarity 63.6%; Pred. No. 0.28;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1 LATYYFGLDV 11  
Db 107 LTYTYGMDV 117

RESULT 11  
US-11-017-550-47  
Sequence 47, Application US/11017550  
Publication No. US20050250183A1  
GENERAL INFORMATION:  
APPLICANT: The Scripps Research Institute  
APPLICANT: Schultz, Peter G  
APPLICANT: Wang, Lei  
APPLICANT: Anderson, John C  
APPLICANT: Chin, Jason  
APPLICANT: Liu, David R  
APPLICANT: Megliery, Thomas  
APPLICANT: Meggers, Eric L  
APPLICANT: Mehl, Ryan A  
APPLICANT: Pasternak, Miro  
APPLICANT: Santoro, Stephen W  
TITLE OF INVENTION: In Vivo Incorporation of Unnatural Amino Acids  
FILE REFERENCE: 54-000120US  
CURRENT APPLICATION NUMBER: US/11/017,550  
CURRENT FILING DATE: 2004-12-17  
PRIOR APPLICATION NUMBER: US/10/126,927  
PRIOR FILING DATE: 2002-04-19  
PRIOR APPLICATION NUMBER: US 60/285,030  
PRIOR FILING DATE: 2001-04-19  
PRIOR APPLICATION NUMBER: US 60/355,514  
PRIOR FILING DATE: 2002-02-06  
NUMBER OF SEQ ID NOS: 79  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 47  
LENGTH: 306  
TYPE: PRT  
ORGANISM: Methanococcus jannaschii  
US-11-017-550-47

Query Match 71.7%; Score 43; DB 7; Length 306;  
Best Local Similarity 77.8%; Pred. No. 0.5;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Oy 3 TYYFGLDV 11  
Db 158 TYYLGVGV 166

RESULT 12  
US-11-054-515-3091  
Sequence 3091, Application US/11054515  
Publication No. US2005025532A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
FILE REFERENCE: P5523P3  
CURRENT APPLICATION NUMBER: US/11/054,515  
CURRENT FILING DATE: 2005-02-10  
PRIOR APPLICATION NUMBER: 60/543,296  
PRIOR FILING DATE: 2004-02-11  
PRIOR APPLICATION NUMBER: 60/580,347  
PRIOR FILING DATE: 2004-06-18  
PRIOR APPLICATION NUMBER: 10/293,418  
PRIOR FILING DATE: 2002-11-14  
PRIOR APPLICATION NUMBER: 60/331,469  
PRIOR FILING DATE: 2001-11-16  
PRIOR APPLICATION NUMBER: 60/340,817  
PRIOR FILING DATE: 2001-12-19  
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PRIOR APPLICATION NUMBER: 60/277,379  
PRIOR FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/276,248  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/240,816  
PRIOR FILING DATE: 2000-10-17  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 3247  
SEQ ID NO 3091  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-054-515-3091

Query Match 70.0%; Score 42; DB 7; Length 13;  
Best Local Similarity 75.0%; Pred. No. 0.035;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 4 YYFGLDV 11  
Db 6 YYYGMDV 13

RESULT 13  
US-11-054-515-2817  
Sequence 2817, Application US/11054515  
Publication No. US2005025532A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
FILE REFERENCE: P5523P3  
CURRENT APPLICATION NUMBER: US/11/054,515  
CURRENT FILING DATE: 2005-02-10  
PRIOR APPLICATION NUMBER: 60/543,296  
PRIOR FILING DATE: 2004-02-11  
PRIOR APPLICATION NUMBER: 60/580,347  
PRIOR FILING DATE: 2004-06-18  
PRIOR APPLICATION NUMBER: 10/293,418  
PRIOR FILING DATE: 2002-11-14  
PRIOR APPLICATION NUMBER: 60/331,469  
PRIOR FILING DATE: 2001-11-16  
PRIOR APPLICATION NUMBER: 60/340,817

```
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2817
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2817
```

```
Query Match          70.0%; Score 42; DB 7; Length 17;
Best Local Similarity 75.0%; Pred. No. 0.046;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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```
QY      4 YYYFGLDV 11
        |||:|:|
Db      10 YYYGMDV 17
```

```
RESULT 14
US-11-054-515-2735
; Sequence 2735; Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2735
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2735
```

```
Query Match          70.0%; Score 42; DB 7; Length 19;
Best Local Similarity 75.0%; Pred. No. 0.051;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 YYYFGLDV 11
        |||:|:|
Db      12 YYYGMDV 19
```

```
RESULT 15
US-11-054-515-2899
; Sequence 2899; Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2899
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2899
```

```
Query Match          70.0%; Score 42; DB 7; Length 19;
Best Local Similarity 75.0%; Pred. No. 0.051;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 YYYFGLDV 11
        |||:|:|
Db      12 YYYGMDV 19
```

```
Search completed: December 4, 2005, 04:37:48
Job time : 3.20833 secs
```



GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: December 4, 2005, 04:09:54 ; Search time 95.5625 Seconds  
(without alignments)  
50.576 Million cell updates/sec

Title: US-10-632-706-128  
Perfect score: 66  
Sequence: 1 GPMELVGYFDS 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

## Database :

A\_Geneseq\_21: \*  
1: geneseqp1980s: \*  
2: geneseqp1990s: \*  
3: geneseqp2000s: \*  
4: geneseqp2001s: \*  
5: geneseqp2002s: \*  
6: geneseqp2003as: \*  
7: geneseqp2003bs: \*  
8: geneseqp2004s: \*  
9: geneseqp2005s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	66	100.0	11	8	ADR38726 Mouse, hea
2	44	66.7	306	6	ABU45531 Protein e
3	44	66.7	367	6	ABU47042 Protein e
4	44	66.7	367	6	ABU47877 Protein e
5	44	65.2	207	8	ADH12894 Francisel
6	42	63.6	415	7	ABM89126 Rice abio
7	41	62.1	114	4	AAO08773 Human pol
8	41	62.1	121	2	AA885504 Vhnu for
9	41	62.1	475	6	ABU20453 Protein e
10	41	62.1	792	7	ADCO7986 Rice prot
11	41	62.1	1352	4	ABM67542 Drosophi
12	40	60.6	146	6	ABP56556 Chimpanze
13	40	60.6	283	6	ABM70292 Phototrab
14	40	60.6	477	8	ADY22314 Plant ful
15	40	60.6	885	3	AA632050 Arabidops
16	40	60.6	931	3	AA632049 Arabidops
17	40	60.6	956	3	AA632048 Arabidops
18	39.5	59.8	511	8	ADX89844 Plant ful
19	39	59.1	79	3	AA613553 Arabidops
20	39	59.1	103	3	AA613552 Arabidops
21	39	59.1	112	3	AA613551 Arabidops
22	39	59.1	166	4	AA606860 Human foe
23	39	59.1	211	8	ADM57065 A thalian
24	39	59.1	233	3	AA605440 Arabidops

25	39	59.1	233	3	AA638801 Arabidops
26	39	59.1	242	5	ABG69053 Amino aci
27	39	59.1	254	3	AA630761 Arabidops
28	39	59.1	257	3	AA638800 Arabidops
29	39	59.1	257	3	AA605439 Arabidops
30	39	59.1	266	3	AA605438 Arabidops
31	39	59.1	266	3	AA638799 Arabidops
32	39	59.1	266	5	AB892172 Herbicida
33	39	59.1	274	9	ABM85054 M. xantho
34	39	59.1	278	3	AA630760 Arabidops
35	39	59.1	287	3	AA630759 Arabidops
36	39	59.1	537	8	ADT60469 Plant pol
37	39	59.1	670	6	ABU18890 Protein e
38	39	59.1	696	4	ABG20404 Novel hum
39	39	59.1	725	4	AAU48754 Propionib
40	39	59.1	775	6	ABM65954 Propionib
41	39	59.1	775	6	ABM45273 Propionib
42	39	59.1	877	3	AA636913 Arabidops
43	39	59.1	885	3	AA636912 Arabidops
44	39	59.1	949	3	AA636911 Arabidops
45	38	57.6	48	4	AA695055 Human rep

## ALIGNMENTS

RESULT 1  
ADR38726 standard; peptide; 11 AA.  
ID ADR38726 standard; peptide; 11 AA.  
AC ADR38726;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Mouse heavy chain variable region CDR3 seqid 128.  
XX  
KW antibacterial; antibody; botulinum neurotoxin type A; BONT/A;  
KW BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
KW toxin neutralisation; botulinum neurotoxin poisoning; mouse;  
KW heavy chain variable region; complementarily determining region; CDR3.  
XX  
OS Mus sp.  
XX  
PN US2004175385-A1.  
XX  
PD 09-SEP-2004.  
XX  
PF 01-AUG-2003; 2003US-00632706.  
XX  
PR 31-AUG-1998; 98US-00144886.  
XX 01-AUG-2002; 2002US-0400721P.  
XX (REGC ) UNIV CALIFORNIA.  
XX Marks JD, Amersdorfer P;  
XX WPI; 2004-652009/63.  
XX  
PS New isolated antibody that neutralises botulinum neurotoxin type A,  
PT useful for diagnosing botulism or for treating pathologies associated  
PT with botulinum neurotoxin poisoning.  
XX  
XX Example 3; SEQ ID NO 128; 110pp; English.  
XX  
XX The invention describes an isolated antibody (I) that specifically binds  
XX to an epitope specifically bound by an antibody expressed by a specific  
XX clone where (I) binds to and neutralises botulinum neurotoxin type A  
XX (BONT/A). An isolated antibody (I) that specifically binds to an epitope  
XX specifically bound by an antibody expressed by a clone chosen from clone  
XX S25, C25, C39, 1G6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1,  
XX 3-8, 3-10 and ING1, where (I) binds to and neutralises botulinum  
XX neurotoxin type A (BONT/A). Also described are: a polypeptide (II)  
XX comprising BONT/A neutralising epitope having an epitope that is

CC specifically bound by an antibody expressed by clones as mentioned in (1)  
CC ; producing (1) ; and a composition (iii) comprising several anti-  
CC botulinum neurotoxin antibodies, where each antibody is specific for a  
CC different epitope of a botulinum neurotoxin and the combination of  
CC antibodies shows greater toxin neutralisation than the single antibodies  
CC in surplus. The following are disclosed: a pharmaceutical composition  
CC comprising (1) ; and a kit comprising (1) . (1) is useful for neutralising  
CC BONT/A antibody and for neutralising a botulinum neurotoxin which  
CC involves contacting neurotoxin with (1) in surplus, where each of (1) is  
CC specific for a different epitope of the botulinum neurotoxin and the  
CC combination of antibodies shows greater toxin neutralisation than the  
CC single antibodies in surplus. (1) is useful for diagnosing the botulinum  
CC or for treating pathologies associated with botulinum neurotoxin  
CC poisoning. (1) exhibits specificity and affinity towards BONT/A. (1)  
CC enables rapid detection or diagnosis of botulism. This is the amino acid  
CC sequence of mouse heavy chain variable region complementarity determining  
CC region 3 (CDR3) from anti-botulinum neurotoxin antibodies.  
XX  
SQ Sequence 11 AA;  
Query Match 100.0%; Score 66; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. NO. 0.00019;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 GPMELVGYFDS 11  
Db 1 GPMELVGYFDS 11  
RESULT 2  
ABU45531  
ID ABU45531 standard; protein; 306 AA.  
XX  
AC ABU45531;  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by Prokaryotic essential gene #31058.  
XX  
DE Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
OS Salmomella paratyphl.  
XX  
PN WO200277183-A2.  
XX  
PD 03-OCT-2002.  
XX  
PE 21-MAR-2002; 2002MO-US009107.  
XX  
PR 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX  
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zykkind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX  
DR WPI: 2003-029926/02.  
XX  
DR N-PSDB; ACA49401.  
XX  
PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
PA Claim 25; SEQ ID NO 73455; 1766pp; English.  
XX  
CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid

CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 306 AA;  
Query Match 66.7%; Score 44; DB 6; Length 306;  
Best Local Similarity 69.2%; Pred. NO. 40;  
Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;  
OY 1 GPMELV----GYF 9  
Db 66 GPMELVAGPGGYF 78  
RESULT 3  
ABU47042  
ID ABU47042 standard; protein; 367 AA.  
XX  
AC ABU47042;  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by Prokaryotic essential gene #32569.  
XX  
DE Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
OS Salmomella typhimurium.  
XX  
PN WO200277183-A2.  
XX  
PD 03-OCT-2002.  
XX  
PE 21-MAR-2002; 2002MO-US009107.  
XX  
PR 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX  
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zykkind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX  
DR WPI: 2003-029926/02.  
XX  
DR N-PSDB; ACA50912.  
XX

PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
PS Claim 25; SEQ ID NO 74966; 1766bp; English.  
XX  
CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 367 AA;  
Query Match 66.7%; Score 44; DB 6; Length 367;  
Best Local Similarity 69.2%; Pred. No. 48;  
Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;  
Qy 1 GPMELV---GYF 9  
Db 127 GPMELVLPFGYF 139  
RESULT 4  
ABU47877  
ID ABU47877 standard; protein; 367 AA.  
XX  
AC ABU47877;  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by Prokaryotic essential gene #33404.  
XX  
DE Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
OS *Salmonella typhi*.  
XX  
PN WO200277183-A2.  
XX  
PD 03-OCT-2002.  
XX  
PE 21-MAR-2002; 2002WO-US009107.  
XX  
PR 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX  
PI Wang L, Zamudio C, Malone C, Haseelbeck R, Ohlsen KL, Zykkind JW;  
PI Wall D, Trawick JD, Carr GU, Yamamoto R, Forsyth RA, Xu HH;  
XX  
DR WPI; 2003-029926/02.  
DR N-PSDB; ACAS1747..  
XX  
PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
PS Claim 25; SEQ ID NO 75801; 1766bp; English.  
XX  
CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 367 AA;  
Query Match 66.7%; Score 44; DB 6; Length 367;  
Best Local Similarity 69.2%; Pred. No. 48;  
Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;  
Qy 1 GPMELV---GYF 9  
Db 127 GPMELVLPFGYF 139  
RESULT 5  
ADH12894  
ID ADH12894 standard; protein; 207 AA.  
XX  
AC ADH12894;  
XX  
DT 25-MAR-2004 (first entry)  
XX  
DE *Francisella tularensis* immunogenic protein 75, SEQ ID NO:75.  
XX  
DE Immunogenic protein; protective immune response; vaccine;  
XX  
KW genetic vaccine; antibacterial.  
XX  
OS *Francisella tularensis*.

XX WO2004003009-A2.  
 PN  
 XX 08-JAN-2004.  
 PD  
 XX 26-JUN-2003; 2003WO-GB002718.  
 XX  
 PR 28-JUN-2002; 2002GB-00014942.  
 XX  
 PA (MINA ) UK SEC FOR DEFENCE.  
 XX  
 PI Tidball RM, Mayers CN, Duffield ML, Miller J, Rowe SC.  
 XX  
 DR WPI; 2004-083016/08.  
 DR N-PSDB; ADH12994.  
 XX  
 PT New protein, useful as a vaccine for producing a protective immune  
 PT response in a mammal against infection by *Francisella tularensis*, or  
 PT preventing or treating *Francisella tularensis* infection in a mammal.  
 XX  
 PS Claim 1; SEQ ID NO 75; 217pp; English.  
 XX  
 CC The invention relates to 100 potentially immunogenic proteins from  
 CC *Francisella tularensis* (ADH12820-ADH12919) and nucleic acids encoding  
 CC them (ADH12920-ADH13019) which may be used in vaccines. The nucleic acids  
 CC may be contained within a vaccine, bacterial or plasmid vector. The  
 CC invention also relates to a pharmaceutical composition comprising the  
 CC protein or the nucleic acid in combination with a pharmaceutical carrier  
 CC or excipient. The proteins and nucleic acids are useful in vaccine  
 CC compositions for producing a protective immune response against  
 CC *Francisella tularensis* infection in a mammal, or for preventing or  
 CC treating *Francisella tularensis* infection in a mammal. The present  
 CC sequence represents a *Francisella tularensis* protein of the invention.  
 XX  
 SQ Sequence 207 AA;

Query Match 65.2%; Score 43; DB 8; Length 207;  
 Best Local Similarity 100.0%; Pred. No. 39;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPMELVVG 7  
 |||||  
 DB 120 GPMELVVG 126

RESULT 6  
 ABM89126  
 ID ABM89126 standard; protein; 415 AA.  
 XX  
 AC ABM89126;  
 XX  
 DT 02-JUN-2005 (first entry)  
 XX  
 DE Rice abiotic stress responsive polypeptide SEQ ID NO:7372.  
 XX  
 KW abiotic stress tolerance; transgenic plant; plant; cereal; agriculture.  
 XX  
 OS *Oryza sativa*.  
 XX  
 PN WO2003008540-A2.  
 XX  
 PD 30-JAN-2003.  
 XX  
 PF 21-JUN-2002; 2002WO-US019668.  
 XX  
 PR 22-JUN-2001; 2001US-0300112P.  
 PR 24-AUG-2001; 2001US-0314662P.  
 PR 26-SEP-2001; 2001US-0325277P.  
 PR 21-NOV-2001; 2001US-0332132P.  
 XX  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 XX  
 PI Kreps J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;

PI Moughamer T, Provart N, Rieke D, Zhu T,  
 XX  
 DR WPI; 2003-248011/24.  
 XX  
 PT New stress-responsive nucleic acid, useful for altering the  
 PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold  
 PT stress, salt stress or osmotic stress.  
 XX  
 PS Claim 1; SEQ ID NO 7372; 89pp; English.  
 XX  
 CC The invention relates to novel abiotic stress responsive polynucleotides  
 CC and polypeptides. Also disclosed are vectors, expression cassettes, host  
 CC cells, and plants containing such polynucleotides. Also disclosed are  
 CC methods for using the polynucleotides and polypeptides to alter the  
 CC responsiveness of a plant to abiotic stress. The invention is useful in  
 CC agriculture. The nucleic acid is useful for determining whether a test  
 CC plant has been exposed to an abiotic stress condition. It is also useful  
 CC for selecting an agent that alters abiotic stress regulated  
 CC polynucleotide expression in a plant cell, and to identify a homolog or  
 CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid  
 CC molecule and the polypeptide encoded by it are useful in altering the  
 CC responsiveness of a plant to an abiotic stress, such as cold stress, salt  
 CC stress, osmotic stress or any of their combinations. The present sequence  
 CC is used in the exemplification of the invention  
 XX  
 SQ Sequence 415 AA;

Query Match 63.6%; Score 42; DB 7; Length 415;  
 Best Local Similarity 75.0%; Pred. No. 1,2e+02;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 GPMELVVG 8  
 |||||  
 DB 176 GPMELTGF 183

RESULT 7  
 AA008773  
 ID AA008773 standard; protein; 114 AA.  
 XX  
 AC AA008773;  
 XX  
 DT 06-NOV-2001 (first entry)  
 XX  
 DE Human polypeptide SEQ ID NO 22665.  
 XX  
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
 KW vaccine; peptide therapy; stem cell growth factor; hematopoiesis;  
 KW tissue growth factor; immunomodulatory; cancer; leukemia;  
 KW nervous system disorders; arthritis; inflammation.  
 XX  
 OS *Homo sapiens*.  
 XX  
 PN WO200164835-A2.  
 XX  
 PD 07-SEP-2001.  
 XX  
 PF 26-FEB-2001; 2001WO-US004927.  
 XX  
 PR 28-FEB-2000; 2000US-00515126.  
 PR 18-MAY-2000; 2000US-00577409.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Liu C, Drmanac RT;  
 XX  
 DR WPI; 2001-514838/56.  
 DR N-PSDB; AA188704.  
 XX  
 PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing  
 PT and treating e.g. leukemia, inflammation and immune disorders.  
 XX  
 PS Claim 20; SEQ ID NO 22665; 1399pp + Sequence Listing; English.

XX The invention relates to human polynucleotides (AA179941-AA193841) and  
CC the encoded proteins (AA000010-AA013910) that exhibit activity elating to  
CC cytokine, cell proliferation or cell differentiation or which may induce  
CC production of other cytokines in other cell populations. The  
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
CC peptide therapy. The polypeptides have various cytokine-like activities,  
CC e.g. stem cell growth factor activity, haematopoiesis regulating  
CC activity, tissue growth factor activity, immunomodulatory activity and  
CC activin/inhibin activity and may be useful in the diagnosis and/or  
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
CC inflammation. Note: The sequence data for this patent did not form part  
CC of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX

SO Sequence 114 AA;

Query Match 62.1%; Score 41; DB 4; Length 114;  
Best Local Similarity 55.6%; Pred. No. 46;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPMELVGVF 9  
|||:|:|:  
Db 76 GPMKFLGFF 84

RESULT 8  
AAR88504

ID AAR88504 standard; protein; 121 AA.

XX AAR88504;

XX 31-JUN-1996 (first entry)

XX Vhm for antibody BT34/A5.

XX Antibody; variable heavy chain; Vhm; human; monoclonal; Mab; BT34/A5;

XX BT32/A6; cell cycle independent; tumour specific; glioma; therapy;

XX detection; complementarity determining region; CDR.

XX Homo sapiens.

XX Key Location/Qualifiers  
FH 31..35  
FT /note="Complementarity determining region (specifically  
FT Region claimed)"  
FT 50..66  
FT /note="Complementarity determining region (specifically  
FT Region claimed)"  
FT 99..110  
FT /note="Complementarity determining region (specifically  
FT Region claimed)"

XX WO9535374-A1.

XX 28-DEC-1995.

XX 16-JUN-1995; 95WO-CA000361.

XX 21-JUN-1994; 94US-00264093.

XX (DANM/) DAN M D.

XX Dan MD;

XX WPI; 1996-058411/06.

XX N-PSDB; AAT10938.

XX Novel monoclonal antibodies, BT34/A5 and BT32/A6 - used to characterise

XX glioma specific cell surface antigens, and in the treatment of glioma.

XX Claim 8; Page 33; 53pp; English.

CC AAR88504-R88510 represent regions of the human monoclonal antibodies  
CC (Mab's) BT34/A5 and BT32/A6. This sequence represents the variable region  
CC of the heavy chain, subgroup mu, (Vhm) of BT34/A5. The complementarity  
CC determining regions (CDR's) of this sequence are specifically claimed.  
CC This sequence preferably has an N-terminal extension comprising the  
CC signal sequence represented in AAR88505. The BT34/A5 and BT32/A6 Mab's  
CC recognise a cell cycle independent tumour specific antigen. They also  
CC bind equally well to tumour cells in vitro regardless of their culture  
CC viability, growth characteristics, or culture density. The antibodies  
CC effectively label the tumour cells by binding to the antigen present on  
CC the cell surface. The Mab's are useful in the detection and the treatment  
CC of glioma. These Mab's are specific for glioma and show none of the cross  
CC reactivity seen with previous antibodies  
XX

SO Sequence 121 AA;

Query Match 62.1%; Score 41; DB 2; Length 121;  
Best Local Similarity 60.0%; Pred. No. 49;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPMELVGVFD 10  
|||:|:|:  
Db 100 GWMDLNVPD 109

RESULT 9  
ABU20453

ID ABU20453 standard; protein; 475 AA.

XX ABU20453;

XX 19-JUN-2003 (first entry)

XX Protein encoded by Prokaryotic essential gene #5960.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX Bacterioides fragilis.

XX WO200277183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

XX 06-SEP-2001; 2001US-00948993.

XX 25-OCT-2001; 2001US-0342923P.

XX 08-FEB-2002; 2002US-00672851.

XX 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

XX N-PSDB; ACA24323.

XX Claim 25; SEQ ID NO 48377; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of  
XX the 6213 antisense sequences given in the specification where expression  
XX of the nucleic acid inhibits proliferation of a cell. Also included are:  
XX (1) a vector comprising a promoter operably linked to the nucleic acid  
XX encoding a polypeptide whose expression is inhibited by the antisense  
XX nucleic acid; (2) a host cell containing the vector; (3) an isolated  
XX polypeptide or its fragment whose expression is inhibited by the  
XX antisense nucleic acid; (4) an antibody capable of specifically binding

CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation; or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one  
CC of the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC [ftp.wipo.int/pub/published\\_pct\\_sequences](http://wipo.int/pub/published_pct_sequences)  
XX  
XX  
XX Sequence 475 AA;

Query Match	62.1%	Score	41	DB	6	Length	475
Best Local	Similarity	54.5%	Pred.	NO.	2.1e+02		
Matches	6	Conservative	3	Mismatches	2	Indels	0
						Gaps	0

```
QY      1  GPWELVGYFDS  11
         | | : | : | |
Db      404  GDMKLIYYDS  414
```

## RESULT 10

ID ADC07986 standard; protein; 792 AA.

AC ADC07986;

DT 18-DEC-2003 (first entry)

DB Rice protein sequence Seg ID252 related to grain filling

KM plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;  
 KM carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;  
 KM tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;  
 KM wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;  
 KM gene; ds; plant.

OS *Oryza sativa*.

PN W02003000905-A2.

PD 03-JAN-2003

PF 21-JUN-2002; 2002WO-IB002450.

PR 22-JUN-2001; 2001US-0300112P.

PR 20-DEC-2001; 2001US-0342327P.

PA (SYGN ) SYNGENTA PARTICIPATIONS AG

PA (SYGN ) SYNGENTA PARTICIPATIONS AG

PI	Zhu T, Cheng W, Briggs S, Cooper B, Golf SA, Moughamer T;
PI	Glazebrook J, Katagiri F, Kreps J, Provant N, Rieke D;

DR WPI; 2003-229341/22.  
DR N-PSDB; ADC07985.

DR WPI; 2003-229341/22.  
DR N-PSDB; ADC07985.

PT New plant genes encoding polypeptides having an activity involved in or associated with the synthesis, metabolism or degradation of carbohydrates

PT in the plant grain useful in generating plants having improved PT nutritional properties.

PS Claim 23; SEQ ID NO 252; 130pp; English.

This invention, in the area of plant biotechnology, relates to novel polynucleotide comprising a nucleotide sequence encoding a protein which is involved in or associated with the synthesis, metabolism or degradation of carbohydrates in the plant grain and the expression of which is up-regulated during grain filling. The plant is selected from corn, tomato, banana, canola, cotton, peanut, soybean, tobacco, sugarcane, wheat, and rice. The invention may be useful for the improvement of protein, oil, starch, fibre and moisture content of the cereal grains. In addition, carbohydrate levels may be modified to a more desirable level using the present invention. The present sequence is the amino acid sequence of a rice protein of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/publishedpat\\_sequences](http://ftp.wipo.int/pub/publishedpat_sequences).

Query Match	62.1%	Score 41	DB 7	Length 792
Best Local Similarity	66.7%	Pred. No.	3.6e+02	
Matches	6	Conservative	2	Mismatches 1
				Indels 0
				Gaps 0

QY 2 PWELVGYFD 10  
||:|:|  
Db 245 PWQLGYGD 253

RESULT 11  
ABB67542

ID ABB67542 standard; protein; 1352 AA.

AC ABB67542;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 29418.

**KW** *Drosophila*; developmental biology; cell signaling; insecticide;

XX

PN WO200171042-A2.

PD 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US009231.

PR 23-MAR-2000; 2000US-0191637P.

XX

XX

XX

DR N-PSDB; ABL11645.

PT New isolated nuclei

PT interactions.

PS Disclosure; SEQ ID NO 29418; 21pp + Sequence Listing; English.

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from *Drosophila*. The invention is useful in developmental biology and in elucidating cell signaling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention

CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA  
CC sequences (AB101840-AB16175) and the encoded proteins (AB57737-  
CC AB572072). The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 1352 AA;

Query Match 62.1%; Score 41; DB 4; Length 1352;  
Best Local Similarity 77.8%; Pred. No. 6.3e+02; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 2;

Oy 3 WELVGYFDS 11  
Db 161 WRNNGYFDS 169

## RESULT 12

ABP56656  
ID ABP56656 standard; protein; 146 AA.

XX AC ABP56656;

XX DT 25-MAR-2003 (first entry)

XX DE Chimpanzee C68 adenovirus E3 16 kDa protein SEQ ID NO:21.

XX KM Chimpanzee C68 adenovirus; rapid screening; bacterial transformant;  
XX KM simian adenovirus; cytotaxtic; antipoxiatic; antimicrobial; vaccine;  
XX KM adenoviral; capsid protein; hexon; penton; fibre protein; cancer;  
XX KM hyperproliferative condition; psoriasis; infection.

XX OS Mastadenovirus.

XX FH Key Location/Qualifiers  
XX FT Misc-difference 62  
XX FT note= "any amino acid"

XX PN WO200300851-A2.

XX PD 03-JAN-2003.

XX PF 20-JUN-2002; 2002WO-US019735.

XX PR 22-JUN-2001; 2001US-0300501P.

XX PR 04-JUN-2002; 2002US-038532P.

XX PA (UNP) UNIV PENNSYLVANIA.

XX PI Gao G, Wilson JM;

XX DR WPI; 2003-184043/18.

XX DR N-PSDB; AB222473.

XX PT New C68 chimpanzee adenoviral capsid protein, useful for preparing a  
XX PT composition for treating hyperproliferative conditions e.g., cancer or  
XX PT psoriasis and as a vaccine against bacterial, fungal, viral or parasitic  
XX PT infection.

XX PS Disclosure; Page 88; 124pp; English.

XX CC The present invention describes a chimpanzee C68 adenoviral capsid  
XX CC protein, which is substantially free of other viral proteins with which  
XX CC it is naturally associated, comprising: (a) a hexon protein comprising  
XX CC 513-amino acid sequence (see ABP56652); (b) a penton protein comprising  
XX CC 534-amino acid sequence (see ABP56647); (c) a fibre protein comprising  
XX CC 425-amino acid sequence (see ABP56662); or (d) a unique fragment of any  
XX CC of (A)-(C) comprising 8-amino acid residues in length. Also described:  
XX CC (1) a novel adenovirus serotype comprising a unique fragment of the C68  
XX CC hexon protein fused to a heterologous adenovirus hexon peptide; (2) a  
XX CC recombinant or pseudotyped adenovirus comprising a capsid of the novel  
XX CC adenovirus serotype encapsidating a molecule for delivery to a target  
XX CC cell; (3) an adenoviral capsid; (4) a pharmaceutical composition; (5)

CC rapid screening of recombinant constructs; and (6) a host cell. The  
CC chimpanzee C68 adenoviral capsid protein has cytotaxtic, antipoxiatic  
CC and antimicrobial activities, and can be used in vaccines. The chimpanzee  
CC C68 adenoviral capsid protein is useful for preparing a composition for  
CC treating hyperproliferative conditions e.g., cancer or psoriasis and as a  
CC vaccine against bacterial, fungal, viral or parasitic infection. The  
CC present sequence represents a chimpanzee C68 adenovirus E3 16 kDa  
CC protein, which is given in the exemplification of the present invention  
XX  
SQ Sequence 146 AA;

Query Match 60.6%; Score 40; DB 6; Length 146;  
Best Local Similarity 85.7%; Pred. No. 89;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GPWELVG 7  
Db 101 GPWEVVG 107

## RESULT 13

ABM70292  
ID ABM70292 standard; protein; 283 AA.

XX AC ABM70292;

XX DT 20-NOV-2003 (first entry)

XX DE Photorhabdus luminescens protein sequence #3389.

XX KM Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;  
XX KM detection; food; gene expression; plant; animal; microorganism; toxin;  
XX KM antibiotic; biopesticide; virulence factor; disease model; plague;  
XX KM whooping cough.

XX OS Photorhabdus luminescens.

XX PN WO200294867-A2.

XX PD 28-NOV-2002.

XX PF 07-FEB-2002; 2002WO-IB003040.

XX PR 07-FEB-2001; 2001FR-00001659.

XX PA (INSP ) INST PASTEUR.

XX PA (CNRS ) CNRS CENT NAT RECH SCI.

XX PI Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;  
XX PI Buchrieser C;

XX DR WPI; 2003-148459/14.

XX PT Genomic sequence of Photorhabdus luminescens and encoded polypeptides,  
XX PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.  
XX PS Claim 2; SEQ ID NO 3389; 1205pp; French.

XX CC The invention relates to the isolation of genes and their encoded  
XX CC proteins from Photorhabdus luminescens. The isolated sequences are  
XX CC sources of probes and primers for detecting the genome of P. luminescens  
XX CC and related species; to study polymorphisms; for gene analysis and for  
XX CC detection/amplification of the genes. Antibodies (Ab) raised against the  
XX CC polypeptides encoded by the genes are used for detection/identification  
XX CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that  
XX CC carry a gene-containing vector are used to select compounds that  
XX CC modulate, regulate, induce or inhibit expression of the genes in plants,  
XX CC animals or microorganisms other than P. luminescens and are able to alter  
XX CC response or sensitivity to toxins and antibiotics produced by P.  
XX CC luminescens. Cells transformed to express the genes are useful for  
XX CC recombinant production of the proteins, particularly toxins and  
XX CC antibacterials useful as insecticides, bactericides and fungicides. The  
XX CC genes, proteins, vectors containing the genes and Ab are also useful



CC therapeutically (to treat microbial infection by bacteria or fungi that  
CC are sensitive to P. lumnescens-encoded toxins or antibiotics) and as  
CC biopesticides. Other uses of the genes and the proteins are as virulence  
CC factors and for identifying targets of human diseases for which P.  
CC lumnescens is a model (particularly plague and whooping cough). This  
CC sequence represents one of the isolated P. lumnescens proteins  
XX  
SQ Sequence 283 AA;  
Query Match 60.6%; Score 40; DB 6; Length 283;  
Best Local Similarity 66.7%; Pred. No. 1.8e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
OY 3 WELVGYFDS 11  
Db 238 WLIVGYFDA 246  
RESULT 14  
ADY22314  
ID ADY22314 standard; protein; 477 AA.  
XX  
AC ADY22314;  
XX  
DT 21-APR-2005 (first entry)  
XX  
DE Plant full length insert polypeptide seqid 70098.  
XX  
KW plant protectant; plant growth regulant; gene therapy; plant;  
KW recombinant DNA construct; physical array; plant breeding marker;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
KW growth rate; cell cycle pathway; disease resistance;  
KW galactomannan production; lignin production; plant growth regulator;  
KW yield; plant growth; plant development; seed oil; protein yield;  
KW protein content.  
XX  
OS Unidentified.  
XX  
PN US2004034888-A1.  
XX  
PD 19-FEB-2004.  
XX  
PF 28-APR-2003; 2003US-00425114.  
XX  
PR 06-MAY-1999; 99US-00304517.  
XX  
PR 05-NOV-2001; 2001US-00985678.  
XX  
PA (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S B.  
PA (TABAS/) TABASKA J E.  
PA (CAOY/) CAO Y.  
XX  
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
XX  
DR WPI; 2004-180133/17.  
XX  
PT New recombinant DNA construct, useful for improving plant tolerance to  
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
PT pests, for conferring increased resistance to plant disease, or for  
PT improving yield.  
XX  
PS Claim 1; SEQ ID NO 70098; 15pp; English.  
XX  
CC The invention describes a recombinant DNA construct comprising a  
CC polynucleotide consisting of a sequence encoding an amino acid sequence  
CC available in electronic form from the US patent office at  
CC ftp://seqdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide  
CC of the invention are also useful in physical arrays of molecules and as  
CC plant breeding markers. The recombinant DNA construct is useful for  
CC improving plant tolerance to cold, heat, drought, herbicides, extreme

CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
CC plant cells by modification of the cell cycle pathway, for conferring  
CC increased resistance to plant disease, for producing galactomannan,  
CC lignin or plant growth regulators, for increasing the rate of homologous  
CC recombination in plants, for improving yield by modification of  
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
CC or by providing improved plant growth and development under at least one  
CC stress condition or for modifying seed oil or protein yield and/or  
CC content. This is the amino acid sequence of a plant full length insert  
CC polypeptide that can be used in the recombinant DNA construct of the  
CC invention.  
XX  
SQ Sequence 477 AA;  
Query Match 60.6%; Score 40; DB 8; Length 477;  
Best Local Similarity 60.0%; Pred. No. 3.1e+02;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
OY 1 GPMELVGYFD 10  
Db 307 GPMEMREFFD 316  
RESULT 15  
AAG32050  
ID AAG32050 standard; protein; 885 AA.  
XX  
AC AAG32050;  
XX  
DT 17-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 38593.  
XX  
KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX  
OS Arabidopsis thaliana.  
XX  
PN EP1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-00301439.  
XX  
PR 25-FEB-1999; 99US-0121825P.  
XX  
PR 05-MAR-1999; 99US-0123180P.  
XX  
PR 09-MAR-1999; 99US-0133548P.  
XX  
PR 23-MAR-1999; 99US-0125788P.  
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PR 25-MAR-1999; 99US-0126264P.  
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PR 29-MAR-1999; 99US-0126785P.  
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PR 01-APR-1999; 99US-0127462P.  
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PR 06-APR-1999; 99US-0128234P.  
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PR 16-APR-1999; 99US-0128645P.  
XX  
PR 19-APR-1999; 99US-0130077P.  
XX  
PR 21-APR-1999; 99US-0130449P.  
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PR 23-APR-1999; 99US-0130510P.  
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PR 28-APR-1999; 99US-0130891P.  
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PR 30-APR-1999; 99US-0132048P.  
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PR 04-MAY-1999; 99US-0132484P.  
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PR 06-MAY-1999; 99US-0132486P.  
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PR 14-MAY-1999; 99US-0134218P.  
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PR 18-MAY-1999; 99US-0134370P.  
XX  
PR 18-MAY-1999; 99US-0134768P.



PR 19-MAY-1999; 99US-0134941P.  
PR 20-MAY-1999; 99US-0135124P.  
PR 21-MAY-1999; 99US-0135353P.  
PR 24-MAY-1999; 99US-0135629P.  
PR 25-MAY-1999; 99US-0136021P.  
PR 27-MAY-1999; 99US-0136392P.  
PR 28-MAY-1999; 99US-0137282P.  
PR 01-JUN-1999; 99US-0137222P.  
PR 03-JUN-1999; 99US-0137528P.  
PR 04-JUN-1999; 99US-0137502P.  
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PR 14-JUN-1999; 99US-0139119P.  
PR 16-JUN-1999; 99US-0139452P.  
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PR 22-JUN-1999; 99US-0139899P.  
PR 23-JUN-1999; 99US-0140353P.  
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PR 24-JUN-1999; 99US-0140695P.  
PR 28-JUN-1999; 99US-0140823P.  
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PR 30-JUN-1999; 99US-0141287P.  
PR 01-JUL-1999; 99US-0141842P.  
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PR 02-JUL-1999; 99US-0142055P.  
PR 06-JUL-1999; 99US-0142390P.  
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PR 09-JUL-1999; 99US-0142920P.  
PR 12-JUL-1999; 99US-0142977P.  
PR 13-JUL-1999; 99US-0143542P.  
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PR 19-JUL-1999; 99US-0144334P.  
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PR 21-JUL-1999; 99US-0144814P.  
PR 21-JUL-1999; 99US-0145086P.  
PR 21-JUL-1999; 99US-0145088P.  
PR 22-JUL-1999; 99US-0145085P.  
PR 22-JUL-1999; 99US-0145087P.  
PR 22-JUL-1999; 99US-0145089P.  
PR 22-JUL-1999; 99US-0145192P.  
PR 23-JUL-1999; 99US-0145145P.  
PR 23-JUL-1999; 99US-0145218P.  
PR 23-JUL-1999; 99US-0145224P.  
PR 26-JUL-1999; 99US-0145276P.  
PR 27-JUL-1999; 99US-0145913P.  
PR 27-JUL-1999; 99US-0145918P.  
PR 27-JUL-1999; 99US-0145919P.  
  
PR 28-JUL-1999; 99US-0145951P.  
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PR 03-AUG-1999; 99US-0147038P.  
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PR 06-AUG-1999; 99US-0147416P.  
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PR 10-AUG-1999; 99US-0148171P.  
PR 11-AUG-1999; 99US-0148119P.  
PR 12-AUG-1999; 99US-0148311P.  
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PR 13-AUG-1999; 99US-0148684P.  
PR 16-AUG-1999; 99US-0149368P.  
PR 17-AUG-1999; 99US-0149175P.  
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PR 20-AUG-1999; 99US-0149722P.  
PR 20-AUG-1999; 99US-0149723P.  
PR 20-AUG-1999; 99US-0149929P.  
PR 23-AUG-1999; 99US-0149902P.  
PR 23-AUG-1999; 99US-0149930P.  
PR 25-AUG-1999; 99US-0150565P.  
PR 26-AUG-1999; 99US-0150884P.  
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PR 27-AUG-1999; 99US-0151080P.  
PR 30-AUG-1999; 99US-0151303P.  
PR 31-AUG-1999; 99US-0151348P.  
PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152330P.  
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PR 13-SEP-1999; 99US-0153758P.  
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PR 24-SEP-1999; 99US-0155659P.  
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PR 22-OCT-1999; 99US-0160989P.  
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PR 25-OCT-1999; 99US-0161405P.  
PR 25-OCT-1999; 99US-0161406P.  
PR 26-OCT-1999; 99US-0161359P.

PR 26-OCT-1999; 99US-0161360P.  
 PR 26-OCT-1999; 99US-0161361P.  
 PR 28-OCT-1999; 99US-0161920P.  
 PR 28-OCT-1999; 99US-0161922P.  
 PR 28-OCT-1999; 99US-0161933P.  
 PR 29-OCT-1999; 99US-0162142P.

Query Match 60.6%; Score 40; DB 3; Length 885;  
 Best Local Similarity 85.7%; Pred. No. 6e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GPMELVG 7  
 |||:  
 Db 411 GPMOLVG 417

Search completed: December 4, 2005, 04:44:57  
 Job time : 98.5625 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: December 4, 2005, 04:31:45 ; Search time 15.5833 Seconds  
(without alignment)  
67.918 Million cell updates/sec

Title: US-10-632-706-128  
Perfect score: 66  
Sequence: 1 GPMELVGYFDS 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	68.2	279	2 T35791	probable transmembr
2	44	66.7	367	2 AD0922	probable undecapre
3	43	65.2	1788	2 T29043	hypothetical prote
4	41	62.1	491	2 E69368	glutamine syntheta
5	41	62.1	550	2 B84900	hypothetical prote
6	41	62.1	619	1 S48729	glucokinase regula
7	41	62.1	697	2 G70704	hypothetical prote
8	40	60.6	724	2 B87015	ABC transporter ML
9	40	60.6	726	2 T44905	ABC-type transport
10	40	60.6	888	2 D84824	probable DNA-dirc
11	40	60.6	931	2 F84637	probable plasma me
12	39	59.1	299	2 D71051	hypothetical prote
13	39	58.1	320	2 T33303	hypothetical prote
14	39	59.1	459	2 S17907	glutamate dehydrog
15	39	59.1	471	2 S28476	rflB protein VC024
16	39	59.1	578	2 B82204	methyl-accepting c
17	39	59.1	949	1 PKMUP1	H+-exporting ATPas
18	38	57.6	173	2 S44403	NADH2 dehydrogenas
19	38	57.6	274	2 G75335	glycerol uptake fa
20	38	57.6	409	2 S63614	male protein homol
21	38	57.6	432	2 T17829	ankyrin repeat pro
22	38	57.6	465	2 T26146	hypothetical prote
23	38	57.6	496	2 G71693	hypothetical prote
24	38	57.6	499	2 G97761	apolipoprotein n-a
25	38	57.6	532	2 AP3498	apolipoprotein N-a
26	38	57.6	1091	2 T34247	hypothetical prote
27	38	57.6	1107	2 T34246	hypothetical prote
28	38	57.6	2100	2 T03223	probable polyketid
29	37	56.1	213	2 C64041	hypothetical prote

30	37	56.1	217	2 A82491	fine protein VCA01
31	37	56.1	226	2 A87664	hypothetical prote
32	37	56.1	235	2 T44679	spou protein homol
33	37	56.1	241	2 T39330	probable 60S acid
34	37	56.1	276	2 A95309	probable ABC trans
35	37	56.1	277	2 AF3216	ABC transporter, m
36	37	56.1	349	2 T31856	hypothetical prote
37	37	56.1	365	2 S61636	hypothetical prote
38	37	56.1	400	2 AF0291	probable drug resi
39	37	56.1	413	2 G95965	conserved hypothet
40	37	56.1	426	2 T08550	choleline monooxygen
41	37	56.1	462	2 I58179	SHR3 receptor subu
42	37	56.1	468	2 T48615	hypothetical prote
43	37	56.1	502	2 S50519	hypothetical prote
44	37	56.1	601	1 A64222	heat shock protein
45	37	56.1	642	2 G69371	acetyl-CoA synthet

## ALIGNMENTS

## RESULT 1

T35791  
probable transmembrane sugar transport protein - Streptomyces coelicolor  
C:Species: Streptomyces coelicolor  
C:Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 09-Jul-2004  
C:Accession: T35791  
R:Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
A:Reference number: Z21570  
A:Accession: T35791  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-279 <SEB>  
A:Cross-references: UNIPROT:O87858; UNIPARC:UPI00000DAC47; EMBL:AL031013; PIDD:CAA19796.  
A:Experimental source: strain A3(2)  
C:Genetics:  
A:Gene: SCOEDB:SC8A6.24  
C:Superfamily: maltose transport protein malC

Query Match 68.2%; Score 45; DB 2; Length 279;  
Best Local Similarity 77.8%; Pred. No. 2.8;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 MELVGYFDS 11  
DB 160 WMLGYFDS 168

## RESULT 2

AD0922  
Probable undecaprenyl-phosphate alpha-N-acetylglucosaminyltransferase STY3637 (imported)  
C:Species: Salmonella enterica subsp. enterica serovar Typhi  
A:Note: this species has also been called Salmonella typhi  
C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 03-Feb-2003  
C:Accession: AD0922  
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, C.; T. Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001  
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A:Reference number: AB0502; MUID:21534947; PMID:11677608  
A:Accession: AD0922  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-367 <PAR>  
A:Cross-references: UNIPARC:UPI000005A58F; GB:AL513382; PIDD:CAD09398.1; PTD:G16504516;  
C:Genetics:  
A:Gene: STY3637

Query Match 66.7%; Score 44; DB 2; Length 367;  
Best Local Similarity 69.2%; Pred. No. 5.6;

Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;  
 QY 1 GPMELVGYFD 9  
 |||||  
 Db 127 GPMELVLPFGYF 139

## RESULT 3

T29043  
 hypothetical protein B0228.2 - *Caenorhabditis elegans*  
 C:Species: *Caenorhabditis elegans*  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C:Accession: T29043

R:Leimach, D.

submitted to the EMBL Data Library, March 1995

A:Description: The sequence of *C. elegans* coemid B0228.

A:Reference number: Z18324

A:Accession: T29043

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1788 <LEI>

A:Cross-references: UNIPROT:O81661; UNIPARC:UPI00000851C9; EMBL:U23168; PIDN:AAC3806.1;

A:Experimental source: strain Bristol N2

C:Genetics:

A:Gene: CESP:B0228.2

A:Introns: 1456/2; 1482/3; 1516/2; 1551/3; 1595/3; 1646/1; 1671/1; 1716/2; 1749/3

Query Match

Best Local Similarity 65.2%; Score 43; DB 2; Length 1788;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPMELVGYFD 10  
 |||||  
 Db 1722 GPMNMGRFD 1731

## RESULT 4

B69368  
 glutamine synthetase (gluA) homolog - *Archaeoglobus fulgidus*

C:Species: *Archaeoglobus fulgidus*

C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004

C:Accession: B69368

R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson

.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sulton, G.G.; Gill, S.; Kirkness, E.F.

Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A:Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artlach, P.; Kaine, B.P.; Sykes, S.

Smith, H.O.; Moese, C.R.; Venter, J.C.

A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae

A:Reference number: A69250; PMID:98049343; PMID:9389475

A:Accession: B69368

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-491 <KLB>

A:Cross-references: UNIPROT:Q29313; UNIPARC:UPI0000056F0D; GB:AE001039; GB:AE000782; NID

C:Superfamily: glutamate-ammonia ligase

Query Match

Best Local Similarity 62.1%; Score 41; DB 2; Length 491;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PWEVLGYFD 10  
 |||||  
 Db 482 PWEFMKYFD 490

## RESULT 5

B84900  
 hypothetical protein At2g46220 [imported] - *Arabidopsis thaliana*

C:Species: *Arabidopsis thaliana* (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004

C:Accession: B84900

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayan, L.; Tallon, L.;  
 euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.

A:Reference number: A84420; PMID:2083487; PMID:10617197

A:Accession: B84900

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-550 <STO>

A:Cross-references: UNIPROT:O82347; UNIPARC:UPI000017A71B; GB:AE002093; NID:G3702327; PII

C:Genetics:

A:Gene: At2g46220

A:Map position: 2

Query Match

Best Local Similarity 62.1%; Score 41; DB 2; Length 550;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GPMELVGYFD 10  
 |||||  
 Db 176 GPMSTRGRFD 185

## RESULT 6

S48729  
 glucokinase regulator - African clawed frog

C:Species: *Xenopus laevis* (African clawed frog)

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004

C:Accession: S48729; S49339

R:Veiga-da-Cunha, M.; Delvaux, M.; Matelet, N.; van Schaftingen, E.

Eur. J. Biochem. 225, 43-51, 1994

A:Title: Cloning and expression of a *Xenopus* liver cDNA encoding a fructose-phosphate-in

A:Reference number: S48729; PMID:95010134; PMID:7925465

A:Accession: S48729

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-619 <VEI>

A:Cross-references: UNIPROT:Q91754; UNIPARC:UPI000012B2E2; EMBL:X80901; NID:G556677; PID:

C:Superfamily: glucokinase regulator

Query Match

Best Local Similarity 62.1%; Score 41; DB 1; Length 619;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GPMELVGYFDS 11  
 |||||  
 Db 17 GPMELVGYEBS 27

## RESULT 7

G70704  
 hypothetical protein RV2326C - *Mycobacterium tuberculosis* (strain H37RV)

C:Species: *Mycobacterium tuberculosis*

C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004

C:Accession: G70704

R:Cole, S.T.; Broesch, R.; Parikh, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S

; Connor, R.; Davies, R.; Devlin, K.; Fellwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A:Authors: Sgares, R.; Sultson, J.E.; Taylor, K.; Whithead, S.; Barrett, B.G.

A:Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome

A:Reference number: A70500; PMID:98295987; PMID:9634230

A:Accession: G70704

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-697 <COL>

A:Cross-references: UNIPROT:P71886; UNIPARC:UPI000013BA74; GB:Z79702; GB:AL123456; NID:G

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: RV2326C

Query Match

Best Local Similarity 62.1%; Score 41; DB 2; Length 697;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
Oy 2 PMWLVGYD 10  
|||:||||  
Db 196 PMWLVGYFN 204

## RESULT 8

B87015

ABC transporter MT0848 [imported] - Mycobacterium leprae

C:Species: Mycobacterium leprae

C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004

C:Accession: B87015

R: Cole, S.T.; Bigmiller, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; He

R.; Davies, R.M.; Devlin, K.; Duthey, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,

eam, M.A.; Rutherford, K.M.

Nature 409, 1007-1011, 2001

A: Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S

A: Title: Massive gene decay in the leprosy bacillus.

A: Reference number: A86909; MUID:21128732; PMID:11234002

A: Accession: B87015

A: Status: preliminary

A: Molecule type: DNA

A: Residues: 1-724 &lt;STO&gt;

A: Cross-references: UNIPROT:Q9CCF9; UNIPARC:UPI00000C6D27; GB:AL450380; NID:g13092926; F

C: Genetics:

A: Gene: ML0848

## Query Match

Best Local Similarity 60.6%; Score 40; DB 2; Length 724;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 2 PMWLVGYF 9  
|||:||||

Db 224 PMWLVGYF 231

## RESULT 9

T44905

ABC-type transporter homolog [imported] - Mycobacterium leprae

C:Species: Mycobacterium leprae

C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 09-Jul-2004

C:Accession: T44905

R: Parkhill, J.; Barrrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, August 1997

A: Reference number: Z22864

A: Accession: T44905

A: Status: preliminary; translated from GB/EMBL/DBJ

A: Molecule type: DNA

A: Residues: 1-726 &lt;PAR&gt;

A: Cross-references: UNIPROT:O32971; UNIPARC:UPI00000BED0E; EMBL:Z98741; PIDN: CAB11403.1

A: Experimental source: cosmid B22

C: Genetics:

A: Note: MLCB22.38C

## Query Match

Best Local Similarity 60.6%; Score 40; DB 2; Length 726;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 2 PMWLVGYF 9  
|||:||||

Db 226 PMWLVGYF 233

## RESULT 10

D84824

probable DNA-directed RNA polymerase II subunit [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004

C:Accession: D84824

R: Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vancken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eilen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J

Nature 402, 761-768, 1999

A: Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A: Reference number: A84420; MUID:20083487; PMID:10617197

A: Accession: D84824

A: Status: preliminary

A: Molecule type: DNA

A: Residues: 1-888 &lt;STO&gt;

A: Cross-references: UNIPROT:O04206; UNIPARC:UPI00000A517F; GB:AE002093; NID:g2088656; PI

C: Genetics:

A: Gene: At2g40030

A: Map position: 2

Query Match 60.6%; Score 40; DB 2; Length 888;  
Best Local Similarity 63.6%; Pred. No. 70;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1 GPMWLVGYFDS 11  
|||:||||

Db 544 GPMWLVGYFDS 554

## RESULT 11

F84637

probable plasma membrane proton ATPase [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 31-Dec-2004

C:Accession: F84637

R: Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vancken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eilen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J

Nature 402, 761-768, 1999

A: Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A: Reference number: A84420; MUID:20083487; PMID:10617197

A: Accession: F84637

A: Status: preliminary

A: Molecule type: DNA

A: Residues: 1-931 &lt;STO&gt;

A: Cross-references: UNIPARC:UPI000016237B; GB:AE002093; NID:g4572678; PIDN: AAD23893.1; G

C: Genetics:

A: Gene: At2g24520

A: Map position: 2

C: Superfamily: Na(+)/(K+)-transporting ATPase alpha chain; ATPase nucleotide-binding dome

Query Match 60.6%; Score 40; DB 2; Length 931;

Best Local Similarity 85.7%; Pred. No. 74;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GPMWLVG 7  
|||:||||

Db 457 GPMWLVG 463

## RESULT 12

D71051

hypothetical protein PH1107 - Pyrococcus horikoshii

C:Species: Pyrococcus horikoshii

C:Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 31-Dec-2004

C:Accession: D71051

R: Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin

M.; Ohtoku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi

DNA Res. 5, 55-76, 1998

A: Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a

A: Reference number: A71000; MUID:98344137; PMID:9679194

A: Accession: D71051

A: Status: preliminary; nucleic acid sequence not shown; translation not shown

A: Molecule type: DNA

A: Residues: 1-299 &lt;KAW&gt;

A: Cross-references: UNIPROT:O58834; UNIPARC:UPI000062FB7; GB:AP000005; NID:g3236132; PI

A: Experimental source: strain OT3

A: Note: this accession replaces an interim accession for a sequence replaced by GenBank

C: Genetics:

A: Gene: PH1107

C: Superfamily: glycosidase, PH1107 type

Query Match 59.1%; Score 39; DB 2; Length 299;  
 Best Local Similarity 60.0%; Pred. No. 33;  
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 PWELVGYFDS 11  
 |||||  
 Db 247 PWELGHVDN 256

## RESULT 13

hypothetical protein R01B10.4 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C>Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004

C:Accession: T33303

R:Langston, Y.; Beck, C.

A:Submitted to the EMBL Data Library, May 1998

A:Description: The sequence of C. elegans cosmid R01B10.

A:Reference number: 221318

A:Accession: T33303

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-320 <LAN>

A:Cross-references: UNIPROT:O61975, UNIPARC:UPI0000080228, EMBL:AF068718; PIDD:AACT17768.

A:Experimental source: strain Bristol N2; clone R01B10

C:Genetics:

A:Gene: CESP:R01B10.4

A:Map position: 5

A:Introns: 25/2; 73/2; 211/3; 241/2

Query Match 59.1%; Score 39; DB 2; Length 320;  
 Best Local Similarity 55.6%; Pred. No. 36;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 WELVGYFDS 11  
 |||||  
 Db 65 WDTIGHFDS 73

## RESULT 14

S17907

glutamate dehydrogenase (NADP) (EC 1.4.1.4) - yeast (*Schwanniomyces occidentalis* var. *occidentalis*)

C:Species: *Schwanniomyces occidentalis* var. *occidentalis*

C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 05-Oct-2004

C:Accession: S17907

R:de Zuyra, P.A.; Connerton, I.F.; Watson, D.C.; Johnston, J.R.

A:Title: Cloning, sequencing and expression of the *Schwanniomyces occidentalis* NADP-depe

A:Reference number: S17907; MUID:92035089; PMID:1934128

A:Accession: S17907

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-459 <DEZ>

A:Cross-references: UNIPROT:P29507, UNIPARC:UPI00001292F9

C:Superfamily: glutamate dehydrogenase

C:Keywords: NADP; oxidoreductase

Query Match 59.1%; Score 39; DB 2; Length 459;  
 Best Local Similarity 66.7%; Pred. No. 52;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PWELVGYFDS 10  
 |||||  
 Db 308 PMAKVGHFD 316

## RESULT 15

S28476

rfbL protease VC0249 [similarity] - *Vibrio cholerae* (strain N16961 serogroup O1)

C:Species: *Vibrio cholerae*

C>Date: 12-Mar-1993 #sequence\_revision 12-Mar-1993 #text\_change 09-Jul-2004

C:Accession: S28476; H82346

R:Manning, P.A.  
 submitted to the EMBL Data Library, May 1991

A:Reference number: S28476

A:Accession: S28476

A:Molecule type: DNA

A:Residues: 1-471 <MAN>

A:Cross-references: UNIPROT:Q06959, UNIPARC:UPI00000D470B; EMBL:X59554; NID:948381; PIDD:

A:Experimental source: strain O17

R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;

Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dreger, I.; Sellers, P.

1; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.

A:Reference number: A82035; MUID:20406833; PMID:10952301

A:Accession: H82346

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-471 <HEI>

A:Cross-references: UNIPARC:UPI00000D470B; GB:AE004113; GB:AE003852; NID:93654648; PIDD:

A:Experimental source: serogroup O1; strain N16961; biotype El Tor

C:Genetics:

A:Gene: rfbL; VC0249

A:Map position: 1

C:Superfamily: 4-connate-CoA ligase; acetate-CoA ligase homology

F:47-468/Domain: acetate-CoA ligase homology <ACT>

Query Match 59.1%; Score 39; DB 2; Length 471;  
 Best Local Similarity 60.0%; Pred. No. 54;  
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 PWELVGYFDS 11  
 |||||  
 Db 329 PMLDGYFEN 338

Search completed: December 4, 2005, 04:53:34  
 Job time : 17.5833 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 4, 2005, 04:31:36 ; Search time 100.375 Seconds  
(without alignments)  
77.318 Million cell updates/sec

Title: US-10-632-706-128  
Perfect score: 66  
Sequence: 1 GPMWLVGFDS 11

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_05.80:\*  
1: uniprot\_sprotc:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	68.2	279	2	087858_STRCO
2	45	68.2	290	2	082M58_STRAM
3	45	68.2	748	2	05NQ32_ZYMMO
4	44	66.7	367	1	MECA_SALTY
5	44	66.7	367	1	MECA_SALTY
6	44	66.7	367	2	05PKK1_SALPA
7	44	66.7	449	2	063N53_BURPS
8	43	65.2	231	2	04K719_PSEPS
9	43	65.2	1201	2	07JYR6_RHOBA
10	43	65.2	1633	1	YF74_CAEEL
11	43	65.2	7548	2	05WRU1_CAEEL
12	42	63.6	272	2	074858_GEOSL
13	42	63.6	381	2	06K1T5_ORYSA
14	42	63.6	454	2	08JYV9_METAC
15	42	63.6	578	2	08D955_VIBVU
16	42	63.6	578	2	07MLB3_VIBVU
17	42	63.6	1275	2	080061_METMA
18	41	62.1	211	2	08KHK7_PSEAE
19	41	62.1	241	2	082347_ARATH
20	41	62.1	273	2	07JUN8_RHOBA
21	41	62.1	318	2	04KEP9_PSEPS
22	41	62.1	491	1	GLNA_ARCFU
23	41	62.1	518	2	05LH40_BACFN
24	41	62.1	518	2	064XZ7_BACFR
25	41	62.1	613	2	06BTL3_DBBHA
26	41	62.1	619	1	06CKR_XENLA
27	41	62.1	619	2	05SKA5_THET8
28	41	62.1	619	2	06PAX3_XENLA
29	41	62.1	697	1	Y2326_MYCTU
30	41	62.1	697	1	Y2353_MYCBO
31	41	62.1	1350	2	09V5J7_DROME

32	41	62.1	1370	2	07KQX6_DROME	07KQX6_drosophila
33	41	62.1	2581	2	07T7T5_VIRU	07T7T5_heterosigma
34	40	60.6	122	2	08EB57_SHEON	08EB57_sheanella
35	40	60.6	146	2	08UY74_GADEN	08UY74_simian aden
36	40	60.6	206	2	06QP97_GADEN	06QP97_simian aden
37	40	60.6	207	2	06QPD3_GADEN	06QPD3_simian aden
38	40	60.6	208	2	06QPG9_GADEN	06QPG9_simian aden
39	40	60.6	210	2	06H1B6_GADEN	06H1B6_simian aden
40	40	60.6	210	2	08BEL6_ADE04	08BEL6_human adeno
41	40	60.6	282	2	07N9W4_PHOCL	07N9W4_photorhabdu
42	40	60.6	304	2	087XQ4_PSESN	087XQ4_pseudomonas
43	40	60.6	319	2	04ZPN4_PSESY	04ZPN4_pseudomonas
44	40	60.6	323	2	04INB2_GIBZE	04INB2_gibberella
45	40	60.6	392	2	08LRJ7_PETRY	08LRJ7_petunia hyb

ALIGNMENTS

RESULT 1	087858_STRCO	PRELIMINARY;	PRT;	279 AA.
AC	087858;			
DT	01-NOV-1998 (TREMblrel, 08, Created)			
DT	01-NOV-1998 (TREMblrel, 08, Last sequence update)			
DT	01-MAR-2004 (TREMblrel, 26, Last annotation update)			
DE	Putative transmembrane sugar transport protein.			
CN	OrderedLocustNames=SC06603; ORFNames=SC86.24;			
OS	Streptomyces coelicolor.			
OC	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;			
OC	Streptomycinae; Streptomycetaceae; Streptomyces.			
OX	NCBI_TaxID=1902;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=A3(2) / M145;			
RX	MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;			
RA	Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,			
RA	Thomson N.R., James K.D., Harris D.E., Quail M.A., Klesner H.,			
RA	Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,			
RA	Cronin A., Fraser A., Gobie A., Hidalgo J., Hornsby T., Howarth S.,			
RA	Huang C.-H., Klesner T., Larke L., Murphy L.D., Oliver K., O'Neill S.,			
RA	Rabinowitz E., Rajadream M.A., Rutherford K.M., Rutter S.,			
RA	Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,			
RA	Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,			
RA	Hopwood D.A.,			
RT	"Complete genome sequence of the model actinomycete Streptomyces			
RT	coelicolor A3(2)."			
RL	Nature 417:141-147(2002).			
CC	-1- FUNCTION: Part of a binding-protein-dependent transport system.			
CC	Probably responsible for the translocation of the substrate across			
CC	the membrane (By similarity).			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).			
CC	-1- SIMILARITY: Belongs to the binding-protein-dependent transport			
CC	system permease family.			
DR	EMBL: AL39128; CAA19796.1; -; Genomic_DNA.			
DR	PIR: T35791; T35791.			
DR	GO: GO:0016021; C: Integral to membrane; IEA.			
DR	GO: GO:0016020; C: Membrane; IEA.			
DR	GO: GO:0005351; F: Sugar porter activity; IEA.			
DR	GO: GO:0005215; F: Transporter activity; IEA.			
DR	GO: GO:0006810; P: Transport; IEA.			
DR	InterPro: IPR000515; BPD transp.			
DR	Pfam: PF00528; BPD transp_1; 1.			
DR	PROSITE: PS50928; ABC_TWI; 1.			
RW	Complete proteome; Sugar transport; Transmembrane; Transport.			
SQ	SEQUENCE 279 AA; 3035 MW; 886063385B8F3BFA CRC64;			
Qy	Query Match 68.2%; Score 45; DB 2; Length 279;			
	Best Local Similarity 77.8%; Pred. No. 25;			
	Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;			
	3 WELVGFDS 11			
	:			

```

Db      160 WMLIGYFDS 168

RESULT 2
ID      Q82M58_STRAW PRELIMINARY;      PRT;      290 AA.
AC      Q82M58;
DT      01-JUN-2003 (TREMBLrel. 24, Created)
DT      01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT      01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE      Purative sugar ABC transporter permealase protein.
GN      OrderedLocuNames=SAV1802;
OS      Streptomyces avermectilis.
OC      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC      Streptomycinae; Streptomycetaceae; Streptomycetes.
OX      NCBI_TaxID=33903;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC      STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX      MEDLINE=21477403; PubMed=1572948; DOI=10.1073/pnas.21143318;
RA      Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA      Shinose S., Takahashi Y., Horikawa H., Nakazawa H., Ogonoe T.,
RA      Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT      "Genome sequence of an industrial microorganism Streptomyces
RT      avermectilis: deducing the ability of producing secondary
RT      metabolites."
RT      Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX      MEDLINE=22608306; PubMed=12692562; DOI=10.1038/nbt820;
RA      Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA      Sakaki Y., Hattori M., Omura S.;
RT      "Complete genome sequence and comparative analysis of the industrial
RT      microorganism Streptomyces avermectilis."
RT      Nat. Biotechnol. 21:526-531(2003).
CC      -1- FUNCTION: Part of a binding-protein-dependent transport system.
CC      Probably responsible for the translocation of the substrate across
CC      the membrane (By similarity).
CC      -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC      -1- SIMILARITY: Belongs to the binding-protein-dependent transport
CC      system permealase family.
DR      EMBL; BA000030; BAC69513.1; -; Genomic DNA.
DR      GO; GO:0016021; C:integral to membrane; IEA.
DR      GO; GO:0016020; C:membrane; IEA.
DR      GO; GO:0005351; F:sugar porter activity; IEA.
DR      GO; GO:0005215; F:transporter activity; IEA.
DR      GO; GO:0006810; P:transport; IEA.
DR      InterPro; IPR00515; BPD_transp.
DR      Pfam; PF00528; BPD_transp_1; 1.
DR      PROSITE; PS50928; ABC_TM1; 1.
KW      Complete proteome; Transmembrane; Transport.
SQ      SEQUENCE 290 AA; 31323 MW; 92650429419A5B9 CRC64;

Query Match      68.2%; Score 45; DB 2; Length 290;
Best Local Similarity 77.8%; Pred. No. 26;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 WELVGYFDS 11
Db      171 WMLIGYFDS 179

RESULT 3
OSNO32_ZYMO PRELIMINARY;      PRT;      748 AA.
ID      OSNO32_ZYMO PRELIMINARY;
AC      OSNO32;
DT      01-FEB-2005 (TREMBLrel. 29, Created)
DT      01-FEB-2005 (TREMBLrel. 29, Last sequence update)
DT      01-FEB-2005 (TREMBLrel. 29, Last annotation update)
DE      Polytubonucleotide nucleotidyltransferase (EC 2.7.7.8).
GN      Name=pnp; OrderedLocuNames=ZMO0549;
OS      Zymomonas mobilis.

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OC      Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC      Sphingomonadaceae; Zymomonas.
OX      NCBI_TaxID=542;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC      STRAIN=ATCC 31821 / ZM4 / CP4.
RX      PubMed=15592456; DOI=10.1038/nbt1045;
RA      Seo J.-S., Chong H., Park H.-S., Yoon K.-O., Jung C., Kim J.-J.,
RA      Hong J.-H., Kim H., Kim J.-H., K1 J.-I., Park C.-J., Oh H.-M.,
RA      Lee J.-S., Jin S.-J., Um H.-W., Lee H.-J., Oh S.-J., Kim J.-Y.,
RA      Kang H.-L., Lee S.-Y., Lee K.-J., Kang H.-S.;
RT      "The genome sequence of the ethanologenic bacterium Zymomonas mobilis
RT      ZM4."
RT      Nat. Biotechnol. 23:63-68(2005).
RL      EMBL; AE008692; AA089173.1; -; Genomic DNA.
DR      GO; GO:0000175; F:3'-5'-exoribonuclease activity; IEA.
DR      GO; GO:0004654; F:polynucleotide nucleotidyltransferase a. . .; IEA.
DR      GO; GO:0003723; F:RNA binding; IEA.
DR      GO; GO:0016740; F:transferase activity; IEA.
DR      GO; GO:0006356; P:RNA processing; IEA.
DR      InterPro; IPR001247; 3_ExoRNase.
DR      InterPro; IPR004087; KH.
DR      InterPro; IPR004088; KH_type_1.
DR      InterPro; IPR012162; PNPase.
DR      InterPro; IPR03029; S1.
DR      Pfam; PF00013; KH_1; 1.
DR      Pfam; PF003726; PNPase; 1.
DR      Pfam; PF01138; RNase_PH; 2.
DR      Pfam; PF03725; RNase_PH_C; 2.
DR      Pfam; PF00575; S1; 1.
DR      PIRSF; PIRSF005499; PNPase; 1.
DR      SMART; SM00316; KH; 1.
DR      SMART; SM00316; S1; 1.
DR      SMART; SM00316; KH; 1.
DR      PROSITE; PS50084; KH_TYPE_1; 1.
DR      PROSITE; PS50126; S1; 1.
KW      Complete proteome; Nucleotidyltransferase; Transferase.
SQ      SEQUENCE 748 AA; 81949 MW; EB8C43821F85F6B CRC64;

Query Match      68.2%; Score 45; DB 2; Length 748;
Best Local Similarity 80.0%; Pred. No. 67;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 WELVGYFDS 11
Db      230 WELVGYFDS 239

RESULT 4
WECA_SALTI STANDARD;      PRT;      367 AA.
ID      WECA_SALTI
AC      Q82386;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      10-MAY-2005 (Rel. 47, Last annotation update)
DE      Undecaprenyl-phosphate alpha-N-acetylglucosaminyl 1-phosphate
DE      transferase (EC 2.7.8.-) (UDP-GlcNAc:undecaprenyl-1-phosphate GlcNAc-1-
DE      phosphate transferase).
GN      Name=weca; Synonyms=srfE; OrderedLocuNames=STY3637, t3379;
OS      Salmoneella typhi;
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC      Enterobacteriaceae; Salmoneella.
OX      NCBI_TaxID=601;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC      STRAIN=CT18;
RX      MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
RA      Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA      Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebatista M.,
RA      Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA      Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA      Feltham T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jegerle K.,
RA      Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA      Quail M.A., Rutherford K.M., Simmonds M., Skellern J., Stevens K.,

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RA Whitehead S., Barrell B.G.,  
 RT "Complete genome sequence of a multiple drug resistant *Salmonella*  
 RT enterica serovar Typhi CT18.";  
 RL Nature 413:848-852(2001).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=Ty2 / ATCC 700931;  
 RX MEDLINE=22531367; PubMed=12644504;  
 RX DOI=10.1128/JB.185.7.2330-2337.2003;  
 RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,  
 RA Burland V., Kodoyianni Y., Schwartz D.C., Blatner F.R.,  
 RT "Comparative genomics of *Salmonella enterica* serovar Typhi strains Ty2  
 RT and CT18.";  
 RL J. Bacteriol. 185:2330-2337(2003).  
 CC -1- FUNCTION: Catalyzes the synthesis of Und-PP-GlcNAc (lipid I), the  
 CC first lipid-linked intermediate involved in ECA synthesis. This  
 CC lipid is also an acceptor for the addition of subsequent sugars to  
 CC complete the biosynthesis of O-antigen (By similarity).  
 CC -1- CATALYTIC ACTIVITY: UDP-N-acetyl-D-glucosamine + undecaprenyl  
 CC phosphate = UMP + N-acetyl-alpha-D-glucosaminylidiphospho-  
 CC undecaprenol.  
 CC -1- COFACTOR: Magnesium and manganese (By similarity).  
 CC -1- PATHWAY: Synthesis of enterobacterial common antigen (ECA).  
 CC SYNTHESIS OF LIPOLYACCHARIDE O-ANTIGEN.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane  
 CC (By similarity).  
 CC -1- SIMILARITY: Belongs to the glycosyltransferase 4 family. Weca  
 CC subfamily.  
 CC -----  
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 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
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 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC DR EMBL; AL627279; CA09398.1; -; Genomic DNA.  
 CC DR EMBL; AE016845; AAC070903.1; -; Genomic DNA.  
 CC DR InterPro; IPR012750; ECA Weca rel.  
 CC DR InterPro; IPR000715; Glyco\_trans\_4.  
 CC DR Pfam; PF00953; Glycos\_transf\_4; 1.  
 CC DR TIGRFam; TIGR02380; ECA\_weca; 1.  
 CC KW Complete proteome; Glycosyltransferase; Inner membrane;  
 CC Lipopolysaccharide biosynthesis; Magnesium; Manganese; Membrane;  
 CC Transferrase; Transmembrane.  
 CC FT TRANSMEM 3 23 Potential.  
 CC FT TRANSMEM 45 65 Potential.  
 CC FT TRANSMEM 69 89 Potential.  
 CC FT TRANSMEM 106 126 Potential.  
 CC FT TRANSMEM 129 149 Potential.  
 CC FT TRANSMEM 158 178 Potential.  
 CC FT TRANSMEM 187 207 Potential.  
 CC FT TRANSMEM 213 233 Potential.  
 CC FT TRANSMEM 242 262 Potential.  
 CC FT TRANSMEM 294 314 Potential.  
 CC FT TRANSMEM 318 338 Potential.  
 CC SQ SEQUENCE 367 AA; 41086 MW; 28DA31CB1AE2D930 CRC64;  
 Query Match 66.7%; Score 44; DB 1; Length 367;  
 Best Local Similarity 69.2%; Pred. No. 49;  
 Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;  
 Oy 1 GPMELV-----GYF 9  
 Db 127 GPMELVLCGPGF 139  
 RESULT 5  
 MECA SALTY STANDARD; PRT; 367 AA.  
 ID MECA SALTY STANDARD; PRT; 367 AA.  
 AC 0916R7; 033788; (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Undecaprenyl-phosphate alpha-N-acetylglucosaminyl 1-phosphate  
 DE transferase (EC 2.7.8.-) (UDP-GlcNAc:undecaprenyl-phosphate GlcNAc-1-  
 DE phosphate transferase).  
 GN Name=Weca; Synonyms=rfe; OrderedLocNames=STM31918; ORFNames=STM1.72;  
 OS *Salmonella typhimurium*.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; *Salmonella*.  
 OC NCBI\_TaxId=602;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=L72 / SCS1412 / ATCC 700720.  
 RX MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;  
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,  
 RA Courtney L., Porwollik S., Ali J., Dante M., Du P., Hou S., Layman D.,  
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewel N., Mulvaney E.,  
 RA Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,  
 RA Waterston R., Wilson R.K.;  
 RT "Complete genome sequence of *Salmonella enterica* serovar Typhimurium  
 RT L72.";  
 RL Nature 413:852-856(2001).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE OF 111-367.  
 RC STRAIN=L72;  
 RX MEDLINE=98409259; PubMed=9738879; DOI=10.1007/s004380050787;  
 RA Mouslim C., Cano D.A., Casadesus J.;  
 RT "The sfx, rfe and meth genes of *Salmonella typhimurium* and their  
 RT involvement in the His(c) pleiotropic response.";  
 RL Mol. Gen. Genet. 259:46-53(1998).  
 CC -1- FUNCTION: Catalyzes the synthesis of Und-PP-GlcNAc (lipid I), the  
 CC first lipid-linked intermediate involved in ECA synthesis. This  
 CC lipid is also an acceptor for the addition of subsequent sugars to  
 CC complete the biosynthesis of O-antigen (By similarity).  
 CC -1- CATALYTIC ACTIVITY: UDP-N-acetyl-D-glucosamine + undecaprenyl  
 CC phosphate = UMP + N-acetyl-alpha-D-glucosaminylidiphospho-  
 CC undecaprenol.  
 CC -1- COFACTOR: Magnesium and manganese (By similarity).  
 CC -1- ENZYME REGULATION: Inhibited by tunicamycin.  
 CC -1- PATHWAY: Synthesis of enterobacterial common antigen (ECA).  
 CC SYNTHESIS OF LIPOLYACCHARIDE O-ANTIGEN.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane  
 CC (By similarity).  
 CC -1- SIMILARITY: Belongs to the glycosyltransferase 4 family. Weca  
 CC subfamily.  
 CC -----  
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 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC DR EMBL; AF233324; AAF33469.1; -; Genomic DNA.  
 CC DR EMBL; AE008883; ALU22767.1; -; Genomic DNA.  
 CC DR EMBL; AJ002275; CAA05287.1; -; Genomic DNA.  
 CC DR StyGene; SG27272; rfe.  
 CC DR InterPro; IPR012750; ECA Weca rel.  
 CC DR InterPro; IPR000715; Glyco\_trans\_4.  
 CC DR Pfam; PF00953; Glycos\_transf\_4; 1.  
 CC DR TIGRFam; TIGR02380; ECA\_weca; 1.  
 CC KW Complete proteome; Glycosyltransferase; Inner membrane;  
 CC Lipopolysaccharide biosynthesis; Magnesium; Manganese; Membrane;  
 CC Transferrase; Transmembrane.  
 CC FT TRANSMEM 3 23 Potential.  
 CC FT TRANSMEM 45 65 Potential.  
 CC FT TRANSMEM 69 89 Potential.  
 CC FT TRANSMEM 106 126 Potential.  
 CC FT TRANSMEM 129 149 Potential.  
 CC FT TRANSMEM 158 178 Potential.  
 CC FT TRANSMEM 187 207 Potential.  
 CC FT TRANSMEM 213 233 Potential.  
 CC FT TRANSMEM 242 262 Potential.  
 CC FT TRANSMEM 294 314 Potential.  
 CC FT TRANSMEM 318 338 Potential.  
 CC FT CONFLICT 118 120 HLG -> ALS (in Ref. 2).

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FT CONFLICT 128 138 PHELVLPFGY -> ALGVSAWPLMH (in Ref. 2).
FT CONFLICT 146 148 MAA -> LMG (in Ref. 2).
FT CONFLICT 220 S -> C (in Ref. 2).
SQ SEQUENCE 367 AA; 41087 MM; 1EDA31CB1AE2D938 CRC64;

Query Match 66.7%; Score 44; DB 1; Length 367;
Best Local Similarity 69.2%; Pred. No. 49;
Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 GPMELV---GYF 9
Db 127 GPMELVLPFGYF 139

RESULT 6
05PKK1_SALPA PRELIMINARY; PRT; 367 AA.
AC 05PKK1;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE Putative undecaprenyl-phosphate alpha-N-
acetylglucosaminyltransferase.
GN Name=rfc; OrderedLocNames=SPA3758;
OS Salmonella paratyphi-a.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=54388;
RX [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 9150;
RX PubMed=15531882; DOI=10.1038/ng1470;
RA McClelland M., Sanderson K.E., Clifton S.W., Latreille P.,
RA Porwollik S., Sabo A., Meyer R., Bieri T., Ozeraky P., McClelland M.,
RA Harting C.R., Wang C., Nguyen C., Berghof A., Elliott G.,
RA Kohlberg S., Strong C., Du F., Carter J., Kremzki C., Layman D.,
RA Leonard S., Sun H., Fulton L., Nash W., Miner T., Minx P.,
RA Delhaunty K., Fronick C., Magrini V., Nhan M., Warren W., Florea L.,
RA Splich J., Wilson R.K.;
RT "Comparison of genome degradation in Paratyphi A and Typhi, human-
restricted serovars of Salmonella enterica that cause typhoid.";
RL Nat. Genet. 36:1268-1274(2004).
DR EMBL; CP000026; AAV79540.1; -; Genomic DNA.
DR GO; GO:0019866; C:inner membrane; IEA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016752; P:transferase activity; transferring glycosyl. . .; IEA.
DR GO; GO:0006629; P:lipid metabolism; IEA.
DR InterPro; IPR00715; Glyco_trans_4.
DR Pfam; PF00953; Glyco_transf_4.1.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
KM Complete proteome; Glycosyltransferase; Transferase.
SQ SEQUENCE 367 AA; 41086 MM; 1EDA31CB1AE2D938 CRC64;

Query Match 66.7%; Score 44; DB 2; Length 367;
Best Local Similarity 69.2%; Pred. No. 49;
Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 GPMELV---GYF 9
Db 127 GPMELVLPFGYF 139

RESULT 7
063NS3_BURPS PRELIMINARY; PRT; 449 AA.
AC 063NS3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=BPS0443;

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OS Burkholderia pseudomallei (Pseudomonas pseudomallei).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; pseudomallei group.
OX NCBI_TaxID=28450;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K96243;
RX PubMed=15377794; DOI=10.1073/pnas.0403302101;
RA Holden M.T.G., Tildall R.W., Peacock S.J., Cerdeno-Tarrega A.-M.,
RA Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.L.,
RA Bentley S.D., Sebahia M., Thomson N.R., Bason N., Beacham I.R.,
RA Brooks K., Brown K.A., Brown N.P., Challis G.L., Cherevach I.,
RA Chillingworth T., Cronin A., Crosslet B., Davis P., Desnazer D.,
RA Felwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagsels K.,
RA Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
RA Rabinowitsch E., Rutherford K., Sanders M., Simmonds M.,
RA Songvilay S., Stevens K., Tumapa S., Vearatchaveest M.,
RA Whitehead S., Yeats C., Barrett B.G., Oyston P.C.F., Parkhill J.;
RT "Genomic plasticity of the causative agent of melioidosis,"
RT Burkholderia pseudomallei."
RL Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
DR EMBL; BX571966; CAH37899.1; -; Genomic DNA.
KM Complete proteome; Hypothetical protein.
SQ SEQUENCE 449 AA; 49531 MM; F1618B746D15240 CRC64;

Query Match 66.7%; Score 44; DB 2; Length 449;
Best Local Similarity 75.0%; Pred. No. 60;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPMELVGY 8
Db 183 GPMRLIGY 190

RESULT 8
04K719_PSEF PRELIMINARY; PRT; 231 AA.
AC 04K719;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Phosphoserine phosphatase, putative.
GN ORFNames=PFL_4883;
OS Pseudomonas fluorescens (strain Pf-5).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=220664;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PF-5;
RX PubMed=15980661; DOI=10.1038/nbt1110;
RA Paulsen I.T., Press C., Ravel J., Kobayashi D., Myers G.S.,
RA Mavrodidi D., DeBoy R.T., Seehardt R., Ren O., Madupu R., Dodson R.J.,
RA Durkin S., Brinkay L.M., Daugherty S.C., Sullivan S.A., Rosovitz M.,
RA Gwinn M.L., Zhou L., Nelson W.C., Weidman J., Watkins K., Tan K.,
RA Khouli H.M., Pierson E., Pierson L., III, Thomasow L., Loper J.;
RT "Complete genome sequence of the plant commensal Pseudomonas
fluorescens Pf-5."
RL Nat. Biotechnol. 23:873-878(2005).
DR EMBL; CP000076; AAY94113.1; -; Genomic DNA.
SQ SEQUENCE 231 AA; 25717 MM; A4DEA84C59107CF2 CRC64;

Query Match 65.2%; Score 43; DB 2; Length 231;
Best Local Similarity 80.0%; Pred. No. 46;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PHELVGYFDS 11
Db 61 PAELVGYFDS 70

RESULT 9
07UYRE_RHOBA

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ID Q7UYR6: RHODA PRELIMINARY; PRT; 1201 AA.
AC Q7UYR6;
DT 01-OCT-2003 (TREMblrel. 25, Created)
DT 01-OCT-2003 (TREMblrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE Hypoetical protein.
GN Rhodopirellula baltica.
OS OrderedLocuNames=RB426;
OC Rhodopirellula baltica.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxId=117;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heilmann K., Rabus R.,
RA Schlesner H., Amann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
RT strain 1."
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
DR EMBL; BX294133; CAD71575.1; -; Genomic_DNA.
DR GO; GO:0020037; F:heme binding; IEA.
DR GO; GO:006118; P:electron transport; IEA.
DR InterPro; IPR012282; Cytochrome_c_R.
DR InterPro; IPR011444; DUF1549.
DR InterPro; IPR011429; PSC3.
DR Pfam; PF07635; PSCy1; 1.
DR Pfam; PF07583; PSCy2; 1.
DR Pfam; PF07587; PSD1; 1.
KW Complete proteome; Hypoetical protein.
SQ SEQUENCE 1201 AA; 134482 MW; 7286827735130D01 CRC64;

Query Match 65.2%; Score 43; DB 2; Length 1201;
Best Local Similarity 72.7%; Pred. No. 2.4e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GPMELVGYFDS 11
Db 1029 GIMELVGYTDS 1039

RESULT 10
VP74_CABEL STRAND; PRT; 1633 AA.
AC Q09221; Q10908;
DT 01-NOV-1995 (Rel. 32, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Hypoetical protein B0228.4 in chromosome II.
GN ORFNames=B0228.4/B0228.2;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxId=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE REVISION.
RG Wormbase consortium;
RL Submitted (JUL-2002) to the EMBL/Genbank/DBJ databases.

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CC removed.
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CC EMBL; U23168; AAC38806.2; -; Genomic DNA.
DR Ensembl; B0228.4; Caenorhabditis elegans.
DR Wormbase; WBGene0015061; B0228.4.
DR WormPep; B0228.4; CE31282.
DR InterPro; IPR010734; Copine.
DR Pfam; PF07002; Copine; 1.
DR PRINTS; PR00453; VMPADOMAIN.
KW Complete proteome; Hypoetical protein.
FT COMEBIAS 155 165 Cys-rich.
FT COMEBIAS 316 338 Lys-rich.
FT COMEBIAS 892 1019 Glu-rich.
SQ SEQUENCE 1633 AA; 183328 MW; 3B4EB46800B7A44D CRC64;

Query Match 65.2%; Score 43; DB 1; Length 1633;
Best Local Similarity 60.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPMELVGYFD 10
Db 1567 GPMNMGRFD 1576

RESULT 11
Q5WRU1_CABEL PRELIMINARY; PRT; 7548 AA.
AC Q5WRU1_CABEL;
DT 25-OCT-2004 (TREMblrel. 28, Created)
DT 25-OCT-2004 (TREMblrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMblrel. 28, Last annotation update)
DE Hypoetical protein B0228.4.
GN ORFNames=B0228.4;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxId=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL; U23168; AAU87832.1; -; Genomic_DNA.
DR Ensembl; B0228.4; Caenorhabditis elegans.
DR Wormbase; WBGene0015061; B0228.4.
DR WormPep; B0228.4; CE37470.
DR InterPro; IPR010734; Copine.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF07002; Copine; 1.
DR SMART; SM00327; VWA; 1.
KW Complete proteome; Hypoetical protein.
SQ SEQUENCE 7548 AA; 840584 MW; 8BEC3CC03D12C1C8 CRC64;

Query Match 65.2%; Score 43; DB 2; Length 7548;
Best Local Similarity 60.0%; Pred. No. 1.5e+03;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPMELVGYFD 10
Db 7482 GPMNMGRFD 7491

RESULT 12
Q748S8_GEOSL PRELIMINARY; PRT; 272 AA.
AC Q748S8;
DT 05-JUL-2004 (TREMblrel. 27, Created)
DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
DE Glutamate racemase (EC 5.1.1.3).
GN Name=mxr1; OrderedLocuNames=GSU2923;
```

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OS Geobacter sulfurreducens.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
OC Geobacteraceae; Geobacter.
OX NCBI_TaxID=35554;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PCA / ATCC 51573;
RX PubMed=14671304; DOI=10.1126/science.1088727;
RA Mehe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
RA Heidelberg J.F., Wu D., Wu M., Ward N.L., Beaman M.J., Dodson R.J.,
RA Madupu R., Brinkac L.M., Daugherty S.C., Deboy R.T., Durkin A.S.,
RA Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
RA Davidson T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
RA Weidman J.E., Khouli H.M., Feldblyum T.V., Ullrich T.R.,
RA Van Aken S.E., Lovley D.R., Fraser C.M.;
RT "Genome of Geobacter sulfurreducens: metal reduction in subsurface
RT environments.";
RU Science 302:1967-1969 (2003).
DR EMBL; AE017180; AAR36315.1; -; Genomic_DNA.
DR HSSP; P56868; 1B74.
DR TIGR; GSU2923; -.
DR GO; GO:0008881; F:glutamate racemase activity; IEA.
DR GO; GO:0016853; P:isomerase activity; IEA.
DR GO; GO:0009252; P:peptidoglycan biosynthesis; IEA.
DR InterPro; IPR001920; Asp/Glu_race.
DR InterPro; IPR004391; Glu_race.
DR Pfam; PF01177; Asp_Glu_race; 1.
DR TIGRFAMs; TIGR00067; glut_race; 1.
DR PROSITE; PS00923; ASP_GLU_RACEMASE_1; 1.
DR PROSITE; PS00924; ASP_GLU_RACEMASE_2; 1.
KW Complete proteome; Isomerase.
SQ SEQUENCE 272 AA; 29521 MW; 674BA01437EC4163 CRC64;

Query Match
Best Local Similarity 63.6%; Score 42; DB 2; Length 272;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PHELVGYFDS 11
Db 2 PWKATGIFDS 11

RESULT 13
Q6KIT5_ORYSA PRELIMINARY; PRT; 381 AA.
AC Q6KIT5;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DS Hypothetical protein OSJNBa0038P01.38.
GN Name=OSJNBa0038P01.38;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Oryza sativa nippondare (GA) genomic DNA, chromosome 2, BAC
RT clone:OSJNBa0038P01.1;
RT Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP006457; BAD22515.1; -; Genomic_DNA.
DR Gramene; Q6KIT5; -.
DR GO; GO:000512; P:ubiquitin cycle; IEA.
DR InterPro; IPR001810; F-box.
DR Pfam; PF00646; F-box; 1.
KW Hypothetical protein.
SQ SEQUENCE 381 AA; 42714 MW; A50564C2F7224FC4 CRC64;

Query Match
Best Local Similarity 63.6%; Score 42; DB 2; Length 381;
Matches 6; Conservative 75.0%; Pred. No. 1.1e+02;

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Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GPMELVGY 8
Db 176 GPMELVGY 183

RESULT 14
Q8TV9 METAC PRELIMINARY; PRT; 454 AA.
AC Q8TV9;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DS Hypothetical protein MA3668.
GN OrderedlocusNames=MA3668;
OS Methanococcus acetiivorans.
OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=1193238; DOI=10.1101/gr.223902;
RA Galagan J.E., Nisbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA Fitzhugh W., Calvo S., Engels R., Smirnov S., Atcoor D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., DeArelano K., Johnson R.,
RA Linton L., McEwan P., McKernan K., Talamas J., Turrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A., Smith K.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA Ferry J.G., Jarell K.F., Jing H., Macario A.J.L., Paulsen I.T.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT and physiological diversity.";
RU Genome Res. 12:532-542(2002).
DR EMBL; AE011076; AAM07023.1; -; Genomic_DNA.
DR InterPro; IPR010180; Cas_CXXC_CXXC.
DR TIGRFAMs; TIGR01908; cas_CXXC_CXXC; 1.
KW Complete proteome.
SQ SEQUENCE 454 AA; 52893 MW; 2BBDA6A6E629B0A0 CRC64;

Query Match
Best Local Similarity 66.7%; Score 42; DB 2; Length 454;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GPMELVGY 9
Db 319 GPMELVGY 327

RESULT 15
Q8D959_VIBVU PRELIMINARY; PRT; 578 AA.
ID Q8D959_VIBVU
AC Q8D959;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DS Methyl-accepting chemotaxis protein.
GN OrderedlocusNames=VVI2747;
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=672;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CMCP6;
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RA Choy H.B.;
RT "Complete genome sequence of Vibrio vulnificus CMCP6.";
RT Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.

```

DR EMBL; AE016806; AA011091.1; -; Genomic\_DNA.  
 DR HSSP; P02942; 1QJ7.  
 DR GO; GO:0019866; C:inner membrane; IEA.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0004871; F:signal transducer activity; IEA.  
 DR GO; GO:0004871; F:signal transducer activity; IEA.  
 DR GO; GO:0006935; P:chemotaxis; IEA.  
 DR GO; GO:0007165; P:signal transduction; IEA.  
 DR InterPro; IPR004089; Chmtaxis transd.  
 DR InterPro; IPR003660; His\_kin\_HAMP.  
 DR Pfam; PF00672; HAMP; 1.  
 DR Pfam; PF00015; MCPsignal; 1.  
 DR SMART; SM00304; HAMP; 1.  
 DR SMART; SM00283; MA; 1.  
 DR PROSITE; PS50111; CHEMOTAXIS\_TRANSDUC\_2; 1.  
 DR PROSITE; PS50885; HAMP; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 578 AA; 63178 MW; 55004ADCT356DA18 CRC64;

Query Match 63.6%; Score 42; DB 2; Length 578;  
 Best Local Similarity 75.0%; Pred. No. 1.7e+02;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 Oy 3 WELVGYFD 10  
 |||:||||  
 Db 204 WELIGYID 211

Search completed: December 4, 2005, 04:52:22  
 Job time : 102.375 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 4, 2005, 03:59:51 ; Search time 23.6042 Seconds  
(without alignments)  
38.528 Million cell updates/sec

Title: US-10-632-706-128  
Perfect score: 66  
Sequence: 1 GPMELVGYFDS 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA: \*  
1: /cgn2\_6/ptodata/1/1aa/5\_COMB.pep: \*  
2: /cgn2\_6/ptodata/1/1aa/6\_COMB.pep: \*  
3: /cgn2\_6/ptodata/1/1aa/H\_COMB.pep: \*  
4: /cgn2\_6/ptodata/1/1aa/PTUS\_COMB.pep: \*  
5: /cgn2\_6/ptodata/1/1aa/RE\_COMB.pep: \*  
6: /cgn2\_6/ptodata/1/1aa/backfill1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	62.1	12	1	US-08-264-093-17 Sequence 17, Appl
2	41	62.1	121	1	US-08-264-093-3 Sequence 3, Appl
3	39	59.1	274	2	US-09-902-540-14253 Sequence 14253, A
4	38	57.6	332	2	US-09-561-763-5 Sequence 5, Appl
5	38	57.6	332	2	US-09-431-367B-5 Sequence 5, Appl
6	38	57.6	493	2	US-09-949-016-10836 Sequence 10836, A
7	38	57.6	1207	2	US-09-976-594-4 Sequence 4, Appl
8	37	56.1	427	2	US-09-902-540-15261 Sequence 15261, A
9	37	56.1	484	2	US-09-543-681A-6615 Sequence 6615, Ap
10	36	54.5	132	2	US-09-311-021-162 Sequence 162, App
11	36	54.5	140	2	US-09-698-341-29 Sequence 29, Appl
12	36	54.5	174	2	US-09-902-540-13916 Sequence 13916, A
13	36	54.5	194	2	US-08-260-202A-15 Sequence 15, Appl
14	36	54.5	194	1	US-08-260-202A-24 Sequence 24, Appl
15	36	54.5	194	1	US-08-017-114-15 Sequence 15, Appl
16	36	54.5	194	1	US-08-017-114-17 Sequence 17, Appl
17	36	54.5	194	2	US-08-505-307-15 Sequence 15, Appl
18	36	54.5	194	2	US-08-505-307-17 Sequence 17, Appl
19	36	54.5	194	2	US-09-609-151A-15 Sequence 15, Appl
20	36	54.5	194	2	US-09-609-151A-17 Sequence 17, Appl
21	36	54.5	194	4	PCR-US94-02034-15 Sequence 15, Appl
22	36	54.5	194	4	PCR-US94-02034-17 Sequence 17, Appl
23	36	54.5	206	2	US-09-902-540-16467 Sequence 16467, A
24	36	54.5	235	2	US-09-252-991A-29814 Sequence 29814, A
25	36	54.5	266	2	US-09-252-991A-21116 Sequence 21116, A
26	36	54.5	321	2	US-09-134-000C-3783 Sequence 3783, Ap
27	36	54.5	500	2	US-09-538-092-831 Sequence 831, App

28	36	54.5	521	2	US-09-221-294-2 Sequence 2, Appl
29	36	54.5	589	2	US-09-489-039A-8395 Sequence 8395, Ap
30	36	54.5	710	2	US-09-518-550-28 Sequence 28, Appl
31	36	54.5	729	2	US-10-104-047-3450 Sequence 3450, Ap
32	36	54.5	751	2	US-09-252-991A-22770 Sequence 22770, A
33	36	54.5	792	2	US-09-994-192-2 Sequence 2, Appl
34	36	54.5	797	2	US-09-994-192-4 Sequence 4, Appl
35	36	54.5	1542	2	US-09-949-016-9215 Sequence 9215, Ap
36	36	54.5	3177	1	US-08-477-451-4 Sequence 4, Appl
37	36	54.5	5532	2	US-09-914-286-6 Sequence 6, Appl
38	35	53.0	61	2	US-08-978-741-3 Sequence 3, Appl
39	35	53.0	61	2	US-09-333-729A-5 Sequence 5, Appl
40	35	53.0	99	2	US-09-330-134B-45 Sequence 45, Appl
41	35	53.0	142	2	US-09-902-540-13948 Sequence 13948, A
42	35	53.0	160	2	US-09-668-673B-7 Sequence 7, Appl
43	35	53.0	160	2	US-10-389-532-7 Sequence 7, Appl
44	35	53.0	166	2	US-09-302-626B-52 Sequence 52, Appl
45	35	53.0	166	2	US-09-303-518D-886 Sequence 886, App

ALIGNMENTS

RESULT 1  
US-08-264-093-17  
Sequence 17, Application US/08264093  
Parent No. 5639863  
GENERAL INFORMATION:  
APPLICANT: Michael D. Dan  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO  
TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ridout & Maybee  
STREET: 2300 Richmond-Adelaide Centre  
STREET: 101 Richmond Street West  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5H 2J7  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette - 3.5 inch, 1.4 MB storage  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: MS-DOS 6.00  
SOFTWARE: ASCII Editor  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/264, 093  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA: No. 5639863 applicable  
ATTORNEY/AGENT INFORMATION:  
NAME: Lake, James R.  
REGISTRATION NUMBER: 31081  
REFERENCE/DOCKET NUMBER: NOVOP/106A/7551  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 868-1482  
TELEFAX: (416) 362-0823  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: not applicable  
TOPOLOGY: linear  
US-08-264-093-17  
Query Match 62.1%; Score 41; DB 1; Length 12;  
Best Local Similarity 60.0%; Pred. No. 0.51;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
DB 1 GPMELVGYFD 10  
2 GVMIDLNYFD 11

## RESULT 2

US-08-264-093-3

Sequence 3, Application US/08264093

Patent No. 5639863

GENERAL INFORMATION:

APPLICANT: Michael D. Dan

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO

TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE

TITLE OF INVENTION: ANTIGEN

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ridout &amp; Maybee

STREET: 2300 Richmond-Adelaide Centre

STREET: 101 Richmond Street West

CITY: Toronto

STATE: Ontario

COUNTRY: Canada

ZIP: M5H 2J7

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: MS-DOS 6.00

SOFTWARE: ASCII Editor

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/264,093

FILING DATE:

CLASSIFICATION: 536

PRIOR APPLICATION DATA: No. 5639863 applicable

ATTORNEY/AGENT INFORMATION:

NAME: Lake, James R.

REGISTRATION/DOCKET NUMBER: 31081

TELECOMMUNICATION INFORMATION:

TELEPHONE: (416) 868-1482

TELEFAX: (416) 362-0823

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 121 amino acids

TYPE: amino acid

STRANDEDNESS: not applicable

TOPOLOGY: linear

US-08-264-093-3

Query Match US-08-264-093-3 Score 41; DB 1; Length 121;

Best Local Similarity 60.0%; Pred. No. 6.7;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPMELVGYFD 10

DB 100 GWMDLNLYFD 109

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ORGANISM: Myxococcus xanthus

US-09-902-540-14253

Query Match

Best Local Similarity 59.1%; Score 39; DB 2; Length 274;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 WELVGYFDS 11

DB 153 WNLKGYFDT 161

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ORGANISM: Myxococcus xanthus

US-09-902-540-14253

Query Match

Best Local Similarity 59.1%; Score 39; DB 2; Length 274;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 WELVGYFDS 11

DB 153 WNLKGYFDT 161

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ORGANISM: Myxococcus xanthus

US-09-902-540-14253

Query Match

Best Local Similarity 59.1%; Score 39; DB 2; Length 274;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 WELVGYFDS 11

DB 153 WNLKGYFDT 161

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ORGANISM: Myxococcus xanthus

US-09-902-540-14253

Query Match

Best Local Similarity 59.1%; Score 39; DB 2; Length 274;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 WELVGYFDS 11

DB 153 WNLKGYFDT 161

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ORGANISM: Myxococcus xanthus

US-09-902-540-14253

Query Match

Best Local Similarity 59.1%; Score 39; DB 2; Length 274;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 WELVGYFDS 11

DB 153 WNLKGYFDT 161

Db

Db

Db

Db



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US-09-949-016-10836
; Sequence 10836, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMERISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10836
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10836

Query Match          57.6%; Score 38; DB 2; Length 493;
Best Local Similarity 60.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy      2  GPWELVGYFDS 11
      |||:|||||
Db      69  PWTAKVDYFDN 78

RESULT 7
US-09-976-594-4
; Sequence 4, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LAYER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 1207
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 1863336CD1
US-09-976-594-4

Query Match          57.6%; Score 38; DB 2; Length 1207;
Best Local Similarity 77.8%; Pred. No. 3.1e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      1  GPWELVGYF 9
      |||:|||||
Db      389  GPTEAVGYF 397

RESULT 8
US-09-902-540-15261
; Sequence 15261, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
```

```
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 15261
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-15261

Query Match          56.1%; Score 37; DB 2; Length 427;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy      1  GPWELVGYF 9
      |||:|||||
Db      82  GPESFVGYF 90

RESULT 9
US-09-543-681A-6615
; Sequence 6615, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETTON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709,1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 6615
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-6615

Query Match          56.1%; Score 37; DB 2; Length 484;
Best Local Similarity 55.6%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy      3  WEVGYFDS 11
      |||:|||||
Db      155  WALIGYQS 163

RESULT 10
US-09-311-021-162
; Sequence 162, Application US/09311021
; Patent No. 6706869
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agostino, Michael J.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI 6300-11A
; CURRENT APPLICATION NUMBER: US/09/311,021
; CURRENT FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 162
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-09-311-021-162

Query Match 54.5%; Score 36; DB 2; Length 132;  
Best Local Similarity 55.6%; Pred. No. 59;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPMVLVGYF 9  
|||: |||  
Db 121 GPMVDLPYF 129

RESULT 11

US-09-698-341-29  
; Sequence 29, Application US/09698341  
; Patent No. 6946273  
; GENERAL INFORMATION:  
; APPLICANT: Sorige, Joseph  
; APPLICANT: Hurlbut Hogrefe, Holly  
; APPLICANT: Connie, Hansen  
; TITLE OF INVENTION: Compositions and Methods Utilizing DNA Polymerases  
; FILE REFERENCE: 25436/1560  
; CURRENT APPLICATION NUMBER: US/09/698,341  
; CURRENT FILING DATE: 2000-10-27  
; PRIOR APPLICATION NUMBER: 60/162,600  
; PRIOR FILING DATE: 1999-10-29  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 29  
; LENGTH: 140  
; TYPE: PRT  
; ORGANISM: Thermococcus sp. JDF-3  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (92)...(92)  
; OTHER INFORMATION: X = Unknown  
US-09-699-341-29

Query Match 54.5%; Score 36; DB 2; Length 140;  
Best Local Similarity 50.0%; Pred. No. 63;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GPMVLVGYF 10  
|||: |||  
Db 55 GPMVDIVYLD 64

RESULT 12

US-09-902-540-13916  
; Sequence 13916, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 13916  
; LENGTH: 174  
; TYPE: PRT  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-13916

Query Match 54.5%; Score 36; DB 2; Length 174;  
Best Local Similarity 85.7%; Pred. No. 81;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 LVGYFDS 11

Db 6 LIGYFDS 12  
|||: |||

RESULT 13

US-08-260-202A-15  
; Sequence 15, Application US/08260202A  
; Patent No. 5573910  
; GENERAL INFORMATION:  
; APPLICANT: Deretic, Vojo  
; APPLICANT: Martin, Daniel W.  
; TITLE OF INVENTION: DETECTION OF CONVERSION TO MUCOIDY IN  
; TITLE OF INVENTION: PSEUDOMONAS AERUGINOSA INFECTING CYSTIC FIBROSIS PATIENTS  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P. O. Box 4433  
; CITY: Houston  
; STATE: TX  
; COUNTRY: USA  
; ZIP: 77210-4433  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/260,202A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/260,202  
; FILING DATE: 15-JUN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/017,114  
; FILING DATE: 12-FEB-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hodgins, Daniel S.  
; REGISTRATION NUMBER: 31,026  
; REFERENCE/DOCKET NUMBER: UTSK:221\HOD  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (512) 474-7577  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 194 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-260-202A-15

Query Match 54.5%; Score 36; DB 1; Length 194;  
Best Local Similarity 71.4%; Pred. No. 91;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPMVLVGYF 7  
|||: |||  
Db 81 GPMRVNG 87

RESULT 14

US-08-260-202A-24  
; Sequence 24, Application US/08260202A  
; Patent No. 5573910  
; GENERAL INFORMATION:  
; APPLICANT: Deretic, Vojo  
; APPLICANT: Martin, Daniel W.  
; TITLE OF INVENTION: DETECTION OF CONVERSION TO MUCOIDY IN  
; TITLE OF INVENTION: PSEUDOMONAS AERUGINOSA INFECTING CYSTIC FIBROSIS PATIENTS  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P. O. Box 4433

CITY: Houston  
STATE: TX  
COUNTRY: USA  
ZIP: 77210-4433  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/260,202A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/260,202  
FILING DATE: 15-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/017,114  
FILING DATE: 12-FEB-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Hodgins, Daniel S.  
REGISTRATION NUMBER: 31,026  
REFERENCE/DOCKET NUMBER: UTSK:221\HOD  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 194 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-260-202A-24

Query Match 54.5%; Score 36; DB 1; Length 194;  
Best Local Similarity 71.4%; Pred. No. 91;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPMELVG 7  
||| :||  
Db 81 GPMRMVG 87

RESULT 15  
US-08-017-114-15  
Sequence 15, Application US/08017114  
Patent No. 5591838  
GENERAL INFORMATION:  
APPLICANT: Detecic, Vojo  
APPLICANT: Martin, Daniel W.  
TITLE OF INVENTION: DETECTION OF CONVERSION TO MUCCOIDY IN  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P. O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/017,114  
FILING DATE: 19930212  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Hodgins, Daniel S.  
REGISTRATION NUMBER: 31,026  
REFERENCE/DOCKET NUMBER: UTSK:205/HOD

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512/320-7200  
TELEFAX: 512/474-7577  
TELEX: N/A  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 194 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-017-114-15

Query Match 54.5%; Score 36; DB 1; Length 194;  
Best Local Similarity 71.4%; Pred. No. 91;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPMELVG 7  
||| :||  
Db 81 GPMRMVG 87

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Job time : 23.6042 secs

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OW protein - protein search, using sw model1

Run on: December 4, 2005, 04:07:28 ; Search time 78.8333 Seconds  
(without alignments)  
58.302 Million cell updates/sec

Title: US-10-632-706-128

Perfect score: 66

Sequence: 1 GPMELVGYFDS 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_MA\_Main:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*
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- 6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	66	100.0	11	US-10-632-706-128	Sequence 128, App
2	45	68.2	290	US-10-156-761-9341	Sequence 9341, Ap
3	44	66.7	306	US-10-282-122A-73455	Sequence 73455, A
4	44	66.7	367	US-10-282-122A-74966	Sequence 74966, A
5	44	66.7	367	US-10-282-122A-75801	Sequence 75801, A
6	42	63.6	381	US-10-437-963-192224	Sequence 192224,
7	41	62.1	125	US-10-425-115-253365	Sequence 253365,
8	41	62.1	171	US-10-424-599-186545	Sequence 186545,
9	41	62.1	475	US-10-282-122A-48377	Sequence 48377, A
10	41	62.1	475	US-10-437-963-187947	Sequence 187947,
11	41	62.1	792	US-10-481-032A-252	Sequence 252, App
12	41	62.1	1352	US-11-097-143-29418	Sequence 29418, A
13	40	60.6	50	US-10-424-599-182764	Sequence 182764,
14	40	60.6	78	US-10-425-115-319649	Sequence 319649,
15	40	60.6	146	US-10-477-527-21	Sequence 21, Appl
16	40	60.6	160	US-10-425-115-333207	Sequence 333207,
17	40	60.6	477	US-10-425-114-70098	Sequence 70098, A
18	40	60.6	507	US-10-424-599-229226	Sequence 229226,
19	40	60.6	891	US-10-425-115-229314	Sequence 229314,
20	40	60.6	931	US-10-732-923-22388	Sequence 22388, A
21	40	60.6	949	US-10-732-923-22387	Sequence 22387, A
22	40	60.6	1355	US-10-437-963-110486	Sequence 110486,
23	39.5	58.8	511	US-10-425-114-52508	Sequence 52508, A
24	39	58.1	118	US-10-424-599-157468	Sequence 157468,
25	39	59.1	207	US-10-424-599-153966	Sequence 153966,
26	39	59.1	235	US-10-732-923-22418	Sequence 22418, A
27	39	59.1	460	US-10-424-599-224678	Sequence 224678,

28	39	59.1	522	US-10-437-963-194057	Sequence 194057,
29	39	59.1	537	US-10-739-930-10546	Sequence 10546, A
30	39	59.1	658	US-10-437-963-121136	Sequence 121136,
31	39	59.1	670	US-10-282-122A-46814	Sequence 46814, A
32	39	59.1	696	US-10-450-763-50763	Sequence 50763, A
33	39	59.1	949	US-10-732-923-22382	Sequence 22382, A
34	39	59.1	949	US-10-732-923-22383	Sequence 22383, A
35	39	59.1	954	US-10-437-963-204079	Sequence 204079,
36	39	59.1	1199	US-10-437-963-121132	Sequence 121132,
37	39	59.1	1441	US-10-437-963-111662	Sequence 111662,
38	38	57.6	48	US-09-764-891-5713	Sequence 3713, Ap
39	38	57.6	71	US-10-425-115-277808	Sequence 277808,
40	38	57.6	84	US-10-437-963-150254	Sequence 150254,
41	38	57.6	96	US-10-437-963-141911	Sequence 141911,
42	38	57.6	135	US-10-424-599-205846	Sequence 205846,
43	38	57.6	167	US-10-767-701-60011	Sequence 60011, A
44	38	57.6	185	US-10-424-599-230098	Sequence 230098,
45	38	57.6	207	US-10-425-114-53925	Sequence 53925, A

## ALIGNMENTS

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RESULT 1
US-10-632-706-128
; Sequence 128, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 128
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-128

Query Match      100.0%; Score 66; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00072;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 GPMELVGYFDS 11
Db      1 GPMELVGYFDS 11

RESULT 2
US-10-156-761-9341
; Sequence 9341, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYPEPTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
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; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 9341
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9341

Query Match      68.2%; Score 45; DB 4; Length 290;
Best Local Similarity 77.8%; Pred. No. 38;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      3  WELVGFDS 11
        |||:|||||
Db      171 WMLIGYFDS 179

RESULT 3
US-10-282-122A-73455
; Sequence 73455, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zykkind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Foreyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 73455
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Salmonella paratyphi A
US-10-282-122A-73455

Query Match      66.7%; Score 44; DB 4; Length 306;
Best Local Similarity 69.2%; Pred. No. 58;
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Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy      1  GPWELV---GYF 9
        |||:|||||
Db      66  GPWELVLPFGYF 78

RESULT 4
US-10-282-122A-74966
; Sequence 74966, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zykkind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Foreyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 74966
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Salmonella typhimurium
US-10-282-122A-74966

Query Match      66.7%; Score 44; DB 4; Length 367;
Best Local Similarity 69.2%; Pred. No. 69;
Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy      1  GPWELV---GYF 9
        |||:|||||
Db      127  GPWELVLPFGYF 139

RESULT 5
US-10-282-122A-75801
; Sequence 75801, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
```

APPLICANT: Malone, Cheryl  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Kari  
APPLICANT: Zykend, Judith  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John  
APPLICANT: Carr, Grant  
APPLICANT: Yamamoto, Robert  
APPLICANT: Forsyth, R.  
APPLICANT: Xu, H.  
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
FILE REFERENCE: ELITRA.034A  
CURRENT APPLICATION NUMBER: US/10/282.122A  
CURRENT FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/230,335  
PRIOR FILING DATE: 2000-09-06  
PRIOR APPLICATION NUMBER: 60/230,347  
PRIOR FILING DATE: 2000-09-09  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/267,636  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 78614  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 75801  
LENGTH: 367  
TYPE: PRT  
ORGANISM: Salmonella typhi  
US-10-282-122A-75801

Query Match 66.7%; Score 44; DB 4; Length 367;  
Best Local Similarity 69.2%; Pred. No. 69;  
Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 GPMELV---GYF 9  
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Db 127 GPMELVLCGPGYF 139

RESULT 6  
US-10-437-963-192224  
Sequence 192224, Application US/10437963  
Publication No. US20040123343A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
APPLICANT: Wu, Wei  
APPLICANT: Boukharov, Andrey A.  
APPLICANT: Barbazuk, Brad  
APPLICANT: Li, Ping  
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
FILE REFERENCE: 38-21(53223)B  
CURRENT APPLICATION NUMBER: US/10/437,963  
CURRENT FILING DATE: 2003-05-14  
NUMBER OF SEQ ID NOS: 204966  
SEQ ID NO 192224  
LENGTH: 381

TYPE: PRT  
ORGANISM: Oryza sativa  
FEATURE:  
OTHER INFORMATION: Clone ID: PAT\_MRT4530\_88472C.1.pep  
US-10-437-963-192224

Query Match 63.6%; Score 42; DB 4; Length 381;  
Best Local Similarity 75.0%; Pred. No. 1.5e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPMELVGY 8  
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Db 176 GPMELTGF 183

RESULT 7  
US-10-425-115-253365  
Sequence 253365, Application US/10425115  
Publication No. US20040214272A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Zhou, Yihua  
APPLICANT: Kovalic, David K.  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
FILE REFERENCE: 38-21(53222)B  
CURRENT APPLICATION NUMBER: US/10/425,115  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 369326  
SEQ ID NO 253365  
LENGTH: 125  
TYPE: PRT  
ORGANISM: Zea mays  
FEATURE:  
OTHER INFORMATION: Clone ID: MRT4577\_16264C.1.pep  
US-10-425-115-253365

Query Match 62.1%; Score 41; DB 4; Length 125;  
Best Local Similarity 66.7%; Pred. No. 78;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPMELVGYF 9  
|||  
Db 75 GPMELKGF 83

RESULT 8  
US-10-424-599-186545  
Sequence 186545, Application US/10424599  
Publication No. US20040031072A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
FILE REFERENCE: 38-21(53223)B  
CURRENT APPLICATION NUMBER: US/10/424,599  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 285684  
SEQ ID NO 186545  
LENGTH: 171  
TYPE: PRT  
ORGANISM: Glycine max  
FEATURE:  
OTHER INFORMATION: Clone ID: PAT\_MRT3847\_139463C.1.pep  
US-10-424-599-186545

Query Match 62.1%; Score 41; DB 4; Length 171;  
Best Local Similarity 60.0%; Pred. No. 1e+02;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 GPMELVGYFD 10  
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Db 14 GPMDEMKYFD 23

RESULT 9  
US-10-282-122A-48377  
; Sequence 48377, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangshu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Foreyth, R.  
; APPLICANT: Xu, H.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA.034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A  
; PRIOR FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/230,335  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/230,347  
; PRIOR FILING DATE: 2000-09-09  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; Remaining prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 78614  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 48377  
; LENGTH: 475  
; TYPE: PRT  
; ORGANISM: Bacteroides fragilis  
US-10-282-122A-48377

Query Match 62.1%; Score 41; DB 4; Length 475;  
Best Local Similarity 54.5%; Pred. No. 2.7e+02;  
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 GPMELVGYFDS 11  
|||: |||  
Db 404 GPMKLIYYDS 414

RESULT 10  
US-10-437-963-187947  
; Sequence 187947, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barabzik, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 187947  
; LENGTH: 475  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(475)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_845C.1.pep  
US-10-437-963-187947

Query Match 62.1%; Score 41; DB 4; Length 475;  
Best Local Similarity 70.0%; Pred. No. 2.7e+02;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GPMELVGYFD 10  
|||: |||  
Db 115 GPMEGKGYHD 124

RESULT 11  
US-10-481-032A-252  
; Sequence 252, Application US/10481032A  
; Publication No. US20050177901A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhu, Tong  
; APPLICANT: Cheng, Wenqiong  
; APPLICANT: Briggs, Steven  
; APPLICANT: Cooper, Bret  
; APPLICANT: Goff, Stephen A.  
; APPLICANT: Moughamer, Todd  
; APPLICANT: Glazebrook, Jane  
; APPLICANT: Katagiri, Fumitaki  
; APPLICANT: Kreps, Joel  
; APPLICANT: Provart, Nicolas  
; APPLICANT: Rhee, Darrell  
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES  
; FILE REFERENCE: 60148USPCT  
; CURRENT APPLICATION NUMBER: US/10/481,032A  
; CURRENT FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: US 60/300,112  
; PRIOR FILING DATE: 2001-06-22  
; PRIOR APPLICATION NUMBER: US 60/325,277  
; PRIOR FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: US 60/342,327  
; PRIOR FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: PCT/IB02/02450  
; PRIOR FILING DATE: 2002-06-21  
; NUMBER OF SEQ ID NOS: 1201  
; SOFTWARE: PatentIn Ver. 2.2  
; SEQ ID NO 252  
; LENGTH: 792  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (12)..(14)  
; OTHER INFORMATION: Xaa = any naturally occurring amino acid  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (16)..(16)



OTHER INFORMATION: Xaa = any naturally occurring amino acid  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (399)..(399)  
OTHER INFORMATION: Xaa = any naturally occurring amino acid  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (493)..(493)  
OTHER INFORMATION: Xaa = any naturally occurring amino acid  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (669)..(669)  
OTHER INFORMATION: Xaa = any naturally occurring amino acid  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (671)..(671)  
OTHER INFORMATION: Xaa = any naturally occurring amino acid  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (673)..(673)  
OTHER INFORMATION: Xaa = any naturally occurring amino acid  
US-10-481-032A-252

Query Match 62.1%; Score 41; DB 5; Length 792;  
Best Local Similarity 66.7%; Pred. No. 4.3e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PWEVLGYFD 10  
Db 245 PWEVLGYFD 253

RESULT 12  
US-11-097-143-29418  
Sequence 29418, Application US/11097143  
Publication No. US20050208558A1  
GENERAL INFORMATION:  
APPLICANT: Venter, J. Craig  
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID  
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE  
FILE REFERENCE: CL000728  
CURRENT FILING DATE: 2005-04-04  
PRIOR APPLICATION NUMBER: 60/157,832  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: 60/160,191  
PRIOR FILING DATE: 1999-10-19  
PRIOR APPLICATION NUMBER: 60/161,932  
PRIOR FILING DATE: 1999-10-28  
PRIOR APPLICATION NUMBER: 60/164,769  
PRIOR FILING DATE: 1999-11-12  
PRIOR APPLICATION NUMBER: 60/173,383  
PRIOR FILING DATE: 1999-12-28  
PRIOR APPLICATION NUMBER: 60/175,693  
PRIOR FILING DATE: 2000-01-12  
PRIOR APPLICATION NUMBER: 60/184,831  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: 60/191,637  
NUMBER OF SEQ ID NOS: 43008  
SOFTWARE: Pat-Seq for Windows Version 4.0  
SEQ ID NO 29418  
LENGTH: 1352  
TYPE: PRT  
ORGANISM: DROSOPHILA  
US-11-097-143-29418

Query Match 62.1%; Score 41; DB 6; Length 1352;  
Best Local Similarity 77.8%; Pred. No. 7.2e+02;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 WEVLGYFDS 11  
Db 161 WRNVLGYFDS 169

RESULT 13  
US-10-424-599-182764  
Sequence 182764, Application US/10424599  
Publication No. US20040031072A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa Thomas J  
APPLICANT: Kovacic David K  
APPLICANT: Zhou Yihua  
APPLICANT: Cao Yongwei  
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
FILE REFERENCE: 38-21(53223)B  
CURRENT FILING DATE: US/10/424,599  
NUMBER OF SEQ ID NOS: 285684  
SEQ ID NO 182764  
LENGTH: 50  
TYPE: PRT  
ORGANISM: Glycine max  
FEATURE:  
OTHER INFORMATION: Clone ID: PAT\_MRT3847\_13604C.1.pcp  
US-10-424-599-182764

Query Match 60.6%; Score 40; DB 4; Length 50;  
Best Local Similarity 66.7%; Pred. No. 48;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GPWEVLGYF 9  
Db 32 GKWEVLGYF 40

RESULT 14  
US-10-425-115-319649  
Sequence 319649, Application US/10425115  
Publication No. US20040214272A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovacic, David K.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants  
FILE REFERENCE: 38-21(53222)B  
CURRENT FILING DATE: US/10/425,115  
NUMBER OF SEQ ID NOS: 369326  
SEQ ID NO 319649  
LENGTH: 78  
TYPE: PRT  
ORGANISM: Zea mays  
FEATURE:  
OTHER INFORMATION: Clone ID: MRT4577\_54590C.1.pcp  
US-10-425-115-319649

Query Match 60.6%; Score 40; DB 4; Length 78;  
Best Local Similarity 66.7%; Pred. No. 73;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GPWEVLGYF 9  
Db 21 GPWEVLGYF 29

RESULT 15  
US-10-477-527-21  
Sequence 21, Application US/10477527  
Publication No. US20040171807A1

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; GENERAL INFORMATION:
; APPLICANT: The Trustees of the University of Pennsylvania
; APPLICANT: Gao, Guangping
; APPLICANT: Wilson, James M.
; TITLE OF INVENTION: Method for Rapid Screening of Bacterial Transformants and Novel S
; TITLE OF INVENTION: Adenovirus Proteins
; FILE REFERENCE: UPM-N2630PCT
; CURRENT APPLICATION NUMBER: US/10/477,527
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/300,501
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/385,632
; PRIOR FILING DATE: 2002-06-04
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 146
; TYPE: PRT
; ORGANISM: chimpanzee C68 adenovirus protein
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (62)..(62)
; OTHER INFORMATION: Xaa can be any amino acid
US-10-477-527-21

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Query Match      60.6%; Score 40; DB 4; Length 146;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      1 GPMELVG 7
DB      101 GPMELVG 107

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Search completed: December 4, 2005, 04:37:29  
 Job time : 79.833 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:08:08 ; Search time 3.20833 Seconds  
(without alignments)  
16.417 Million cell updates/sec

Title: US-10-632-706-128

Perfect score: 66  
Sequence: 1 GPMELVGFDS 11

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications NA New:\*  
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3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
7: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	54.5	792	6	US-10-467-657-6026
2	36	54.5	792	6	US-10-467-657-7528
3	35	53.0	356	6	US-10-467-657-1210
4	34	51.5	322	7	US-11-074-176-36
5	34	51.5	723	6	US-10-467-657-1916
6	34	51.5	926	6	US-10-841-129-2
7	33.5	50.8	478	7	US-11-037-829A-4
8	33.5	50.8	198	7	US-11-082-389-302
9	33	50.0	281	7	US-11-082-389-304
10	33	50.0	431	7	US-11-055-822-76
11	33	50.0	724	6	US-10-131-826A-60
12	33	50.0	1510	7	US-11-055-822-72
13	33	50.0	2725	7	US-11-113-424-52
14	32	48.5	456	6	US-10-467-657-4150
15	32	48.5	533	6	US-11-147-047-33
16	32	48.5	771	7	US-11-147-047-34
17	31.5	47.7	532	7	US-11-184-380-6
18	31.5	47.7	544	6	US-10-719-311-18
19	31.5	47.7	588	7	US-11-184-380-5
20	31.5	47.7	598	6	US-10-719-311-16
21	31.5	47.7	724	7	US-11-184-380-4
22	31.5	47.7	734	6	US-10-719-311-4
23	31.5	47.7	735	7	US-11-184-380-24
24	31	47.0	142	6	US-10-821-234-1030
25	31	47.0	229	6	US-10-510-386-228

26	31	47.0	290	6	US-10-793-626-214	Sequence 214, App
27	31	47.0	393	6	US-10-821-234-1292	Sequence 192, Ap
28	31	47.0	490	6	US-10-131-826A-310	Sequence 310, Ap
29	31	47.0	626	6	US-10-467-657-6426	Sequence 6426, Ap
30	31	47.0	626	6	US-10-467-657-7618	Sequence 7618, Ap
31	31	47.0	745	7	US-11-109-156-14	Sequence 14, App1
32	31	47.0	766	2	US-10-522-789-2	Sequence 2, App1
33	30	45.5	31	6	US-10-467-657-2188	Sequence 2188, Ap
34	30	45.5	180	6	US-10-665-455-11	Sequence 11, App1
35	30	45.5	221	7	US-11-055-822-82	Sequence 82, App1
36	30	45.5	389	6	US-10-979-821-2	Sequence 2, App1
37	30	45.5	400	6	US-10-793-626-3116	Sequence 3116, Ap
38	30	45.5	450	6	US-10-467-657-2126	Sequence 2126, Ap
39	30	45.5	457	7	US-11-055-822-80	Sequence 80, App1
40	30	45.5	479	6	US-10-821-234-871	Sequence 871, App
41	30	45.5	934	7	US-10-858-730-8	Sequence 8, App1
42	30	45.5	1857	7	US-11-102-217-2	Sequence 2, App1
43	29.5	44.7	178	6	US-10-939-890-116	Sequence 116, App
44	29.5	44.7	178	6	US-10-508-263-32	Sequence 32, App1
45	29.5	44.7	178	6	US-10-508-263-46	Sequence 46, App1

#### ALIGNMENTS

RESULT 1  
US-10-467-657-6026  
Sequence 6026, Application US/10467657  
Publication No. US20050260581A1  
GENERAL INFORMATION:  
APPLICANT: CHIRON SPA  
APPLICANT: FONTANA Maria Rita  
APPLICANT: PIZZA Mariagrazia  
APPLICANT: MASIGNANI Vega  
APPLICANT: MONACI Elisabetta  
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/10/467,657  
CURRENT FILING DATE: 2003-08-11  
PRIOR APPLICATION NUMBER: GB-0103424.8  
PRIOR FILING DATE: 2001-02-12  
NUMBER OF SEQ ID NOS: 9218  
SOFTWARE: Seqwin99, version 1.04  
SEQ ID NO 6026  
LENGTH: 792  
TYPE: PRT  
ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-6026

Query Match 54.5%; Score 36; DB 6; Length 792;  
Best Local Similarity 75.0%; Pred. No. 27;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 ELVGFDS 11  
||:||||:  
Db 390 ELVGFDSN 397

RESULT 2  
US-10-467-657-7528  
Sequence 7528, Application US/10467657  
Publication No. US20050260581A1  
GENERAL INFORMATION:  
APPLICANT: CHIRON SPA  
APPLICANT: FONTANA Maria Rita  
APPLICANT: PIZZA Mariagrazia  
APPLICANT: MASIGNANI Vega  
APPLICANT: MONACI Elisabetta  
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/10/467,657  
CURRENT FILING DATE: 2003-08-11  
PRIOR APPLICATION NUMBER: GB-0103424.8

;; PRIOR FILING DATE: 2001-02-12  
;; NUMBER OF SEQ ID NOS: 9218  
;; SOFTWARE: SeqMin99, version 1.04  
;; SEQ ID NO 7528  
;; LENGTH: 792  
;; TYPE: PRT  
;; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-7528

Query Match 54.5%; Score 36; DB 6; Length 792;  
Best Local Similarity 75.0%; Pred. No. 27;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 ELVGYFDS 11  
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Db 390 ELVGYFDN 397

RESULT 3  
US-10-467-657-1210  
;; Sequence 1210, Application US/10467657  
;; Publication No. US20050260581A1  
;; GENERAL INFORMATION:  
;; APPLICANT: CHIRON SPA  
;; APPLICANT: FONTANA Maria Rita  
;; APPLICANT: PIZZA Mariagrazia  
;; APPLICANT: MASIGNANI Vega  
;; APPLICANT: MONACI Elisabetta  
;; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
;; FILE REFERENCE:  
;; CURRENT APPLICATION NUMBER: US/10/467,657  
;; CURRENT FILING DATE: 2003-08-11  
;; PRIOR APPLICATION NUMBER: GB-0103424.8  
;; PRIOR FILING DATE: 2001-02-12  
;; NUMBER OF SEQ ID NOS: 9218  
;; SOFTWARE: SeqMin99, version 1.04  
;; SEQ ID NO 1210  
;; LENGTH: 356  
;; TYPE: PRT  
;; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-1210

Query Match 53.0%; Score 35; DB 6; Length 356;  
Best Local Similarity 62.5%; Pred. No. 19;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPMELVGY 8  
||:||||:  
Db 45 GPMELVGY 52

RESULT 4  
US-11-074-176-36  
;; Sequence 36, Application US/11074176  
;; Publication No. US20050250135A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Kleenhammer, Todd R.  
;; APPLICANT: Russell, William M.  
;; APPLICANT: Allemann, Eric  
;; APPLICANT: McAlliff, Olivia  
;; APPLICANT: Perill, Andrea Azcarate  
;; TITLE OF INVENTION: Nucleic Acid Sequences Encoding  
;; TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore  
;; FILE REFERENCE: 5051-694  
;; CURRENT APPLICATION NUMBER: US/11/074,176  
;; CURRENT FILING DATE: 2005-03-07  
;; PRIOR APPLICATION NUMBER: 60/551,161  
;; PRIOR FILING DATE: 2004-03-08  
;; NUMBER OF SEQ ID NOS: 381  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 36  
;; LENGTH: 322  
;; TYPE: PRT

;; ORGANISM: Lactobacillus acidophilus  
US-11-074-176-36

Query Match 51.5%; Score 34; DB 7; Length 322;  
Best Local Similarity 85.7%; Pred. No. 25;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 ELVGYFD 10  
||:||||:  
Db 43 ELVGYFD 49

RESULT 5  
US-10-467-657-1916  
;; Sequence 1916, Application US/10467657  
;; Publication No. US20050260581A1  
;; GENERAL INFORMATION:  
;; APPLICANT: CHIRON SPA  
;; APPLICANT: FONTANA Maria Rita  
;; APPLICANT: PIZZA Mariagrazia  
;; APPLICANT: MASIGNANI Vega  
;; APPLICANT: MONACI Elisabetta  
;; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
;; FILE REFERENCE:  
;; CURRENT APPLICATION NUMBER: US/10/467,657  
;; CURRENT FILING DATE: 2003-08-11  
;; PRIOR APPLICATION NUMBER: GB-0103424.8  
;; PRIOR FILING DATE: 2001-02-12  
;; NUMBER OF SEQ ID NOS: 9218  
;; SOFTWARE: SeqMin99, version 1.04  
;; SEQ ID NO 1916  
;; LENGTH: 723  
;; TYPE: PRT  
;; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-1916

Query Match 51.5%; Score 34; DB 6; Length 723;  
Best Local Similarity 53.3%; Pred. No. 55;  
Matches 8; Conservative 0; Mismatches 1; Indels 6; Gaps 1;

QY 1 GPMELV-----GYF 9  
||:||||:  
Db 260 GPMELVNKSAAGYF 274

RESULT 6  
US-10-841-129-2  
;; Sequence 2, Application US/10841129  
;; Publication No. US20050250113A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Zuker, Charles S.  
;; APPLICANT: Erlenbach, Isolda  
;; APPLICANT: Hoon, Mark A.  
;; APPLICANT: Ryba, Nicholas J. P.  
;; APPLICANT: Zhang, Yifeng  
;; APPLICANT: The Regents of the University of California  
;; APPLICANT: The Government of the United States of America  
;; APPLICANT: as represented by The Secretary of the  
;; APPLICANT: Department of Health and Human Services  
;; TITLE OF INVENTION: A Mammalian Magnesium/Manganese Sensing G Protein  
;; TITLE OF INVENTION: Coupled Receptor  
;; FILE REFERENCE: 02307E-145400US  
;; CURRENT APPLICATION NUMBER: US/10/841,129  
;; CURRENT FILING DATE: 2004-05-07  
;; NUMBER OF SEQ ID NOS: 7  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 2  
;; LENGTH: 926  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; OTHER INFORMATION: human magnesium/manganese sensing G protein  
;; OTHER INFORMATION: coupled receptor (GPCR) R5.24, Mg receptor, Mn

OTHER INFORMATION: receptor  
US-10-841-129-2

Query Match 51.5%; Score 34; DB 6; Length 926;  
Best Local Similarity 83.3%; Pred. No. 70;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PWELVG 7  
Db 443 PWELIG 448

## RESULT 7

US-11-037-829A-4  
Sequence 4, Application US/11037829A  
Publication No. US20050255551A1  
GENERAL INFORMATION:  
APPLICANT: Targacept, Inc  
APPLICANT: Catholic Healthcare West  
APPLICANT: Benchrif, Merouane  
APPLICANT: Lukas, Ronald J.  
TITLE OF INVENTION: Methods and Compositions Relating to Chimeric  
FILE REFERENCE: 1103 1520.PCT  
CURRENT APPLICATION NUMBER: US/11/037,829A  
PRIOR FILING DATE: 2005-01-18  
PRIOR APPLICATION NUMBER: US 60/397,380  
PRIOR FILING DATE: 2002-07-19  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4  
LENGTH: 478  
TYPE: PRT  
ORGANISM: Homo sapien  
US-11-037-829A-4

Query Match 50.8%; Score 33.5; DB 7; Length 478;  
Best Local Similarity 58.3%; Pred. No. 45;  
Matches 7; Conservative 1; Mismatches 1; Indels 3; Gaps 1;

Qy 1 GPWELVG---YF 9  
Db 207 GEWELIGVLPYF 218

## RESULT 8

US-11-082-389-302  
Sequence 302, Application US/11082389  
Publication No. US20050244935A1  
GENERAL INFORMATION:  
APPLICANT: Pompejus, Markus  
APPLICANT: Krogger, Burkhard  
APPLICANT: Schröder, Hartwig  
APPLICANT: Zelder, Oskar  
APPLICANT: Haberhauser, Gregor  
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS  
INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE  
TITLE OF INVENTION: TRANSPORT  
FILE REFERENCE: BGI-131CPCN  
CURRENT APPLICATION NUMBER: US/11/082,389  
PRIOR FILING DATE: 2005-03-16  
PRIOR APPLICATION NUMBER: US 09/603024  
PRIOR FILING DATE: 2000-06-23  
PRIOR APPLICATION NUMBER: US 60/141031  
PRIOR FILING DATE: 1999-06-25  
PRIOR APPLICATION NUMBER: US 60/143262  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: US 60/151281  
PRIOR FILING DATE: 1999-08-27  
PRIOR APPLICATION NUMBER: DE 19930487.4  
PRIOR FILING DATE: 1999-07-01  
PRIOR APPLICATION NUMBER: DE 19930489.0  
PRIOR FILING DATE: 1999-07-01

PRIOR APPLICATION NUMBER: DE 19931549.3  
PRIOR FILING DATE: 1999-07-08  
PRIOR APPLICATION NUMBER: DE 19931550.7  
PRIOR FILING DATE: 1999-07-08  
PRIOR APPLICATION NUMBER: DE 19932134.5  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: DE 19941379.7  
PRIOR FILING DATE: 1999-08-31  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 446  
SEQ ID NO 302  
LENGTH: 198  
TYPE: PRT  
ORGANISM: Corynebacterium glutamicum  
FEATURE:  
NAME/KEY: VARIANT  
LOCATION: 4  
OTHER INFORMATION: Xaa = Phe, Ser, Tyr, or Cys  
US-11-082-389-302

Query Match 50.0%; Score 33; DB 7; Length 198;  
Best Local Similarity 66.7%; Pred. No. 24;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WELVGY 8  
Db 99 WOLIGY 104

## RESULT 9

US-11-082-389-304  
Sequence 304, Application US/11082389  
Publication No. US20050244935A1  
GENERAL INFORMATION:  
APPLICANT: Pompejus, Markus  
APPLICANT: Krogger, Burkhard  
APPLICANT: Schröder, Hartwig  
APPLICANT: Zelder, Oskar  
APPLICANT: Haberhauser, Gregor  
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS  
INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE  
TITLE OF INVENTION: TRANSPORT  
FILE REFERENCE: BGI-131CPCN  
CURRENT APPLICATION NUMBER: US/11/082,389  
PRIOR FILING DATE: 2005-03-16  
PRIOR APPLICATION NUMBER: US 09/603024  
PRIOR FILING DATE: 2000-06-23  
PRIOR APPLICATION NUMBER: US 60/141031  
PRIOR FILING DATE: 1999-06-25  
PRIOR APPLICATION NUMBER: US 60/143262  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: US 60/151281  
PRIOR FILING DATE: 1999-08-27  
PRIOR APPLICATION NUMBER: DE 19930487.4  
PRIOR FILING DATE: 1999-07-01  
PRIOR APPLICATION NUMBER: DE 19930489.0  
PRIOR FILING DATE: 1999-07-01  
PRIOR APPLICATION NUMBER: DE 19931549.3  
PRIOR FILING DATE: 1999-07-08  
PRIOR APPLICATION NUMBER: DE 19931550.7  
PRIOR FILING DATE: 1999-07-08  
PRIOR APPLICATION NUMBER: DE 19932134.5  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: DE 19941379.7  
PRIOR FILING DATE: 1999-08-31  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 446  
SEQ ID NO 304  
LENGTH: 281  
TYPE: PRT  
ORGANISM: Corynebacterium glutamicum  
US-11-082-389-304

Query Match 50.0%; Score 33; DB 7; Length 281;  
Best Local Similarity 66.7%; Pred. No. 33;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 3 WEIVGY 8  
Db 153 WOLIGY 158

## RESULT 10

US-11-055-822-76  
Sequence 76, Application US/11055822  
Publication No. US20050260707A1  
GENERAL INFORMATION:  
APPLICANT: Pompejus, Markus  
APPLICANT: Kroeger, Burkhard  
APPLICANT: Schneider, Hartwig  
APPLICANT: Zeider, Oskar  
APPLICANT: Haberhauer, Gregor  
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING  
FILE REFERENCE: BGI-121CPN  
CURRENT APPLICATION NUMBER: US/11/055,822  
CURRENT FILING DATE: 2005-02-11  
PRIOR APPLICATION NUMBER: 09/606,740  
PRIOR FILING DATE: 2000-06-23  
PRIOR APPLICATION NUMBER: 60/141,031  
PRIOR FILING DATE: 1999-06-25  
PRIOR APPLICATION NUMBER: 60/142,101  
PRIOR FILING DATE: 1999-07-02  
PRIOR APPLICATION NUMBER: 60/148,613  
PRIOR FILING DATE: 1999-08-12  
PRIOR APPLICATION NUMBER: 60/187,970  
PRIOR FILING DATE: 2000-03-09  
PRIOR APPLICATION NUMBER: DE 19930476.9  
PRIOR FILING DATE: 1999-07-01  
PRIOR APPLICATION NUMBER: DE 19931415.2  
PRIOR FILING DATE: 1999-07-08  
PRIOR APPLICATION NUMBER: DE 19931418.7  
PRIOR FILING DATE: 1999-07-08  
PRIOR APPLICATION NUMBER: DE 19931419.5  
PRIOR FILING DATE: 1999-07-08  
PRIOR APPLICATION NUMBER: DE 19931420.9  
PRIOR FILING DATE: 1999-07-08  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 1158  
SEQ ID NO 76  
LENGTH: 431  
TYPE: PRT  
ORGANISM: Corynebacterium glutamicum  
US-11-055-822-76

Query Match 50.0%; Score 33; DB 7; Length 431;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GPWEL 5  
Db 284 GPWEL 288

## RESULT 11

US-10-131-826A-60  
Sequence 60, Application US/10131826A  
Publication No. US20050245730A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: DeForge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerltsen, Mary E.

APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P330R1C128  
CURRENT APPLICATION NUMBER: US/10/131,826A  
CURRENT FILING DATE: 2002-04-24  
PRIOR APPLICATION NUMBER: 60/049911  
PRIOR FILING DATE: 1997-06-18  
PRIOR APPLICATION NUMBER: 60/056974  
PRIOR FILING DATE: 1997-08-26  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059115  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059117  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059122  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059184  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059263  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/059352  
PRIOR FILING DATE: 1997-09-19  
PRIOR APPLICATION NUMBER: 60/059588  
PRIOR FILING DATE: 1997-09-19  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 60  
LENGTH: 724  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-131-826A-60

Query Match 50.0%; Score 33; DB 6; Length 724;  
Best Local Similarity 50.0%; Pred. No. 82;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 3 WEIVGYFD 10  
Db 83 WDIVGYFD 90

## RESULT 12

US-11-055-822-72  
Sequence 72, Application US/11055822  
Publication No. US20050260707A1  
GENERAL INFORMATION:  
APPLICANT: Pompejus, Markus  
APPLICANT: Kroeger, Burkhard  
APPLICANT: Schneider, Hartwig  
APPLICANT: Zeider, Oskar  
APPLICANT: Haberhauer, Gregor  
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING  
FILE REFERENCE: BGI-121CPN  
CURRENT APPLICATION NUMBER: US/11/055,822  
CURRENT FILING DATE: 2005-02-11  
PRIOR APPLICATION NUMBER: 09/606,740  
PRIOR FILING DATE: 2000-06-23  
PRIOR APPLICATION NUMBER: 60/141,031  
PRIOR FILING DATE: 1999-06-25  
PRIOR APPLICATION NUMBER: 60/142,101  
PRIOR FILING DATE: 1999-07-02

PRIOR APPLICATION NUMBER: 60/148,613  
PRIOR FILING DATE: 1999-08-12  
PRIOR APPLICATION NUMBER: 60/187,970  
PRIOR FILING DATE: 2000-03-09  
PRIOR APPLICATION NUMBER: DE 19930476.9  
PRIOR FILING DATE: 1999-07-01  
PRIOR APPLICATION NUMBER: DE 19931415.2  
PRIOR FILING DATE: 1999-07-08  
PRIOR APPLICATION NUMBER: DE 19931418.7  
PRIOR FILING DATE: 1999-07-08  
PRIOR APPLICATION NUMBER: DE 19931419.5  
PRIOR FILING DATE: 1999-07-08  
PRIOR APPLICATION NUMBER: DE 19931420.9  
PRIOR FILING DATE: 1999-07-08  
Remaining Prior Application data removed - See File Wrapper or PLM.  
NUMBER OF SEQ ID NOS: 1158  
SEQ ID NO 72  
LENGTH: 1510  
TYPE: PRT  
ORGANISM: Corynebacterium glutamicum  
US-11-055-822-72

Query Match 50.0%; Score 33; DB 7; Length 1510;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPWEL 5  
DB 1063 GPWEL 1067

RESULT 13  
US-11-113-424-52  
Sequence 52, Application US/11113424  
Publication No. US20050260713A1  
GENERAL INFORMATION:  
APPLICANT: Gangolli et al.  
TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same  
FILE REFERENCE: 21402-225  
CURRENT APPLICATION NUMBER: US/11/113,424  
CURRENT FILING DATE: 2005-04-21  
PRIOR APPLICATION NUMBER: 60/256,704  
PRIOR FILING DATE: 2000-12-19  
PRIOR APPLICATION NUMBER: 60/311,590  
PRIOR FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: 60/257,314  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: 60/311,613  
PRIOR FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: 60/315,617  
PRIOR FILING DATE: 2001-08-29  
PRIOR APPLICATION NUMBER: 60/307,506  
PRIOR FILING DATE: 2001-07-24  
PRIOR APPLICATION NUMBER: 60/322,358  
PRIOR FILING DATE: 2001-09-14  
PRIOR APPLICATION NUMBER: 60/294,075  
PRIOR FILING DATE: 2001-05-29  
PRIOR APPLICATION NUMBER: 60/288,153  
PRIOR FILING DATE: 2001-05-02  
NUMBER OF SEQ ID NOS: 190  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 52  
LENGTH: 2725  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-113-424-52

Query Match 50.0%; Score 33; DB 7; Length 2725;  
Best Local Similarity 60.0%; Pred. No. 2.9e+02;  
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GPWELVGYFD 10  
DB 1063 GPWELVGYFD 1067

DB 503 GPWYLAIFYND 512  
RESULT 14  
US-10-467-657-4150  
Sequence 4150, Application US/10467657  
Publication No. US20050260581A1  
GENERAL INFORMATION:  
APPLICANT: CHIRON SPA  
APPLICANT: FORTANA Maria Rita  
APPLICANT: PIZZA Mariagrazia  
APPLICANT: MASIGNANI Vega  
APPLICANT: MONACI Elisabetta  
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/10/467,657  
CURRENT FILING DATE: 2003-08-11  
PRIOR APPLICATION NUMBER: GB-0103424.8  
PRIOR FILING DATE: 2001-02-12  
NUMBER OF SEQ ID NOS: 9218  
SOFTWARE: Seqwin99, version 1.04  
SEQ ID NO 4150  
LENGTH: 456  
TYPE: PRT  
ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-4150

Query Match 48.5%; Score 32; DB 6; Length 456;  
Best Local Similarity 57.1%; Pred. No. 78;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PWEIYVY 8  
DB 154 PWEIYVY 160

RESULT 15  
US-11-147-047-33  
Sequence 33, Application US/11147047  
Publication No. US2005026068A1  
GENERAL INFORMATION:  
APPLICANT: Agarwal, Panaj  
APPLICANT: Murdock, Paul R.  
APPLICANT: Rizvi, Safia K.  
APPLICANT: Smith, Randall F.  
APPLICANT: Xiang, Zhaoyang  
TITLE OF INVENTION: NOVEL COMPOUNDS  
FILE REFERENCE: GPS0016  
CURRENT APPLICATION NUMBER: US/11/147,047  
CURRENT FILING DATE: 2005-06-07  
PRIOR APPLICATION NUMBER: US/10/221,097  
PRIOR FILING DATE: 2002-09-06  
PRIOR APPLICATION NUMBER: PCT/US01/07143  
PRIOR FILING DATE: 2001-03-05  
PRIOR APPLICATION NUMBER: 60/187,107  
PRIOR FILING DATE: 2000-03-06  
PRIOR APPLICATION NUMBER: 60/236,874  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/188,916  
PRIOR FILING DATE: 2000-03-13  
PRIOR APPLICATION NUMBER: 60/237,846  
PRIOR FILING DATE: 2000-10-03  
NUMBER OF SEQ ID NOS: 52  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 33  
LENGTH: 533  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-147-047-33

Query Match 48.5%; Score 32; DB 7; Length 533;  
Best Local Similarity 83.3%; Pred. No. 90;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy	2	PWELVG	7
Db	178	PWEAVG	183

Search completed: December 4, 2005, 04:37:49  
Job time : 4.20833 secs



GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: December 4, 2005, 04:09:54 ; Search time 130.312 Seconds  
(without alignments)  
50.576 Million cell updates/sec

Title: US-10-632-706-197  
Perfect score: 89  
Sequence: 1 EPDMLMGDRGALDV 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

A\_Geneseq\_21:\*

1: geneeqp1980s:\*  
2: geneeqp1990s:\*  
3: geneeqp2000s:\*  
4: geneeqp2001s:\*  
5: geneeqp2002s:\*  
6: geneeqp2003as:\*  
7: geneeqp2003bs:\*  
8: geneeqp2004s:\*  
9: geneeqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	89	100.0	15	ADR38727	Adt38727 Mouse hea
2	89	100.0	15	ADR38728	Adt38728 Mouse hea
3	89	100.0	15	ADR38792	Adt38792 Mouse hea
4	89	100.0	15	ADR38795	Adt38795 Mouse hea
5	89	100.0	15	ADR38798	Adt38798 Mouse hea
6	89	100.0	15	ADR38729	Adt38729 Mouse hea
7	89	100.0	15	ADR38801	Adt38801 Mouse hea
8	89	100.0	15	ADR38801	Adt38801 Mouse hea
9	89	100.0	15	ADR38801	Adt38801 Mouse hea
10	89	100.0	15	ADR38801	Adt38801 Mouse hea
11	89	100.0	15	ADR38801	Adt38801 Mouse hea
12	89	100.0	15	ADR38801	Adt38801 Mouse hea
13	89	100.0	15	ADR38801	Adt38801 Mouse hea
14	89	100.0	15	ADR38801	Adt38801 Mouse hea
15	89	100.0	15	ADR38801	Adt38801 Mouse hea
16	89	100.0	15	ADR38801	Adt38801 Mouse hea
17	89	100.0	15	ADR38801	Adt38801 Mouse hea
18	89	100.0	15	ADR38801	Adt38801 Mouse hea
19	89	100.0	15	ADR38801	Adt38801 Mouse hea
20	89	100.0	15	ADR38801	Adt38801 Mouse hea
21	89	100.0	15	ADR38801	Adt38801 Mouse hea
22	89	100.0	15	ADR38801	Adt38801 Mouse hea
23	89	100.0	15	ADR38801	Adt38801 Mouse hea
24	89	100.0	15	ADR38801	Adt38801 Mouse hea

25	44	49.4	687	8	ADG42446	Adg42446 Bacterial
26	43	48.3	100	8	ADG65091	Adg65091 Novel hum
27	43	48.3	345	2	AAV38595	AAV38595 Neisseria
28	43	48.3	345	2	ABE49036	ABE49036 N. gonorr
29	43	48.3	383	6	AAV38596	AAV38596 Neisseria
30	43	48.3	383	6	ABP79536	ABP79536 N. gonorr
31	43	48.3	383	6	ABE49038	ABE49038 N. gonorr
32	43	48.3	546	2	AAW26164	AAW26164 KF-1 prot
33	43	48.3	582	4	AAU30396	AAU30396 Novel hum
34	43	48.3	616	8	ADS20416	ADS20416 Crab-eat1
35	43	48.3	683	2	AAW26163	AAW26163 Mouse KF-
36	43	48.3	683	2	ADZ04210	ADZ04210 Novel apo
37	43	48.3	685	2	AAW26165	AAW26165 Human KF-
38	43	48.3	685	9	ADU07646	ADU07646 Cyclin-de
39	43	48.3	685	9	ADZ04207	ADZ04207 Novel apo
40	43	48.3	732	9	ABM94428	ABM94428 M. xanthu
41	43	48.3	2519	7	ABM88218	ABM88218 Rice abio
42	42.5	47.8	315	4	ABM09181	ABM09181 Pseudomon
43	42.5	47.8	315	6	ABU15664	ABU15664 Protein e
44	42.5	47.8	320	7	ABO69555	ABO69555 Pseudomon
45	42	47.2	53	4	AAU65794	AAU65794 Propionib

## ALIGNMENTS

RESULT 1  
ADR38727  
ID ADR38727 standard; peptide, 15 AA.  
AC ADR38727;  
XX 02-DEC-2004 (first entry)  
DT Mouse heavy chain variable region CDR3 seqid 129.  
DE  
XX antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;  
XX BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
XX toxin neutralisation; botulinum neurotoxin poisoning; mouse;  
XX heavy chain variable region; complementarily determining region; CDR3.  
OS Mus sp.  
XX  
XX US2004175385-A1.  
XX  
XX 09-SEP-2004.  
XX  
XX 01-AUG-2003; 2003US-00632706.  
XX  
XX 31-AUG-1998; 98US-00144886.  
XX 01-AUG-2002; 2002US-0400721P.  
XX  
XX (REGC ) UNIV CALIFORNIA.  
XX  
XX Marks JD, Amerdort P;  
XX WPI; 2004-652009/63.  
XX  
XX New isolated antibody that neutralizes botulinum neurotoxin type A,  
XX useful for diagnosing botulism or for treating pathologies associated  
XX with botulinum neurotoxin poisoning.  
XX  
XX Example 3; SEQ ID NO 129; 110pp; English.  
XX  
XX The invention describes an isolated antibody (I) that specifically binds  
XX to an epitope specifically bound by an antibody expressed by a specific  
XX clone where (I) binds to and neutralises botulinum neurotoxin type A  
XX (BoNT/A). An isolated antibody (I) that specifically binds to an epitope  
XX specifically bound by an antibody expressed by a clone chosen from clone  
XX S25, C25, C39, I06, 3D12, B4, I03, nuc25, A11, A12, WRI(V), WRI(T), 3-1,  
XX 3-8, 3-10 and IN01, where (I) binds to and neutralizes botulinum  
XX neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)  
XX comprising BoNT/A neutralising epitope having an epitope that is

CC specifically bound by an antibody expressed by clones as mentioned in (I)  
CC ; producing (I) ; and a composition (II) comprising several anti-  
CC botulinum neurotoxin antibodies, where each antibody is specific for a  
CC different epitope of a botulinum neurotoxin and the combination of  
CC antibodies shows greater toxin neutralisation than the single antibodies  
CC in surplus. The following are disclosed: a pharmaceutical composition  
CC comprising (I) ; and a kit comprising (I). (I) is useful for neutralising  
CC BoNT/A antibody and for neutralising a botulinum neurotoxin which  
CC involves contacting neurotoxin with (I) in surplus, where each of (I) is  
CC specific for a different epitope of the botulinum neurotoxin and the  
CC combination of antibodies shows greater toxin neutralisation than the  
CC single antibodies in surplus. (I) is useful for diagnosing the botulism  
CC or for treating pathologies associated with botulinum neurotoxin  
CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)  
CC enables rapid detection or diagnosis of botulism. This is the amino acid  
CC sequence of mouse heavy chain variable region complementarity determining  
CC region 3 (CDR3) from anti-botulinum neurotoxin antibodies.  
CC  
XX  
SQ Sequence 15 AA;  
Query Match 100.0%; Score 89; DB 8; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EPDWLWMDRGALDV 15  
Db 1 EPDWLWMDRGALDV 15  
RESULT 2  
ADR38728 standard; peptide; 15 AA.  
XX ADR38728;  
XX  
XX 02-DEC-2004 (first entry)  
XX  
XX Mouse heavy chain variable region CDR3 seqid 130.  
XX  
XX  
XX antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;  
XX BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
XX toxin neutralisation; botulinum neurotoxin poisoning; mouse;  
XX heavy chain variable region; complementarity determining region; CDR3.  
XX  
XX Mus sp.  
XX  
XX US2004175385-A1.  
XX  
XX 09-SEP-2004.  
XX  
XX 01-AUG-2003; 2003US-00632706.  
XX  
XX 31-AUG-1998; 98US-00144886.  
XX  
XX 01-AUG-2002; 2002US-0400721P.  
XX  
XX (REGC ) UNIV CALIFORNIA.  
XX  
XX Marks JD, Amerdorfer P;  
XX  
XX WPI; 2004-652009/63.  
XX  
XX  
XX New isolated antibody that neutralizes botulinum neurotoxin type A,  
XX useful for diagnosing botulism or for treating pathologies associated  
XX with botulinum neurotoxin poisoning.  
XX  
XX Example 3; SEQ ID NO 130; 110pp; English.  
XX  
XX The invention describes an isolated antibody (I) that specifically binds  
XX to an epitope specifically bound by an antibody expressed by a specific  
XX clone where (I) binds to and neutralises botulinum neurotoxin type A  
XX (BoNT/A). An isolated antibody (I) that specifically binds to an epitope  
XX specifically bound by an antibody expressed by a clone chosen from clone  
XX S25, C25, C39, IC6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WRI(V), WRI(T), 3-1,

CC 3-8, 3-10 and INGI, where (I) binds to and neutralizes botulinum  
CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)  
CC comprising BoNT/A neutralising epitope having an epitope that is  
CC specifically bound by an antibody expressed by clones as mentioned in (I)  
CC ; producing (I) ; and a composition (III) comprising several anti-  
CC botulinum neurotoxin antibodies, where each antibody is specific for a  
CC different epitope of a botulinum neurotoxin and the combination of  
CC antibodies shows greater toxin neutralisation than the single antibodies  
CC in surplus. The following are disclosed: a pharmaceutical composition  
CC comprising (I) ; and a kit comprising (I). (I) is useful for neutralising  
CC BoNT/A antibody and for neutralising a botulinum neurotoxin which  
CC involves contacting neurotoxin with (I) in surplus, where each of (I) is  
CC specific for a different epitope of the botulinum neurotoxin and the  
CC combination of antibodies shows greater toxin neutralisation than the  
CC single antibodies in surplus. (I) is useful for diagnosing the botulism  
CC or for treating pathologies associated with botulinum neurotoxin  
CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)  
CC enables rapid detection or diagnosis of botulism. This is the amino acid  
CC sequence of mouse heavy chain variable region complementarity determining  
CC region 3 (CDR3) from anti-botulinum neurotoxin antibodies.  
CC  
XX  
SQ Sequence 15 AA;  
Query Match 100.0%; Score 89; DB 8; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EPDWLWMDRGALDV 15  
Db 1 EPDWLWMDRGALDV 15  
RESULT 3  
ADR38792 standard; peptide; 15 AA.  
XX ADR38792;  
XX  
XX 02-DEC-2004 (first entry)  
XX  
XX Mouse heavy chain anti-BoNT-antibody CD3 seqid 194.  
XX  
XX  
XX antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;  
XX BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
XX toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;  
XX CDR3; complementarity determining region 1.  
XX  
XX Mus sp.  
XX  
XX US2004175385-A1.  
XX  
XX 09-SEP-2004.  
XX  
XX 01-AUG-2003; 2003US-00632706.  
XX  
XX 31-AUG-1998; 98US-00144886.  
XX  
XX 01-AUG-2002; 2002US-0400721P.  
XX  
XX (REGC ) UNIV CALIFORNIA.  
XX  
XX Marks JD, Amerdorfer P;  
XX  
XX WPI; 2004-652009/63.  
XX  
XX  
XX New isolated antibody that neutralizes botulinum neurotoxin type A,  
XX useful for diagnosing botulism or for treating pathologies associated  
XX with botulinum neurotoxin poisoning.  
XX  
XX Example 4; SEQ ID NO 194; 110pp; English.  
XX  
XX The invention describes an isolated antibody (I) that specifically binds  
XX to an epitope specifically bound by an antibody expressed by a specific  
XX clone where (I) binds to and neutralises botulinum neurotoxin type A

(BONT/A). An isolated antibody (I) that specifically binds to an epitope specifically bound by an antibody expressed by a clone chosen from clone S25, C25, C39, 1C6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WR1(V), WR1(T), 3-1, 3-8, 3-10 and INGI, where (I) binds to and neutralizes botulinum neurotoxin type A (BONT/A). Also described are: a polypeptide (II) comprising BONT/A neutralising epitope having an epitope that is specifically bound by an antibody expressed by clones as mentioned in (I); producing (I); and a composition (III) comprising several anti-botulinum neurotoxin antibodies, where each antibody is specific for a different epitope of a botulinum neurotoxin and the combination of antibodies shows greater toxin neutralisation than the single antibodies in surplus. The following are disclosed: a pharmaceutical composition comprising (I); and a kit comprising (I). (I) is useful for neutralising BONT/A antibody and for neutralising a botulinum neurotoxin which involves contacting neurotoxin with (I) in surplus, where each of (I) is specific for a different epitope of the botulinum neurotoxin and the combination of antibodies shows greater toxin neutralisation than the single antibodies in surplus. (I) is useful for diagnosing the botulinism or for treating pathologies associated with botulinum neurotoxin poisoning. (I) exhibits specificity and affinity towards BONT/A. (I) enables rapid detection or diagnosis of botulinism. This is the amino acid sequence of mouse heavy chain anti-BONT-antibody CDR3.

XX Sequence 15 AA;

SQ Query Match 100.0%; Score 89; DB 8; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.8e-06; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EPDMLMGDRGALDV 15

|||||

1 EPDMLMGDRGALDV 15

Db

RESULT 4  
ADR38795  
ID ADR38795 standard; peptide; 15 AA.

XX ADR38795;

XX 02-DEC-2004 (first entry)

XX Mouse heavy chain anti-BONT-antibody CDR3 seqid 197.

XX antibacterial; antibody; botulinum neurotoxin type A; BONT/A;  
XX BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
XX toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;  
XX CDR3; complementarity determining region 1.

XX Mus sp.

XX US2004175385-A1.

XX 09-SEP-2004.

XX 01-AUG-2003; 2003US-00632706.

XX 31-AUG-1998; 98US-00144886.

XX 01-AUG-2002; 2002US-0400721P.

XX (REGC ) UNIV CALIFORNIA.

XX Marks JD, Amerdorfer P;

XX WPI; 2004-652009/63.

XX New isolated antibody that neutralizes botulinum neurotoxin type A,  
XX useful for diagnosing botulinism or for treating pathologies associated  
XX with botulinum neurotoxin poisoning.

XX Example 4; SEQ ID NO 197; 110pp; English.

XX The invention describes an isolated antibody (I) that specifically binds

to an epitope specifically bound by an antibody expressed by a specific clone where (I) binds to and neutralises botulinum neurotoxin type A (BONT/A). An isolated antibody (I) that specifically binds to an epitope specifically bound by an antibody expressed by a clone chosen from clone S25, C25, C39, 1C6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WR1(V), WR1(T), 3-1, 3-8, 3-10 and INGI, where (I) binds to and neutralizes botulinum neurotoxin type A (BONT/A). Also described are: a polypeptide (II) comprising BONT/A neutralising epitope having an epitope that is specifically bound by an antibody expressed by clones as mentioned in (I); producing (I); and a composition (III) comprising several anti-botulinum neurotoxin antibodies, where each antibody is specific for a different epitope of a botulinum neurotoxin and the combination of antibodies shows greater toxin neutralisation than the single antibodies in surplus. The following are disclosed: a pharmaceutical composition comprising (I); and a kit comprising (I). (I) is useful for neutralising BONT/A antibody and for neutralising a botulinum neurotoxin which involves contacting neurotoxin with (I) in surplus, where each of (I) is specific for a different epitope of the botulinum neurotoxin and the combination of antibodies shows greater toxin neutralisation than the single antibodies in surplus. (I) is useful for diagnosing the botulinism or for treating pathologies associated with botulinum neurotoxin poisoning. (I) exhibits specificity and affinity towards BONT/A. (I) enables rapid detection or diagnosis of botulinism. This is the amino acid sequence of mouse heavy chain anti-BONT-antibody CDR3.

SQ Sequence 15 AA;

Query Match 100.0%; Score 89; DB 8; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.8e-06; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EPDMLMGDRGALDV 15

|||||

1 EPDMLMGDRGALDV 15

Db

RESULT 5  
ADR38798  
ID ADR38798 standard; peptide; 15 AA.

XX ADR38798;

XX 02-DEC-2004 (first entry)

XX Mouse heavy chain anti-BONT-antibody CDR3 seqid 200.

XX antibacterial; antibody; botulinum neurotoxin type A; BONT/A;  
XX BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
XX toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;  
XX CDR3; complementarity determining region 1.

XX Mus sp.

XX US2004175385-A1.

XX 09-SEP-2004.

XX 01-AUG-2003; 2003US-00632706.

XX 31-AUG-1998; 98US-00144886.

XX 01-AUG-2002; 2002US-0400721P.

XX (REGC ) UNIV CALIFORNIA.

XX Marks JD, Amerdorfer P;

XX WPI; 2004-652009/63.

XX New isolated antibody that neutralizes botulinum neurotoxin type A,  
XX useful for diagnosing botulinism or for treating pathologies associated  
XX with botulinum neurotoxin poisoning.

XX Example 4; SEQ ID NO 200; 110pp; English.



PT New isolated antibody that neutralizes botulinum neurotoxin type A,  
PT useful for diagnosing botulism or for treating pathologies associated  
PT with botulinum neurotoxin poisoning.

XX Example 4; SEQ ID NO 203; 110pp; English.

CC The invention describes an isolated antibody (I) that specifically binds  
CC to an epitope specifically bound by an antibody expressed by a specific  
CC clone where (I) binds to and neutralizes botulinum neurotoxin type A  
CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope  
CC specifically bound by an antibody expressed by a clone chosen from clone  
CC S25, C25, C39, 1C6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WR1(V), WR1(T), 3-1,  
CC 3-8, 3-10 and IN61, where (I) binds to and neutralizes botulinum  
CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)  
CC comprising BoNT/A neutralising epitope having an epitope that is  
CC specifically bound by an antibody expressed by clones as mentioned in (I)  
CC ; producing (I); and a composition (III) comprising several anti-  
CC botulinum neurotoxin antibodies, where each antibody is specific for a  
CC different epitope of a botulinum neurotoxin and the combination of  
CC antibodies shows greater toxin neutralisation than the single antibodies  
CC in surplus. The following are disclosed: a pharmaceutical composition  
CC comprising (I); and a kit comprising (I). (I) is useful for neutralising  
CC BoNT/A antibody and for neutralising a botulinum neurotoxin which  
CC involves contacting neurotoxin with (I) in surplus, where each of (I) is  
CC specific for a different epitope of the botulinum neurotoxin and the  
CC combination of antibodies shows greater toxin neutralising than the  
CC single antibodies in surplus. (I) is useful for diagnosing the botulinum  
CC or for treating pathologies associated with botulinum neurotoxin  
CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)  
CC enables rapid detection or diagnosis of botulism. This is the amino acid  
CC sequence of mouse heavy chain anti-BoNT-antibody CDR3.

XX Sequence 15 AA;

Qy Query Match 84.3%; Score 75; DB 8; Length 15;  
Best Local Similarity 93.3%; Pred. No. 0.00023;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Db 1 EPPDLWMDRGALDV 15  
1 EPPDLWMDRGALDV 15

RESULT 8

ABG20331  
ID ABG20331 standard; protein; 334 AA.

XX ABG20331;

DT 13-FEB-2002 (first entry)

DE Novel human diagnostic protein #20322.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

OS WO200175067-A2.

PN 11-OCT-2001.

PD 30-MAR-2001; 2001WO-US008631.

PF 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

DR N-PSDB; AAS84518.

XX New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.

PS Claim 20; SEQ ID NO 50690; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
CC sequences. (I) is useful as hybridisation probes, polymerase chain  
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
CC and in recombinant production of (II). The polynucleotides are also used  
CC in diagnostics as expressed sequence tags for identifying expressed  
CC genes. (I) is useful in gene therapy techniques to restore normal  
CC activity of (II) or to treat disease states involving (II). (II) is  
CC useful for generating antibodies against it, detecting or quantitating a  
CC polypeptide in tissue, as molecular weight markers and as a food  
CC supplement. (II) and its binding partners are useful in medical imaging  
CC of sites expressing (II). (I) and (II) are useful for treating disorders  
CC involving aberrant protein expression or biological activity. The  
CC polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic  
CC amino acid sequences of the invention. Note: The sequence data for this  
CC patent did not appear in the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 334 AA;

Qy Query Match 57.3%; Score 51; DB 4; Length 334;  
Best Local Similarity 53.3%; Pred. No. 23;  
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
Db 1 EPPDLWMDRGALDV 15  
263 KPDKSSWGPSCGWDV 277

RESULT 9

ADJ98189  
ID ADJ98189 standard; protein; 201 AA.

XX ADJ98189;

DT 06-MAY-2004 (first entry)

DE Prochlorococcus marinus str MIT 9313 phycol kinase protein.

XX phycol kinase; tocopherol biosynthesis; plant; drought resistance;  
KW enzyme.

XX Prochlorococcus marinus str. MIT 9313.

OS WO2004013312-A2.

PN 12-FEB-2004.

PD 05-AUG-2003; 2003WO-US025276.

PF 05-AUG-2002; 2002US-0400689P.

PR 05-AUG-2003; 2003US-00634548.

XX (MONS ) MONSANTO TECHNOLOGY LLC.

PI Norris SR, Lincoln K, Abad MS, Bilers R, Hartsuyker KK;

XX Hirschberg J, Karunanandaa B, Moshiri F, Stein JC, Valentin HB;

DR WPI; 2004-157125/15.



XX DE19811194-A1.  
XX 16-SEP-1999.  
XX 10-MAR-1998; 98DE-01011194.  
XX 10-MAR-1998; 98DE-01011194.  
XX (META-) METAGEN GES GENOMFORSCHUNG MBH.  
XX Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E, Rosenthal A;  
XX MPI, 1999-519629/44.  
XX N-PSDB; AAZ33505.  
XX New nucleic acid expressed at high level in normal prostatic tissue and  
XX encoded polypeptides, used to treat cancer and screen for therapeutic  
XX agents.  
XX Claim 22; 148; 194pp; German.  
XX This invention describes novel nucleic acid sequences (A) that are  
XX expressed at high level in normal prostatic tissue. Polypeptides (I)  
XX encoded by (A) are used; (a) for identifying agents for treatment of  
XX prostatic cancer and (b) for therapy of prostate cancer, optionally where  
XX expressed by gene therapy methods. (A) is also used to isolate full-  
XX length genes (for gene therapy) and for recombinant production of (I),  
XX which can be used to raise specific antibodies. (A) are identified by  
XX assembly of ESTs (expressed sequence tags) before these are analyzed for  
XX expression pattern (tissue specificity). This approach eliminates many of  
XX the false results, as regards tissue specificity, associated with known  
XX methods that use single (usually short) ESTs. AA18304-148456 represent  
XX peptides encoded by the expressed sequence tags described in the method  
XX of the invention  
XX  
SQ Sequence 59 AA;  
Query Match 52.8%; Score 47; DB 2; Length 59;  
Best Local Similarity 87.5%; Pred. No. 15;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 4 WLLMGDRG 11  
| | | | |  
44 WLLMGSRG 51  
DB  
RESULT 13  
ABG22524  
ID ABG22524 standard; protein; 455 AA.  
XX  
AC ABG22524;  
XX  
DT 18-FEB-2002 (first entry)  
XX  
DE Novel human diagnostic protein #22515.  
XX  
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder.  
XX  
OS Homo sapiens.  
XX  
PM WO200175067-A2.  
XX  
PD 11-OCT-2001.  
XX  
PF 30-MAR-2001; 2001WO-US008631.  
XX  
PR 31-MAR-2000; 2000US-00540217.  
XX  
PR 23-AUG-2000; 2000US-00649167.  
XX  
PA (HYSB-) HYSBQ INC.  
XX

PI Drmanac RT, Liu C, Tang YT;  
XX  
XX MPI; 2001-639362/73.  
XX N-PSDB; AAS86711.  
XX  
XX New isolated polynucleotide and encoded polypeptides, useful in  
XX diagnostics, forensics, gene mapping, identification of mutations  
XX responsible for genetic disorders or other traits and to assess  
XX biodiversity.  
XX  
PS Claim 20; SEQ ID NO 52883; 103pp; English.  
XX  
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)  
XX sequences. (I) is useful as hybridization probes, polymerase chain  
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
XX and in recombinant production of (II). The polynucleotides are also used  
XX in diagnostics as expressed sequence tags for identifying expressed  
XX genes. (I) is useful in gene therapy techniques to restore normal  
XX activity of (II) or to treat disease states involving (II). (II) is  
XX useful for generating antibodies against it, detecting or quantitating a  
XX polypeptide in tissue, as molecular weight markers and as a food  
XX supplement. (II) and its binding partners are useful in medical imaging  
XX of sites expressing (II). (I) and (II) are useful for treating disorders  
XX involving aberrant protein expression or biological activity. The  
XX polypeptide and polynucleotide sequences have applications in  
XX diagnostics, forensics, gene mapping, identification of mutations  
XX responsible for genetic disorders or other traits to assess biodiversity  
XX and to produce other types of data and products dependent on DNA and  
XX amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic  
XX amino acid sequences of the invention. Note: The sequence data for this  
XX patent did not appear in the printed specification, but was obtained in  
XX electronic format directly from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 455 AA;  
Query Match 52.8%; Score 47; DB 4; Length 455;  
Best Local Similarity 53.8%; Pred. No. 1.3e+02;  
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
OY 1 EPDWLWGRGAL 13  
| : | | | : | | :  
93 EQNWLWRCRGVM 105  
DB  
RESULT 14  
ADS23387  
ID ADS23387 standard; protein; 904 AA.  
XX  
AC ADS23387;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Bacterial polypeptide #12420.  
XX  
KW Recombinant DNA construct; transformed plant; improved plant property;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmotic;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;  
KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
KW bacterial polypeptide.  
XX  
OS Bacteria.  
XX  
PM US2003233675-A1.  
XX  
PD 18-DEC-2003.  
XX  
PF 20-FEB-2003; 2003US-00369493.  
XX  
PR 21-FEB-2002; 2002US-0360039P.  
XX







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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:31:45 ; Search time 21.25 Seconds  
(without alignments)  
67.918 Million cell updates/sec

Title: US-10-632-706-197

Sequence: 1 EPDMLMGDRGALDV 15

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: p1r1.\*  
2: p1r2.\*  
3: p1r3.\*  
4: p1r4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	51.7	373	2 D71142	hypothetical prote
2	45.5	51.1	298	2 AE3234	transcriptional re
3	45	50.6	203	2 G70595	probable endo prot
4	45	50.6	2	2 AG0066	probable AMP-bind
5	44.5	50.0	1076	2 T30842	serine-repeat anti
6	44	49.4	237	2 G82768	virulence protein
7	44	49.4	409	2 B75010	hypothetical prote
8	44	49.4	491	2 T10930	3C3.21 protein - S
9	44	49.4	601	2 B95296	probable ABC-type
10	43	48.3	321	2 S77614	phosphoribosylform
11	43	48.3	462	2 T50432	homolog to yeast o
12	43	48.3	683	2 UC5393	zinc finger protei
13	43	48.3	685	2 UC5392	zinc finger protei
14	43	48.3	698	2 AB2593	hypothetical prote
15	42.5	47.8	315	2 H83276	probable lipase PA
16	42	47.2	71	2 G98356	hypothetical prote
17	42	47.2	139	2 AG2925	hypothetical prote
18	42	47.2	397	2 B53240	allergen Amb a II
19	42	47.2	408	1 A69819	probable phospho
20	42	47.2	482	2 A10554	thiamin biosynthes
21	42	47.2	482	2 B90688	probable oxidoredu
22	42	47.2	482	2 T46944	thiamin biosynthes
23	42	47.2	482	2 AB5539	probable oxidoredu
24	42	47.2	482	2 G64771	yeak protein - Bsc
25	42	47.2	486	2 T51431	glucosyltransferas
26	42	47.2	486	2 H87311	hypothetical prote
27	42	47.2	492	2 T38156	citrate lyase - fi
28	42	47.2	566	2 H84037	long-chain fatty-a
29	42	47.2	604	2 T49577	hypothetical prote

30	42	47.2	608	2 T34994	probable long-chain
31	42	47.2	804	2 AG0565	probable membrane
32	42	47.2	804	2 G64780	probable membrane
33	42	47.2	804	2 AB5549	probable oxidoredu
34	42	47.2	804	2 G90698	probable oxidoredu
35	42	47.2	993	2 B97219	conserved membrane
36	41	46.1	36	2 E84416	hypothetical prote
37	41	46.1	248	2 T36093	probable DNA methyl
38	41	46.1	262	2 T75093	hypothetical prote
39	41	46.1	288	2 AG0888	probable Arac-fami
40	41	46.1	359	2 C70735	probable Idsa prot
41	41	46.1	403	2 T10847	Y4hm protein - Rhi
42	41	46.1	408	2 AG0305	probable L-ldicol
43	41	46.1	438	2 T37786	probable RNA-bind
44	41	46.1	442	2 D84600	probable xylose
45	41	46.1	459	2 T27657	hypothetical prote

## ALIGNMENTS

RESULT 1  
D71142  
hypothetical protein PH0351 - *Pyrococcus horikoshii*  
C:Species: *Pyrococcus horikoshii*  
C>Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 09-Jul-2004  
C:Accession: D71142  
R:Kawarayashi, Y.; Sawada, M.; Horikawa, H.; Hata, Y.; Hino, Y.; Yamamoto, S.; Sekine, M.; Ohtoku, Y.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kishida, N.; Oguchi, DNA Res. 5, 55-76, 1998  
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic archaeon, *Pyrococcus horikoshii* strain OT3  
A:Reference number: A71000; MUID:98344137; PMID:9679194  
A:Accession: D71142  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-373 <KAM>  
A:Cross-references: UNIPROT:O58089; UNIPARC:UPI000062DB7; GB:AP000002; NID:g3236129; PIR A:Experimental source: strain OT3  
A>Note: this accession replaces an interim accession for a sequence replaced by GenBank C:Genetics:  
A:Gene: PH0351

Query Match 51.7%; Score 46; DB 2; Length 373;  
Best Local Similarity 43.5%; Pred. No. 19;  
Matches 10; Conservative 1; Mismatches 2; Indels 10; Gaps 1;  
Db 2 PDMLM-----GDRGALD 14  
318 PGWLMGILMLMGRIQNGALD 340

RESULT 2  
AE3234  
transcriptional regulator, *lyrA* family *gcva* [imported] - *Agrobacterium tumefaciens* (str. C:Species: *Agrobacterium tumefaciens*  
C>Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004  
C:Accession: AE3234  
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutysavin, T.; Levy, R.; Li, M.; McClell Science 294, 2317-2323, 2001  
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.  
A:Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.  
A:Reference number: AB2577; MUID:21608550; PMID:11743193  
A:Accession: AE3234  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-298 <KUR>  
A:Cross-references: UNIPROT:Q8U680; UNIPARC:UPI000002D764; GB:AE006690; PIDN:AAI46291.1;  
A:Experimental source: strain C58 (Dupont)  
C:Genetics:  
A:Gene: *gcva*

A:Genome: plasmid  
C:Superfamily: regulatory protein ampr

Query Match 51.1%; Score 45.5; DB 2; Length 298;  
Best Local Similarity 56.2%; Pred. No. 18;  
Matches 9; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

Qy 1 EPDWLW-GDRGALDV 15  
Db 199 EPDWLRWCAQAGVADV 214

## RESULT 3

GPro595  
probable enrd protein - Mycobacterium tuberculosis (strain H37Rv)

C:Species: Mycobacterium tuberculosis  
C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004

C:Accession: G70595  
R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltham, T.; Gentles, S.; Hamlin, N.; Holtroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sultson, J.E.; Taylor, K.; Whitehead, S.; Barrrell, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A:Reference number: A70500; PMID:98295987; PMID:9634230

A:Accession: G70595

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-203 <COL>

A:Cross-references: UNIPROT:O05852; UNIPARC:UPI000016534B; GB:I295120; GB:AL123456; NID:G

A:Experimental source: strain H37Rv

C:Genetics:

A:Gene: enrd

C:Superfamily: cofactor-dependent phosphoglycerate mutase; phosphoglycerate mutase homol

Query Match 50.6%; Score 45; DB 2; Length 203;  
Best Local Similarity 85.7%; Pred. No. 15;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EPDWLW 7  
Db 103 EPDWLW 109

## RESULT 4

AG0066  
probable AMP-binding enzyme-family protein YP00537 [imported] - Yersinia pestis (strain

C:Species: Yersinia pestis  
C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004

C:Accession: AG0066

R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tlball, R.W.; Holden, M.T.G.; Prentice, M.B.

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;

ll, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrrell,

Nature 413, 523-527, 2001

A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: AG0066

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-601 <KUR>

A:Cross-references: UNIPROT:Q82IG5; UNIPARC:UPI000000CD42; GB:AL590842; PIDN:CA089394.1;

C:Genetics:

A:Gene: YP00537

C:Superfamily: Synchocystis long-chain-fatty-acid-CoA ligase; acetate-CoA ligase homol

Query Match 50.6%; Score 45; DB 2; Length 601;  
Best Local Similarity 64.3%; Pred. No. 42;  
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EPDWLW-GDRGALDV 14  
Db 440 EDGWLKTGAGALDV 453

RESULT 5  
T30842  
serine-repeat antigen 3 - Plasmodium vivax

C:Species: Plasmodium vivax  
C:Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 09-Jul-2004

C:Accession: T30842  
R:Kieffer, M.C.; Crawford, K.A.; Boley, L.J.; Landsberg, K.E.; Gibson, H.L.; Kestow, D.C.;  
Mol. Biochem. Parasitol. 78, 55-65, 1996

A:Title: Identification and cloning of a locus of serine repeat antigen (serra)-related ge

A:Reference number: 220898; MUID:96408670; PMID:8813677

A:Accession: T30842

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1076 <RIB>

A:Cross-references: UNIPROT:Q26154; UNIPARC:UPI00000809B3; EMBL:U51723; NID:G1381087; PII

C:Genetics:

A:Insertions: 12/1; 253/1; 302/1

A>Note: V-SERA 3

C:Superfamily: Plasmodium vivax serine-repeat antigen

Query Match 50.0%; Score 44.5; DB 2; Length 1076;  
Best Local Similarity 40.9%; Pred. No. 87;  
Matches 9; Conservative 2; Mismatches 4; Indels 7; Gaps 1;

Qy 1 EPDWL-----WGDRGALDV 15  
Db 743 KPWLWLNWGWKHWGDKTFKCV 764

## RESULT 6

G82768  
virulence protein Xp0754 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004

C:Accession: G82768

R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen-

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717; PMID:10910347

A>Note: for a complete list of authors see reference number A59328 below

A:Accession: G82768

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-237 <SIM>

A:Cross-references: UNIPROT:Q9PFC4; UNIPARC:UPI00000C24F4; GB:AB003916; GB:AB003849; NID

A:Experimental source: strain 9a5c

R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvaranga, R.; A

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.B.A.; Carraro, D.M.; Carrer, H

as-Neto, E.; Docena, C.; El-Dorty, H.; Facinani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kempf, B.L.; Kleijima, J.P.; Krieger, J.E.; Kuramae, E.B.; Laigr

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, S

A:Authors: Martins, B.M.F.; Matsumura, A.Y.; Menck, C.F.M.; Miracca, B.C.; Miyaki, C.Y.

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmeri, D.A

Rodrigues, V.; Rosa, A.J.; de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

A:Authors: da Silva, A.C.; de M.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir

M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

A:Gene: XF0754

C:Superfamily: type IV secretory pathway, VirC component

Query Match 49.4%; Score 44; DB 2; Length 237;  
Best Local Similarity 58.3%; Pred. No. 24;  
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 4 WLWNGDRGALDV 15  
Db 151 WLWNGDRGTRDV 162

RESULT 7  
B75010  
hypochemical protein PAB1063 - Pyrococcus abyssi (strain Orsay)  
C:Species: Pyrococcus abyssi  
C>Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004  
C/Accession: B75010  
R:anonymous, Genoscope  
submitted to the EMBL Data Library, July 1999  
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru  
A:Reference number: A75001  
A:Accession: B75010  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-409 <KAM>  
A:Cross-references: UNIPROT:Q9UT92, UNIPARC:UPI0000034560, GB:AJ248288, GB:AL096836, NIT  
A:Experimental source: strain Orsay  
C:Genetics:  
A:Gene: PAB1063

Query Match 49.4%; Score 44; DB 2; Length 409;  
Best Local Similarity 39.1%; Pred. No. 41;  
Matches 9; Conservative 2; Mismatches 2; Indels 10; Gaps 1;

QY 2 PDWLMW-----GDRGALD 14  
Db 354 PGWILMGLILMLMGRVGNRGLD 376

RESULT 8  
T10930  
3C3.21 protein - Streptomyces coelicolor  
C:Species: Streptomyces coelicolor  
C>Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
C/Accession: T10930  
R:Parkhill, J.; Barrall, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, August 1998  
A:Reference number: Z17215  
A:Accession: T10930  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-491 <PAR>  
A:Cross-references: UNIPROT:O86654, UNIPARC:UPI000000DAD67, EMBL:AL031231, NID:e1315070;  
A:Experimental source: strain A3(2)  
C:Genetics:  
A:Gene: 3C3.21

Query Match 49.4%; Score 44; DB 2; Length 491;  
Best Local Similarity 61.5%; Pred. No. 49;  
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 DWLMGDRGALD 15  
Db 413 EFVLHGRGALD 425

RESULT 9  
E95296  
probable ABC-type iron transport system protein Sma0525 [imported] - Sinorhizobium meli  
C:Species: Sinorhizobium meli  
C>Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 09-Jul-2004  
C/Accession: E95296  
R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowe  
; Kaiman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yen, K.C.  
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001  
A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meli  
A:Reference number: A95262; MUID:21396509; PMID:11481432  
A:Accession: E95296  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-601 <KUR>  
A:Cross-references: UNIPROT:Q930C1, UNIPARC:UPI000000CB03E, GB:AB006469, PIDN:AA64935.1;  
A:Experimental source: strain 1021, megaplasmid pSymbA

R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,  
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Drenno, S.; Federspiel, N.A.; Fisher, R.F.;  
L.; Hyman, R.W.; Jones, T.  
Science 293, 668-672, 2001  
A:Authors: Kahn, D.; Kahn, M.L.; Kaiman, S.; Keating, D.H.; Kise, E.; Komp, C.; Lelaure,  
hebulle, P.; Vandendol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yen, K.  
A:Title: The composite genome of the legume symbiont Sinorhizobium meli  
A:Reference number: A96039; MUID:21368234; PMID:11474104  
A:Contents: annotation  
C:Genetics:  
A:Gene: Sma0525  
A:Genome: plasmid

Query Match 49.4%; Score 44; DB 2; Length 601;  
Best Local Similarity 85.7%; Pred. No. 59;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PDWLMWG 8  
Db 169 PDWLMWG 175

RESULT 10  
S77614  
phosphoribosylformylglycinamide synthase (EC 6.3.5.3) component II - Synecococcus sp.  
N:Alternate names: PGAM synthetase  
C:Species: Synecococcus sp.  
A:Variety: PCC 7942  
C>Date: 29-Jul-1997 #sequence\_revision 24-Oct-1998 #text\_change 31-Dec-2004  
C/Accession: S77614; S77613  
R;Liu, Y.; Tsinoresmas, N.F.  
submitted to the EMBL Data Library, August 1995  
A:Description: Unusual gene arrangement for the putative chromosome replication origin a  
A:Reference number: S77614  
A:Accession: S77614  
A:Molecule type: DNA  
A:Residues: 1-112 <LTV>  
A:Cross-references: UNIPROT:Q55037, UNIPARC:UPI0000176276, EMBL:U33322, NID:g974613; PIDN  
A:Experimental source: PCC 7942  
R;Liu, Y.; Tsinoresmas, N.F.; Golden, S.S.; Kondo, T.; Johnson, C.H.  
Mol. Microbiol. 20, 1071-1081, 1996  
A:Title: Circadian expression of genes involved in the purine biosynthetic pathway of cyr  
A:Reference number: S77612; MUID:96405630; PMID:8809759  
A:Accession: S77613  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 113-321 <LTV>  
A:Cross-references: UNIPARC:UPI00000BE4A4; EMBL:U33211  
A:Experimental source: PCC 7942  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1995  
C:Genetics:  
A:Gene: purL  
A:Function:  
A:Description: catalyzes the condensation of 5'-phosphoribosylformylglycinamide with ATP.  
A:Pathway: purine nucleotide biosynthesis  
A:Note: fourth step in pathway  
C:Keywords: ligase; purine nucleotide biosynthesis

Query Match 48.3%; Score 43; DB 2; Length 321;  
Best Local Similarity 63.6%; Pred. No. 46;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 PDWLMGDRGA 12  
Db 240 PDWLMFABEGA 250

RESULT 11  
T50422  
homolog to yeast orf yor166c. [imported] - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe  
C>Date: 09-Jun-2000 #sequence\_revision 09-Jun-2000 #text\_change 09-Jul-2004  
C/Accession: T50422

R;Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.  
Submitted to the EMBL Data Library, February 2000  
A:Reference number: Z25039  
A:Accession: J50422  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-462 <SER>  
A:Cross-references: UNIPROT:Q9P7J1, UNIPARC:UPI000060AA1B, EMBL:AL157991, PIDN:CAB76224.  
A:Experimental source: strain 972h(-); cosmid C24B10  
C:Genetics:  
A:Gene: SPDB:SPCC24B10.15  
A:Map position: 3

Query Match 48.3%; Score 43; DB 2; Length 462;  
Best Local Similarity 55.6%; Pred. No. 65;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 DMLMGDRG 11  
Db 394 EMDLMAERG 402

## RESULT 12

JC5392  
zinc finger protein KF-1 precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 04-Jun-1997 #sequence\_revision 18-Jul-1997 #text\_change 09-Jul-2004  
A:Accession: JC5393  
R;Yaoojima, K.; Tsujimura, A.; Mizuno, T.; Shigeyoshi, Y.; Inazawa, J.; Kikuno, R.; Kuma

Biochem. Biophys. Res. Commun. 231, 481-487, 1997  
A:Title: Cloning of human and mouse cDNAs encoding novel zinc finger proteins expressed  
A:Reference number: JC5392; MUID:97223484; PMID:9070305  
A:Accession: JC5393  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-683 <YAS>  
A:Cross-references: UNIPROT:O08883; UNIPARC:UPI00000E0601; DBJ:D76445; NID:92058262; PT

A:Experimental source: brain  
C:Comment: This protein is involved in membranous protein-sorting apparatus similarly to  
C:Genetics:  
A:Gene: Kf-1  
C:Superfamily: zinc finger protein KF-1 precursor; RING finger homology  
C:Keywords: glycoprotein; phosphoprotein; zinc  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:326-344/Domain: transmembrane #status predicted <TM1>  
F:352-380/Domain: transmembrane #status predicted <TM2>  
F:631-666/Domain: RING finger homology <RMG>  
F:100,155,228,273,301,356/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:664/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 48.3%; Score 43; DB 2; Length 683;  
Best Local Similarity 85.7%; Pred. No. 95;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EPDWLW 7  
Db 603 EPDWLW 609

## RESULT 13

JC5392  
zinc finger protein KF-1 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 04-Jun-1997 #sequence\_revision 18-Jul-1997 #text\_change 09-Jul-2004  
A:Accession: JC5392  
R;Yaoojima, K.; Tsujimura, A.; Mizuno, T.; Shigeyoshi, Y.; Inazawa, J.; Kikuno, R.; Kuma

Biochem. Biophys. Res. Commun. 231, 481-487, 1997  
A:Title: Cloning of human and mouse cDNAs encoding novel zinc finger proteins expressed  
A:Reference number: JC5392; MUID:97223484; PMID:9070305  
A:Accession: JC5392  
A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA  
A:Residues: 1-685 <YAS>  
A:Cross-references: UNIPROT:O00237, UNIPARC:UPI000073F2A, DBJ:D76444, NID:91945614, PIT  
A:Experimental source: brain  
C:Comment: This protein is involved in membranous protein-sorting apparatus similarly to  
C:Genetics:  
A:Gene: Kf-1  
C:Superfamily: zinc finger protein KF-1 precursor; RING finger homology  
C:Keywords: zinc  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:326-344/Domain: transmembrane #status predicted <TM1>  
F:352-380/Domain: transmembrane #status predicted <TM2>  
F:617-668/Domain: RING finger homology <RMG>

Query Match 48.3%; Score 43; DB 2; Length 685;  
Best Local Similarity 85.7%; Pred. No. 95;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EPDWLW 7  
Db 605 EPDWLW 611

## RESULT 14

A82593  
hypothetical protein XF2169 [imported] - Xylella fastidiosa (strain 9a5c)  
C:Species: Xylella fastidiosa  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
A:Accession: A82593  
R;Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc  
Nature 406, 151-157, 2000  
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A:Reference number: A82515; MUID:20365717; PMID:10910347  
A:Note: for a complete list of authors see reference number A59328 below  
A:Accession: A82593  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-698 <STM>  
A:Cross-references: UNIPROT:Q9PBH5; UNIPARC:UPI0000C2968; GB:AE004030; GB:AB003849; NID

A:Experimental source: strain 9a5c  
R;Simpon, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A  
Brites, M.R.S.; Bueno, M.R.P.; Canarço, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H  
as-Neto, E.; Docena, C.; El-Dorri, H.; Fedini, A.P.; Ferreira, A.J.S.  
Submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm  
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitejima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig  
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins, E  
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;  
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmarini, D.A  
Rodrigues, V.; Rosa, A.C.R.; de M.; de M.; de M.; de M.; de M.; de M.; de M.; de M.; de M.  
A:Authors: da Silva, A.C.R.; de M.; de M.; de M.; de M.; de M.; de M.; de M.; de M.; de M.  
M.; Tsunako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A:Reference number: A59328  
A:Contents: annotation  
C:Genetics:  
A:Gene: XF2169

Query Match 48.3%; Score 43; DB 2; Length 698;  
Best Local Similarity 63.6%; Pred. No. 97;  
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 DMLMGDRGAL 13  
Db 554 DMLMWDNSL 564

## RESULT 15

H83276  
probable lipase PA2949 [imported] - Pseudomonas aeruginosa (strain PA01)  
C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 12-Jul-2004  
A:Accession: H83276  
R;Stover, C.K.; Pham, X.O.; Brwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lim,  
 .; Lory, S.; Olson, M.V.  
 Nature 406, 959-964, 2000  
 A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho  
 A:Reference number: A82950; MUID:20437337; PMID:10984043  
 A:Accession: H83276  
 A:Status: Preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-315 <STO>  
 A:Cross-references: UNIPROT:Q9KJG6; UNIPARC:UPI000000C4BC6; GB:AE004721; GB:AE004091; NID  
 A:Experimental source: strain PA01  
 C:Genetics:  
 A:Gene: PA2949  
 C:Superfamily: tropinesterase

Query Match 47.8%; Score 42.5; DB 2; Length 315;  
 Best Local Similarity 66.7%; Pred.No.54;  
 Matches 10; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Qy 2 PDWLIMGDRG-ALDV 15  
 | |||||  
 Db 249 PTLIMGDRDRVDV 263

Search completed: December 4, 2005, 04:53:46  
 Job time : 33.25 secs

**This page blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 4, 2005, 04:31:36 ; Search time 136.875 Seconds  
(without alignments)  
77.318 Million cell updates/sec

Title: US-10-632-706-197  
Perfect score: 89  
Sequence: 1 EPDMLWMDRGALDV 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	56.2	441	2	OSLQ90_SILPO
2	49	55.1	208	2	OSYQ86_NOCFA
3	49	55.1	405	2	QSN4J9_SYNPF
4	49	55.1	779	2	Q6H084_FREDI
5	48	53.9	217	2	Q7V3U3_PROMM
6	48	53.9	262	2	Q8BJP9_SHEON
7	48	53.9	426	2	Q5SS50_CRYNE
8	48	53.9	448	2	Q9S4Z3_SALEN
9	48	53.9	775	2	Q9S8A1_CANAL
10	48	53.9	784	2	Q8GMI3_STRGL
11	48	53.9	793	2	Q59870_CANAL
12	48	53.9	804	2	Q8ZRP9_SALTY
13	47.5	53.4	527	2	Q6ZDZ2_ORYSA
14	47	52.8	61	2	Q6THZ8_HUMAN
15	47	52.8	364	2	Q7UG34_RHOBA
16	47	52.8	369	2	Q5KNM7_CRYNE
17	47	52.8	375	2	Q55ZB2_CRYNE
18	47	52.8	471	2	Q4RPV5_9SPHN
19	47	52.8	1517	2	Q5AYP9_EMENT
20	47	52.8	1547	2	Q9G1A0_ASPTU
21	47	52.8	1547	2	Q4WDD4_ASPTU
22	46	51.7	214	2	Q4UX96_CORJK
23	46	51.7	350	1	COBT_PSBEM
24	46	51.7	356	2	Q6C1B2_YARLI
25	46	51.7	373	2	Q58089_PYRHO
26	46	51.7	396	2	Q70GME_CHIRE
27	46	51.7	1562	2	Q9Y840_MYCRG
28	45.5	51.1	266	2	Q7D2M8_AGRTS
29	45.5	51.1	298	2	Q8U680_AGRTS
30	45	50.6	91	2	Q854E3_9CAUD
31	45	50.6	141	2	Q9NU66_HUMAN

32	45	50.6	203	2	Q6MW27_MYCTU
33	45	50.6	203	2	Q7TW28_MYCBO
34	45	50.6	228	2	Q7DSX2_MYCBO
35	45	50.6	246	2	Q7U9Y4_SYNPF
36	45	50.6	370	2	Q88JL2_PSEPK
37	45	50.6	381	2	Q5P2Z9_AZOSB
38	45	50.6	450	2	Q5JDB4_PYRKO
39	45	50.6	505	2	Q5LR06_SILPO
40	45	50.6	601	2	Q66EL9_YERPS
41	45	50.6	601	2	Q8ZIG5_YERPE
42	45	50.6	781	2	Q4HY20_GIBZE
43	45	50.6	892	2	Q4KIV4_PSESY
44	45	50.6	907	2	Q4ZN69_PSESY
45	45	50.6	1326	2	Q6ATH6_ORYSA

ALIGNMENTS

RESULT 1					
ID	OSLQ90_SILPO	PRELIMINARY;	PRT;	441 AA.	
AC	QSLQ90;				
DT	01-FEB-2005 (TReMBLrel. 29, Created)				
DT	01-FEB-2005 (TReMBLrel. 29, Last sequence update)				
DT	01-FEB-2005 (TReMBLrel. 29, Last annotation update)				
DE	TRAP dicarboxylate transporter, DctM subunit.				
GN	OrderedLocustNames=SPO2605;				
OS	Silicibacter pomeroyi.				
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;				
OX	Rhodobacteraceae; Silicibacter.				
OX	NCBI_TaxID=89184;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].				
RC	STRAIN=DSS-3 / ATCC 700808 / DSM 15171;				
RX	PubMed=15602564; DOI=10.1038/nature03170;				
RA	Moran M.A., Buchan A., Gonzalez J.M., Heidelberg J.F., Whitman W.B.,				
RA	Brinkac L.M., Heniksen J.R., King G.M., Belas R., Fugua C.,				
RA	Rane E., Sheldon W.M., Ye W., Miller T.R., Carlton J., Raabso D.A.,				
RA	Paulsen I.T., Ren Q., Daugherty S.C., DeBoy R.T., Dodson R.J.,				
RA	Durkin A.S., Madupu R., Nelson W.C., Sullivan S.A., Rosovitz M.J.,				
RA	Haft D.H., Selengut J., Ward N.;				
RT	"Genome sequence of Silicibacter pomeroyi reveals adaptations to the				
RT	marine environment."				
RL	Nature 432:910-913(2004).				
DR	EMBL; CP000031; AA95851.1; -; Genomic_DNA.				
DR	InterPro; IPR010656; DctM.				
DR	InterPro; IPR000252; Deda.				
DR	Pfam; PF06808; DctM; 1.				
DR	Pfam; PF00597; Deda; 1.				
KW	Complete proteome.				
SQ	SEQUENCE 441 AA; 48056 MW; 8B59B0A462757858 CRC64;				
Query Match					
Best Local Similarity 72.7%; Score 50; DB 2; Length 441;					
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;					
QY	5 LWMGDRGALDV 15				
DB					
	38 LWMGDRGVDI 48				
RESULT 2					
ID	OSYQ86_NOCFA	PRELIMINARY;	PRT;	208 AA.	
AC	QSYQ86;				
DT	25-OCT-2004 (TReMBLrel. 28, Created)				
DT	25-OCT-2004 (TReMBLrel. 28, Last sequence update)				
DT	25-OCT-2004 (TReMBLrel. 28, Last annotation update)				
DE	Hypothetical protein.				
GN	OrderedLocustNames=nfa48030;				
OS	Nocardia farcinica.				

```
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Nocardiaceae; Nocardia.
OX NCBI_TaxID=37329;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=IFM 10152.
RX PubMed=15466710; DOI=10.1073/pnas.0406410101;
RA Ishikawa J., Yamashita A., Mikami Y., Hoshino Y., Kurita H., Hotta K.,
RA Shiba T., Hattori M.;
RT "The complete genomic sequence of Nocardia farcinica IFM 10152.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14925-14930(2004).
DR EMBL; AP006618; BAD5655.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 208 AA; 22565 MW; EBE3243D9E52094E CRC64;

Query Match 55.1%; Score 49; DB 2; Length 208;
Best Local Similarity 46.7%; Pred. No. 16;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
```

```
OY 1 EPDWLMGDRGALDV 15
DB 111 DPDWYMLNRDEIDV 125

RESULT 3
OSN4J9 SYNTP6 PRELIMINARY; PRT; 405 AA.
AC OSN4J9;
DT 01-FEB-2005 (TREMBLrel. 29, Created)
DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)
DE Sun protein.
GN Name=sun; OrderedlocusNames=sync0580_d;
OS Synecchococcus sp. (strain PCC 6301) (Anacystis nidulans).
OC Bacteria; Cyanobacteria; Chroococcales; Synecchococcus.
OX NCBI_TaxID=265084;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PCC6301;
RA Sugita M.;
RT "Complete genome structure of the unicellular cyanobacterium Anacystis
nidulans 6301 (Synecchococcus sp. PCC6301).";
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP008231; BAD78770.1; -; Genomic_DNA.
DR GO; GO:0008649; rRNA methyltransferase activity; IEA.
DR GO; GO:0006364; rRNA processing; IEA.
DR InterPro; IPR004573; Fmu_mfrase.
DR InterPro; IPR001678; Fmu_NDI1/Nop2p.
DR InterPro; IPR006077; NusB_Remb_TM44.
DR InterPro; IPR006174; SAM_mfrase.
DR InterPro; IPR000051; SAM_bind.
DR Pfam; PF01189; Noli_Nop2_Fmu; 1.
DR Pfam; PF01029; NusB_1.
DR ProDom; PD005242; NusB_region; 1.
DR TIGRfams; TIGR00563; ramb; 1.
KW Complete proteome.
SQ SEQUENCE 405 AA; 44708 MW; 89F6C51B86590C4 CRC64;

Query Match 55.1%; Score 49; DB 2; Length 405;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 10; Conservative 0; Mismatches 3; Indels 2; Gaps 1;
```

```
OY 2 PDWLMGDRGALD 14
DB 110 PDWLMGDRGALD 124

RESULT 4
OSN084 FREDI PRELIMINARY; PRT; 779 AA.
AC OSN084;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
```

```
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein (Fragment).
OS Fremyella diplosiphon (Calochrix PCC 7601).
OC Bacteria; Cyanobacteria; Nostocales; Microchaetaceae; Microchaete.
OX NCBI_TaxID=1197;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FDJ3;
RX Stowe-Evans E.L., Ford J., Kehoe D.M.;
RT "Genomic DNA Microarray Analysis: Identification of New Genes
RT Regulated by Light Color in the Cyanobacterium Fremyella
RT diplosiphon.";
RL J. Bacteriol. 186:4338-4349(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FDJ3;
RX Stowe-Evans E., Ford J., Kehoe D.M.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY548438; AAT11885.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON TER 779
SQ SEQUENCE 779 AA; 85897 MW; 67144DE6E472F0AD CRC64;
```

```
Query Match 55.1%; Score 49; DB 2; Length 779;
Best Local Similarity 77.8%; Pred. No. 60;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 EPDWLMGCD 9
DB 422 EPDWLMGCD 430

RESULT 5
OSV3J3 PROMM PRELIMINARY; PRT; 217 AA.
AC OSV3J3;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DE Hypothetical protein precursor.
GN OrderedlocusNames=PMT2247;
OS Prochlorococcus marinus (strain MIT 9313).
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=74547;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;
RA Kocap G., Latimer F.W., Lamerdin J.E., Malfatti S., Chain P.,
RA Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
RA Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M.,
RA Shaw E.A., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
RA Webb E.A., Zinser E.R., Chisholm S.W.;
RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
RT niche differentiation.";
RL Nature 424:1042-1047(2003).
DR EMBL; BX572101; CAE32421.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004605; F:phosphatidate cytidyltransferase activity; IEA.
DR GO; GO:0008654; P:phospholipid biosynthesis; IEA.
DR InterPro; IPR000374; PC_trans.
DR Pfam; PF01148; CTP_transf_1; 1.
KW Complete proteome; Hypothetical protein; Signal.
FT SIGNAL 1
SQ SEQUENCE 217 AA; 23832 MW; 522AA449E8033FEC CRC64;
```

```
Query Match 53.9%; Score 48; DB 2; Length 217;
Best Local Similarity 50.0%; Pred. No. 24;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
OY 2 PDWLMGDRGAL 13
DB 139 PDWLMGDRGAL 150
```



## RESULT 6

Q8BJF9\_SHEON PRELIMINARY; PRT; 262 AA.

AC Q8BJF9;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein S00508.  
GN OrderedLocustNames=S00508;  
OS Shewanella oneidensis.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;  
OC Shewanellaceae; Shewanella.  
OX NCBI\_TaxID=70863;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=MR-1;  
RX MEDLINE=22297686; PubMed=1236813; DOI=10.1038/nbt.749;  
RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gallos E.J., Nelson W.C.,  
RA Read T.D., Eisen J.A., Seshadri R., Ward N.L., Mehe B.A.,  
RA Clayton R.A., Meyer T., Teapin A., Scott J., Beanan M.J.,  
RA Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,  
RA Halt D.H., Kolonay J.F., Madupu R., Peterson J.D., Unayam L.A.,  
RA White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Impriali M.,  
RA Lee K., Barry K.J., Lee C., Mueller J., Khouri H.M., Gill J.,  
RA Uterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,  
RA Venter J.C., Neilson K.H., Fraser C.M.,  
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium  
RT Shewanella oneidensis."RL Nat. Biotechnol. 20:1118-1123(2002).  
DR EMBL; AB015498; AAN53589.1; -; Genomic\_DNA.  
DR TIGR; S00508; -;  
KW Complete proteome.  
SQ SEQUENCE 262 AA; 29556 MW; 5E5E6EF4D52DC44C CRC64;

Query Match 53.9%; Score 48; DB 2; Length 262;  
Best Local Similarity 61.5%; Pred. No. 29;  
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 PDWLMGDRGALD 14  
|||:|||||  
Db 58 PDWAIAGDRGTND 70

## RESULT 7

Q55S80\_CRYNE PRELIMINARY; PRT; 426 AA.

AC Q55S80;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Hypothetical protein.  
GN ORFNames=CNBE1140;  
OS Cryptococcus neoformans var. neoformans B-3501A.  
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;  
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.  
OX NCBI\_TaxID=283643;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=B-3501A;  
RA Fung B., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,  
RA Wicks B.L., Fu J., Davis R.W.,  
RT "Cryptococcus neoformans serotype D sequencing."  
RL Submitted (JUL-2004) to the EMBL/Genbank/DBJ databases.  
CC -! CAUTION: The sequence shown here is derived from an  
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; AA01000024; EAL20751.1; -; Genomic\_DNA.  
KW Hypothetical protein.  
SQ SEQUENCE 426 AA; 47024 MW; A0F8D1F268A28310 CRC64;

Query Match 53.9%; Score 48; DB 2; Length 426;

Best Local Similarity 53.3%; Pred. No. 47;  
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 EPDWLMGDRGALDV 15  
|||:|||||:  
Db 328 KPDVEMGDRGALDL 342

## RESULT 8

Q9S4Z3\_SALEN PRELIMINARY; PRT; 448 AA.

AC Q9S4Z3;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein (Fragment).  
OS Salmoneella enteritidis.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Salmoneella.  
OX NCBI\_TaxID=592;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=S1400;  
RX MEDLINE=99377131; PubMed=10447888;  
RA Pattery T., Hernalssteens J.-P., De Greve H.,  
RT "Identification and molecular characterization of a novel Salmoneella  
RT enteritidis pathogenicity islet encoding an ABC transporter."  
RL Mol. Microbiol. 33:791-805(1999).  
DR EMBL; AF102556; AAD51877.1; -; Genomic\_DNA.  
DR GO; GO:0016020; C:membrane; IEA.  
DR InterPro; IPR003838; DUF214.  
DR Pfam; PF02687; FtsX; 1.  
KW Hypothetical protein.  
FT NON\_TER  
SQ SEQUENCE 448 AA; 49706 MW; 389077E50235C42A CRC64;

Query Match 53.9%; Score 48; DB 2; Length 448;  
Best Local Similarity 87.5%; Pred. No. 49;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EPDWLMG 8  
|||:|||||  
Db 408 EPDWRLMG 415

## RESULT 9

Q59SA1\_CANAL PRELIMINARY; PRT; 775 AA.

AC Q59SA1;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Hypothetical protein.  
GN ORFNames=CaO19.10974;  
OS Candida albicans SC5314.  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.  
OX NCBI\_TaxID=237561;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=SC5314;  
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;  
RA Jones T., Federpriel N.A., Chihana H., Dungan J., Kaiman S.,  
RA Magee B.B., Newport G., Thorensen Y.R., Agabian N., Magee P.T.,  
RA Davis R.W., Scherer S.,  
RT "The diploid genome sequence of Candida albicans."  
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=SC5314;  
RA Dungan J., Kuo A., Newport G., Ian C.-Y., Iijima C., Adegbola O.,  
RA Roberts J., Perison K., Donnelly S., Favoreto S., Tzung K.-W.,  
RA Jones T., Scherer S., Agabian N.,

Query Match 53.9%; Score 48; DB 2; Length 775;

RT "Annotation of the Genome of *Candida albicans*.";  
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.  
CC -! CAUTION: The sequence shown here is derived from an  
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
preliminary data.  
CC EMBL; AAC001000154; EAK93359.1; -; Genomic\_DNA.  
DR KW Hypothetical protein.  
SQ SEQUENCE 775 AA; 88474 MW; 685118C6B2C914A8 CRC64;  
  
Query Match 53.9%; Score 48; DB 2; Length 775;  
Best Local Similarity 54.5%; Pred. No. 86;  
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 2 PDMLMGDRGA 12  
Db 718 PEMAVWGSQGA 728  
  
RESULT 10  
O8GM13\_STRGL PRELIMINARY; PRT; 784 AA.  
ID O8GM13;  
AC O8GM13;  
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
DE UvrA-like drug resistance pump.  
OS Streptomyces globisporus.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomycetaceae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxId=1908;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C-1027;  
RX MEDLINE=22171413; PubMed=12183628; DOI=10.1126/science.1072110;  
RA Liu W., Christenson S.D., Standage S., Shen B.;  
RL Science 297:1170-1173 (2002).  
RT "Biosynthesis of the endiayne antitumor antibiotic C-1027."  
CC -! SIMILARITY: Belongs to the ABC transporter family.  
DR EMBL; AY048670; AAL0654.1; -; Genomic\_DNA.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0016887; F:ATPase activity; IEA.  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR003439; ABC transp\_like.  
DR Pfam; PF00005; ABC trans\_2.  
DR PROSITE; PS00211; ABC\_TRANSPORTER\_1; 1.  
DR PROSITE; PS00893; ABC\_TRANSPORTER\_2; 2.  
DR ATP-binding; Membrane; Nucleotide-binding; Transport.  
KW ATP-binding; Membrane; Nucleotide-binding; Transport.  
SQ SEQUENCE 784 AA; 83960 MW; DA8C2D965720A5E7 CRC64;  
  
Query Match 53.9%; Score 48; DB 2; Length 784;  
Best Local Similarity 53.8%; Pred. No. 87;  
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
  
Qy 2 PDMLMGDRGALD 14  
Db 204 PDQMIAKSGRLD 216  
  
RESULT 11  
O59S70\_CANAL PRELIMINARY; PRT; 793 AA.  
ID O59S70;  
AC O59S70;  
DT 10-MAY-2005 (TRENBLrel. 30, Created)  
DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)  
DE Hypothetical protein.  
GN ORFNames=CaO19.3470;  
OS *Candida albicans* SC5314.  
OC Bacteria; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccaromycetales; Candida.  
OX NCBI\_TaxId=237561;

RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=SC5314;  
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;  
RA Jones T., Federpelt N.A., Chihana H., Dungan J., Kalman S.,  
RA Magee B.B., Newport G., Thorsen Y.R., Agabian N., Magee P.T.,  
RA Davis R.W., Scherer S.;  
RT "The diploid genome sequence of *Candida albicans*."  
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334 (2004).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=SC5314;  
RA Dungan J., Kuo A., Newport G., Lan C.-Y., Itijima C., Adegoja O.,  
RA Roberts J., Persson K., Donnelly S., Favoreto S., Tzung K.-W.,  
RA Jones T., Scherer S., Agabian N.;  
RT "Annotation of the genome of *Candida albicans*."  
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.  
CC -! CAUTION: The sequence shown here is derived from an  
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
preliminary data.  
CC EMBL; AAC001000155; EAK93328.1; -; Genomic\_DNA.  
DR KW Hypothetical protein.  
SQ SEQUENCE 793 AA; 90808 MW; 870A0A0508ADF827 CRC64;  
  
Query Match 53.9%; Score 48; DB 2; Length 793;  
Best Local Similarity 54.5%; Pred. No. 88;  
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 2 PDMLMGDRGA 12  
Db 735 PEMAVWGSQGA 745  
  
RESULT 12  
O8ZR90\_SALTY PRELIMINARY; PRT; 804 AA.  
ID O8ZR90;  
AC O8ZR90;  
DT 01-MAR-2002 (TRENBLrel. 20, Created)  
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)  
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
DE Putative inner membrane protein.  
GN Name=ybbp; OrderedlocusNames=STM0508;  
OS *Salmonella typhimurium*.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; *Salmonella*.  
OX NCBI\_TaxId=602;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=LIT;  
RX MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;  
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,  
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,  
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,  
RA Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,  
RA Waterston R., Wilson R.K.;  
RT "Complete genome sequence of *Salmonella enterica* serovar Typhimurium  
LT2."  
RL Nature 413:852-856 (2001).  
DR EMBL; AB008719; AAL19462.1; -; Genomic\_DNA.  
DR GO; GO:0016020; C:membrane; IEA.  
DR InterPro; IPR003838; DUF214.  
DR Pfam; PF02687; Flex; 2.  
KW Complete proteome.  
SQ SEQUENCE 804 AA; 88772 MW; 72A29069A7021F11 CRC64;  
  
Query Match 53.9%; Score 48; DB 2; Length 804;  
Best Local Similarity 87.5%; Pred. No. 89;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 EPDMLMG 8  
Db 764 EPDMLMG 771

RESULT 13  
06ZD22\_ORYSA PRELIMINARY; PRT; 527 AA.  
ID Q6ZD22\_ORYSA PRELIMINARY; PRT; 527 AA.  
AC Q6ZD22;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Hypothetical protein P0507H12.22.  
GN Name=P0507H12.22;  
OS Oryza sativa (japonica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzeae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Sasaki T., Matsumoto T., Yamamoto K.,  
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, PAC  
clone: P0507H12."  
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF004338; BAC03511.1; -; Genomic\_DNA.  
DR Gramene; Q6ZD22; -  
DR GO; GO:0004519; F:endonuclease activity; IEA.  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
DR GO; GO:0006281; P:DNA repair; IEA.  
DR InterPro; IPR004843; M-pesterase.  
DR Pfam; PF00149; Metallophos; 1.  
DR Hypothetical protein.  
SQ SEQUENCE 527 AA; 61478 MW; 265E5E1451BC92EE6 CRC64;

Query Match 53.4%; Score 47.5; DB 2; Length 527;  
Best Local Similarity 50.0%; Pred. No. 70;  
Matches 9; Conservative 3; Mismatches 3; Indels 3; Gaps 1;  
QY 1 EPPWLL--WGDGALDV 15  
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DB 86 EPPWLLDWYMGDKGTGV 103

RESULT 14  
06JH28\_HUMAN PRELIMINARY; PRT; 61 AA.  
ID Q6JH28\_HUMAN PRELIMINARY; PRT; 61 AA.  
AC Q6JH28;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE HCV-E2 binding protein 1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Zhang J., Cheng J., Wang L., Shao Q., Lu Y., Chen T., Hong Y.,  
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY459290; AAR23235.1; -; mRNA.  
SQ SEQUENCE 61 AA; 6607 MW; 4E162AA344E7A56 CRC64;

Query Match 52.8%; Score 47; DB 2; Length 61;  
Best Local Similarity 87.5%; Pred. No. 9.3;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 WLLMGDRG 11  
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DB 46 WLLMGSRG 53

RESULT 15  
07UG34\_RHOBA PRELIMINARY; PRT; 364 AA.  
ID 07UG34\_RHOBA PRELIMINARY; PRT; 364 AA.  
AC 07UG34;

DT 01-OCT-2003 (TREMBlrel. 25, Created)  
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Hypothetical protein.  
GN OrderedLocustNames=RB8157;  
OS Rhodospirillum rubrum.  
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;  
OC Planctomycetaceae; Pirellula.  
OX NCBI\_TaxID=117;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA STRAIN=1;  
RC MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;  
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,  
RA Ludwig W., Gade D., Beck A., Borzym K., Heilmann K., Rabus R.,  
RA Schlesner H., Amann R., Reinhardt R.,  
RT "Complete genome sequence of the marine planctomycete Pirellula sp.  
strain 1."  
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).  
DR EMBL; BX294147; CAD78495.1; -; Genomic DNA.  
DR Complete proteome; Hypothetical protein.  
SQ SEQUENCE 364 AA; 40878 MW; 2284324F0722E6AB CRC64;

Query Match 52.8%; Score 47; DB 2; Length 364;  
Best Local Similarity 58.3%; Pred. No. 57;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 3 DWLLMGDRGALD 14  
|||||:|  
DB 162 DWLLMGDRGALD 173

Search completed: December 4, 2005, 04:52:25  
Job time : 139.875 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model1

Run on: December 4, 2005, 03:59:51 ; Search time 32.1875 Seconds  
(without alignments)  
38.528 Million cell updates/sec

Title: US-10-632-706-197

Perfect score: 89

Sequence: 1 EPDWLWGDRCALDV 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: Issued Patents AA:\*

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3: /cgn2\_6/ptodata/1/1aa/6 COMB.pep:\*

4: /cgn2\_6/ptodata/1/1aa/H\_COMB.pep:\*

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27: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	53.9	229	2	US-09-489-039A-12532
2	45	50.6	614	2	US-09-543-681A-7066
3	44	49.4	80	2	US-09-248-796A-22630
4	43	48.3	345	2	US-09-303-518D-194
5	43	48.3	383	2	US-09-303-518D-194
6	43	48.3	638	2	US-09-949-016-9984
7	43	48.3	732	2	US-09-902-540-13627
8	42.5	47.8	320	2	US-09-252-991A-18301
9	42	47.2	174	2	US-09-854-133-426
10	42	47.2	388	1	US-08-290-448A-80
11	42	47.2	388	1	US-08-290-448A-80
12	42	47.2	388	1	US-08-175-069A-80
13	42	47.2	388	1	US-08-461-939B-80
14	42	47.2	388	2	US-08-464-000-80
15	42	47.2	493	2	US-09-489-039A-12903
16	41	46.1	588	4	PCT-US95-13749-4
17	41	46.1	611	2	US-09-543-681A-7786
18	41	46.1	884	2	US-09-248-796A-20574
19	40.5	45.5	488	2	US-08-311-731A-29
20	40	44.9	392	2	US-09-252-991A-27798
21	40	44.9	497	2	US-09-489-039A-12027
22	40	44.9	576	2	US-09-367-206-1
23	40	44.9	576	2	US-09-367-206-21
24	40	44.9	576	2	US-09-367-206-22
25	40	44.9	576	2	US-09-367-206-23
26	40	44.9	576	2	US-09-298-404-1
27	40	44.9	576	2	US-09-298-404-21

28	40	44.9	576	2	US-09-298-404-22	Sequence 22, Appl
29	40	44.9	576	2	US-09-298-404-23	Sequence 23, Appl
30	40	44.9	776	2	US-09-155-396-3	Sequence 3, Appl
31	39	43.8	113	1	US-08-321-625-44	Sequence 44, Appl
32	39	43.8	13	2	US-09-181-083-44	Sequence 44, Appl
33	39	43.8	13	2	US-09-750-754-44	Sequence 272, Appl
34	39	43.8	93	2	US-09-072-596-772	Sequence 272, Appl
35	39	43.8	93	2	US-09-072-596-772	Sequence 272, Appl
36	39	43.8	93	2	US-10-193-002-272	Sequence 272, Appl
37	39	43.8	93	2	US-10-084-843-277	Sequence 277, Appl
38	39	43.8	141	2	US-09-902-540-14417	Sequence 14417, A
39	39	43.8	170	2	US-09-270-767-45277	Sequence 45277, A
40	39	43.8	194	2	US-09-489-039A-7558	Sequence 7558, Ap
41	39	43.8	226	2	US-09-004-731-8	Sequence 8, Appl
42	39	43.8	226	2	US-08-749-699-8	Sequence 8, Appl
43	39	43.8	226	2	US-09-004-729-8	Sequence 8, Appl
44	39	43.8	258	2	US-09-134-000C-5594	Sequence 5594, Ap
45	39	43.8	286	2	US-09-248-796A-23020	Sequence 23020, A

#### ALIGNMENTS

```
RESULT 1
US-09-489-039A-12532
Sequence 12532, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 12532
LENGTH: 229
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12532

Query Match      53.9%; Score 48; DB 2; Length 229;
Best Local Similarity 57.1%; Pred. NO. 7.8;
Matches      8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy      1 EPDWLWGDRCALDV 14
Db      32 ERSCKWGDRAFD 45

RESULT 2
US-09-543-681A-7066
Sequence 7066, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 7066
LENGTH: 614
TYPE: PRT
ORGANISM: Proteus mirabilis
US-09-543-681A-7066

Query Match      50.6%; Score 45; DB 2; Length 614;
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Best Local Similarity 64.3%; Pred. No. 66;  
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
OY 1 EPDWLMGDRGALD 14  
DB 452 EDGWLRTGDAGALD 465

RESULT 3  
US-09-248-796A-22630  
; Sequence 22630, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; PRIOR FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 22630  
; LENGTH: 80  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-09-248-796A-22630

Query Match  
Best Local Similarity 49.4%; Score 44; DB 2; Length 80;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 PDWMLMGDRGA 12  
DB 12 PDWAVMGSGWA 22

RESULT 4  
US-09-303-518D-194  
; Sequence 194, Application US/09303518D  
; Patent No. 6914131  
; GENERAL INFORMATION:  
; APPLICANT: Scariato, Vincenzo  
; APPLICANT: Maignani, Vega  
; APPLICANT: Rappuoli, Rino  
; APPLICANT: Pizza, Mariagrazia  
; APPLICANT: Grandi, Guido  
; TITLE OF INVENTION: Neisserial Antigens  
; FILE REFERENCE: CHIR0160  
; CURRENT APPLICATION NUMBER: US/09/303,518D  
; CURRENT FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 1098  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 194  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-09-303-518D-194

Query Match  
Best Local Similarity 48.3%; Score 43; DB 2; Length 345;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 PDWMLMGDRG 11  
DB 183 PEMLLFGYRG 192

RESULT 5  
US-09-303-518D-196  
; Sequence 196, Application US/09303518D

; Patent No. 6914131  
; GENERAL INFORMATION:  
; APPLICANT: Scariato, Vincenzo  
; APPLICANT: Maignani, Vega  
; APPLICANT: Rappuoli, Rino  
; APPLICANT: Pizza, Mariagrazia  
; APPLICANT: Grandi, Guido  
; TITLE OF INVENTION: Neisserial Antigens  
; FILE REFERENCE: CHIR0160  
; CURRENT APPLICATION NUMBER: US/09/303,518D  
; CURRENT FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 1098  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 196  
; LENGTH: 383  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-303-518D-196

Query Match  
Best Local Similarity 48.3%; Score 43; DB 2; Length 383;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 PDWMLMGDRG 11  
DB 181 PEMLLFGYRG 190

RESULT 6  
US-09-949-016-9984  
; Sequence 9984, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9984  
; LENGTH: 638  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-9984

Query Match  
Best Local Similarity 48.3%; Score 43; DB 2; Length 638;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 EPDWMLW 7  
DB 558 EPDWMLW 564

RESULT 7  
US-09-902-540-13627  
; Sequence 13627, Application US/09902540  
; Patent No. 6833467  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540  
CURRENT FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: 60/217,883  
PRIOR FILING DATE: 2000-07-10  
NUMBER OF SEQ ID NOS: 16825  
SEQ ID NO 13627  
LENGTH: 732  
TYPE: PRT  
ORGANISM: Myxococcus xanthus  
US-09-902-540-13627

Query Match 48.3%; Score 43; DB 2; Length 732;  
Best Local Similarity 63.6%; Pred. No. 1.6e+02;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 4 WLMGDRALD 14  
Db 126 WLMGDRRAAE 136

RESULT 8  
US-09-252-991A-18301  
Sequence 18301, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 18301  
LENGTH: 320  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-18301

Query Match 47.8%; Score 42.5; DB 2; Length 320;  
Best Local Similarity 66.7%; Pred. No. 79;  
Matches 10; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Qy 2 PDWLMGDRG-ALDV 15  
Db 254 PTLWMGDRDRLDV 268

RESULT 9  
US-09-854-133-426  
Sequence 426, Application US/09854133  
Patent No. 6759508  
GENERAL INFORMATION:  
APPLICANT: Lodes, Michael J.  
APPLICANT: Mohamath, Radoch  
APPLICANT: Henderson, Robert A.  
APPLICANT: Benson, Darin R.  
APPLICANT: Secrist, Heather  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR  
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.475C10  
CURRENT APPLICATION NUMBER: US/09/854,133  
CURRENT FILING DATE: 2001-05-11  
NUMBER OF SEQ ID NOS: 735  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 426  
LENGTH: 174  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-854-133-426

Query Match 47.2%; Score 42; DB 2; Length 174;  
Best Local Similarity 70.0%; Pred. No. 49;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EPDWLMGDR 10  
Db 124 DPGLWLMGDR 133

RESULT 10  
US-08-290-448A-80  
Sequence 80, Application US/08290448A  
Patent No. 5676954  
GENERAL INFORMATION:  
APPLICANT: Rogers, Bruce  
APPLICANT: Klapper, David G.  
APPLICANT: Ratnar, Thorunn  
APPLICANT: Kuo, Mei-chang  
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses  
NUMBER OF SEQUENCES: 93  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/290,448A  
FILING DATE: August 15, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/529,951  
FILING DATE: May 29, 1990  
APPLICATION NUMBER: US 07/325,365  
FILING DATE: March 17, 1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Amy E. Mandragouras  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: INT-018CN  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 80:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 388 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-290-448A-80

Query Match 47.2%; Score 42; DB 1; Length 388;  
Best Local Similarity 46.7%; Pred. No. 1.2e+02;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 EPDWLMGDRALDV 15  
Db 323 EPDMTWMRTQNDV 337

RESULT 11  
US-08-290-448A-80  
Sequence 80, Application US/08290448A  
Patent No. 5698204  
GENERAL INFORMATION:  
APPLICANT: Rogers, Bruce  
APPLICANT: Klapper, David G.  
APPLICANT: Ratnar, Thorunn

APPLICANT: Kuo, Mei-chang  
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses  
NUMBER OF SEQUENCES: 93  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/290,448A  
FILING DATE: August 15, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/529,951  
FILING DATE: May 29, 1990  
APPLICATION NUMBER: US 07/325,365  
FILING DATE: March 17, 1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Amy E. Mandragouras  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: IMI-018CN  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 80:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 388 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-290-448A-80

Query Match 47.2%; Score 42; DB 1; Length 388;  
Best Local Similarity 46.7%; Pred. No. 1.2e+02;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 EPPWLMGDRGALDV 15  
||:|:|:|:|:|:|  
Db 323 EPEWMTWNRQNDV 337

RESULT 12  
US-08-175-069A-80  
Sequence 80, Application US/08175069A  
Patent No. 5776761  
GENERAL INFORMATION:  
APPLICANT: Rogers, Bruce  
APPLICANT: Klapper, David G.  
APPLICANT: Ratner, Thorum  
APPLICANT: Kuo, Mei-chang  
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses  
NUMBER OF SEQUENCES: 93  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/175,069A  
FILING DATE: December 29, 1993

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/529,951  
FILING DATE: May 29, 1990  
APPLICATION NUMBER: US 07/325,365  
FILING DATE: March 17, 1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Amy E. Mandragouras  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: IMI-018DV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 80:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 388 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-175-069A-80

Query Match 47.2%; Score 42; DB 1; Length 388;  
Best Local Similarity 46.7%; Pred. No. 1.2e+02;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 EPPWLMGDRGALDV 15  
||:|:|:|:|:|:|  
Db 323 EPEWMTWNRQNDV 337

RESULT 13  
US-08-461-939B-80  
Sequence 80, Application US/08461939B  
Patent No. 6335019  
GENERAL INFORMATION:  
APPLICANT: Rogers, Bruce  
APPLICANT: Klapper, David G.  
APPLICANT: Ratner, Thorum  
APPLICANT: Kuo, Mei-chang  
TITLE OF INVENTION: Methods For Treating Sensitivity To A  
NUMBER OF SEQUENCES: 93  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,939B  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/464,000  
FILING DATE: 05-JUN-1995  
APPLICATION NUMBER: US 08/290,448  
FILING DATE: 15-AUG-1994  
APPLICATION NUMBER: US 07/529,951  
FILING DATE: 29-MAY-1990  
APPLICATION NUMBER: US 07/325,365  
FILING DATE: 17-MAR-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Amy E. Mandragouras  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: IMI-018CNDV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 80:



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; SEQUENCE CHARACTERISTICS:
; LENGTH: 388 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-461-939B-80

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Query Match	47.2%	Score 42;	DB 2;	Length 388;
Best Local Similarity	46.7%	Pred. No. 1B2e+02;		
Matches	7;	Conservative	2;	Mismatches 6; Indels 0; Gaps 0;

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QY      1 EPDWLLWGDRCALDV 15
         ||::||
Db     323 EPEWMTWNRQTQNDV 337
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RESULT 14  
US-08-464-000-80

1 GENERAL INFORMATION:  
2 APPLICANT: Rogers, Bruce  
3 APPLICANT: Klapper, David G.  
4 APPLICANT: Rafnar, Thorunn  
5 APPLICANT: Kuo, Mei-chang  
6 TITLE OF INVENTION: Allergenic Peptides from Ragweed Pollen  
7 NUMBER OF SEQUENCES: 93  
8 CORRESPONDENCE ADDRESS:

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1  COMPUTER READABLE FORM:
2  MEDIUM TYPE: Floppy disk
3  COMPUTER: IBM PC compatible
4  OPERATING SYSTEM: PC-DOS/MS-DOS
5  SOFTWARE: PatentIn Release #1.0, Version #1.25
6  CURRENT APPLICATION DATA:

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ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 36,207

TELECOMMUNICATION INFORMATION:

TELEFAX: (617) 227-5941

SEQUENCE CHARACTERISTICS:

TYPE: amino acid

MOLECULE TYPE: protein

Query Match Similarity	47.2%;	Score 42;	DB 2;	Length 388;
Best Local Similarity	46.7%;	Pred. NO. 1.2e+02;		
Matches 7; Conservative	2;	Mismatches 6;	Indels 0;	Gaps 0

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QY      1 EPDWLWGDRLD 15
          ||::||
Db      323 EPEWMTWNRQTNDV 337
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RESULT 15  
US-09-489-039A-12903

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1  APPLICANT: Gary Breton et. al
2  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KREBSIELLA
3  TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
4  FILE REFERENCE: 2709,2004001
5  CURRENT APPLICATION NUMBER: US/09/489,039A
6  CURRENT FILING DATE: 2000-01-27
7  PRIOR APPLICATION NUMBER: US 60/117,747
8  PRIOR FILING DATE: 1999-01-29
9  NUMBER OF SEQ ID NOS: 14342
10 SEQ ID NO 12903
11 LENGTH: 493

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Query Match	47.2%	Score 42;	DB 2;	Length 493;
Best Local Similarity	60.0%	Pred. No. 1.5e+02;		
Matches	6;	Conservative	2;	Mismatches 0;
				Gaps 0;

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QY      4 WILMGDRGAL 13
         ||||:|:
Db      463 WILWCERGVM 472
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Search completed: December 4, 2005, 04:09:44
Job time : 33.1875 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 4, 2005, 04:07:28 ; Search time 107.5 Seconds  
(without alignments)  
58.302 Million cell updates/sec

Title: US-10-632-706-197

Perfect score: 89

Sequence: 1 EPDWLWMDRGALDV 15

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	89	100.0	15	US-10-632-706-129	Sequence 129, App
2	89	100.0	15	US-10-632-706-130	Sequence 130, App
3	89	100.0	15	US-10-632-706-131	Sequence 131, App
4	89	100.0	15	US-10-632-706-194	Sequence 194, App
5	89	100.0	15	US-10-632-706-197	Sequence 197, App
6	89	100.0	15	US-10-632-706-200	Sequence 200, App
7	75	84.3	15	US-10-632-706-203	Sequence 203, App
8	51	57.3	334	US-10-450-763-50690	Sequence 50690, A
9	48	53.9	775	US-10-634-548-27	Sequence 27, App
10	48	53.9	775	US-10-159-2574-160	Sequence 160, App
11	47.5	53.4	992	US-10-437-963-134365	Sequence 134365, A
12	47	52.8	435	US-10-450-763-52883	Sequence 52883, A
13	47	52.8	904	US-10-369-493-12420	Sequence 12420, A
14	45	50.6	159	US-10-425-115-240160	Sequence 240160, A
15	45	50.6	372	US-10-283-122A-68332	Sequence 68332, A
16	44.5	50.0	203	US-10-767-701-42189	Sequence 42189, A
17	44.5	50.0	394	US-10-425-115-23354	Sequence 23354, A
18	44	49.4	472	US-10-017-161-1674	Sequence 1674, App
19	44	49.4	472	US-10-292-798-1334	Sequence 1334, App
20	44	49.4	505	US-10-437-963-179634	Sequence 179634, App
21	44	49.4	687	US-10-369-493-20876	Sequence 20876, A
22	43.5	48.9	77	US-10-425-115-263892	Sequence 263892, A
23	43	48.3	264	US-10-156-761-11420	Sequence 11420, A
24	43	48.3	368	US-10-437-963-115853	Sequence 115853, A
25	43	48.3	439	US-10-156-761-13497	Sequence 13497, A
26	43	48.3	616	US-10-808-522-8	Sequence 8, App1
27	43	48.3	1975	US-10-437-963-140079	Sequence 140079, A

28	42.5	47.8	315	4	US-10-282-122A-43588	Sequence 43588, A
29	42	47.2	77	3	US-09-764-847-922	Sequence 922, App
30	42	47.2	77	4	US-10-092-154-922	Sequence 922, App
31	42	47.2	116	4	US-10-424-599-206981	Sequence 206981, App
32	42	47.2	131	3	US-09-864-408A-4566	Sequence 4566, App
33	42	47.2	154	4	US-10-312-354-76	Sequence 354, App
34	42	47.2	174	3	US-09-738-973-426	Sequence 426, App
35	42	47.2	174	3	US-09-854-133-426	Sequence 426, App
36	42	47.2	174	4	US-10-144-649A-426	Sequence 426, App
37	42	47.2	175	5	US-10-450-763-31629	Sequence 31629, A
38	42	47.2	198	4	US-10-767-701-34131	Sequence 34131, A
39	42	47.2	211	5	US-10-450-763-37978	Sequence 37978, A
40	42	47.2	245	4	US-10-437-963-108592	Sequence 108592, A
41	42	47.2	275	4	US-10-425-114-66625	Sequence 66625, A
42	42	47.2	363	4	US-10-282-122A-50322	Sequence 50322, A
43	42	47.2	380	4	US-10-369-493-20944	Sequence 20944, A
44	42	47.2	397	3	US-09-847-208-17	Sequence 17, App1
45	42	47.2	397	5	US-10-809-689-97	Sequence 97, App1

#### ALIGNMENTS

```
RESULT 1
US-10-632-706-129
; Sequence 129, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT FILING DATE: 2003-08-01
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 129
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-129
Query Match 100.0%; Score 89; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 EPDWLWMDRGALDV 15
Db 1 EPDWLWMDRGALDV 15
RESULT 2
US-10-632-706-130
; Sequence 130, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT FILING DATE: 2003-08-01
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
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; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 130
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-130

Query Match      100.0%; Score 89; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EPDWLWMDRGALDV 15
Db      1 EPDWLWMDRGALDV 15

RESULT 3
US-10-632-706-131
; Sequence 131, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 131
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-131

Query Match      100.0%; Score 89; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EPDWLWMDRGALDV 15
Db      1 EPDWLWMDRGALDV 15

RESULT 4
US-10-632-706-194
; Sequence 194, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
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; SEQ ID NO 194
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-194

Query Match      100.0%; Score 89; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EPDWLWMDRGALDV 15
Db      1 EPDWLWMDRGALDV 15

RESULT 5
US-10-632-706-197
; Sequence 197, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 197
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-197

Query Match      100.0%; Score 89; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EPDWLWMDRGALDV 15
Db      1 EPDWLWMDRGALDV 15

RESULT 6
US-10-632-706-200
; Sequence 200, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 200
; LENGTH: 15
; TYPE: PRT
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ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: single chain antibody fragment  
US-10-632-706-200

Query Match 100.0%; Score 89; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.8e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 EPPWLWMDRGALDV 15  
Db 1 EPPWLWMDRGALDV 15

RESULT 7  
US-10-632-706-203  
Sequence 203; Application US/10632706  
Publication No. US20040175385A1  
GENERAL INFORMATION:  
APPLICANT: MARKS, JAMES D.  
APPLICANT: AMERSOORER, PETER  
TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM  
FILE REFERENCE: 407T-895120US  
CURRENT APPLICATION NUMBER: US/10/632,706  
CURRENT FILING DATE: 2003-08-01  
PRIOR APPLICATION NUMBER: US 60/400,721  
PRIOR FILING DATE: 2002-08-01  
PRIOR APPLICATION NUMBER: US 09/144,806  
PRIOR FILING DATE: 1998-08-31  
NUMBER OF SEQ ID NOS: 278  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 203  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: single chain antibody fragment  
US-10-632-706-203

Query Match 84.3%; Score 75; DB 4; Length 15;  
Best Local Similarity 93.3%; Pred. No. 0.00033;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EPPWLWMDRGALDV 15  
Db 1 EPPWLWMDRGALDV 15

RESULT 8  
US-10-450-763-50690  
Sequence 50690; Application US/10450763  
Publication No. US20050196754A1  
GENERAL INFORMATION:  
APPLICANT: Hyseq, Inc  
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
FILE REFERENCE: 790CIT3/US  
CURRENT APPLICATION NUMBER: US/10/450,763  
CURRENT FILING DATE: 2003-06-11  
PRIOR APPLICATION NUMBER: PCT/US01/08631  
PRIOR FILING DATE: 2001-03-30  
PRIOR APPLICATION NUMBER: 09/540,217  
PRIOR FILING DATE: 2000-03-31  
PRIOR APPLICATION NUMBER: 09/649,167  
PRIOR FILING DATE: 2000-08-23  
NUMBER OF SEQ ID NOS: 60736  
SOFTWARE: Custom  
SEQ ID NO 50690  
LENGTH: 334  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: DOMAIN

LOCATION: (267)..(320)  
OTHER INFORMATION: Sodium:neurotransmitter symporter family proteins domain  
OTHER INFORMATION: identified by eMATRIX, accession number BL00610D, p-value=2.000e-  
OTHER INFORMATION: 25, raw score of 20.97  
FEATURE:  
NAME/KEY: DOMAIN  
LOCATION: (44)..(307)  
OTHER INFORMATION: Sodium:neurotransmitter symporter family domain identified by  
OTHER INFORMATION: Pfam, accession name SNF\_E-value=2e-76, Pfam score of 267.3  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(334)  
OTHER INFORMATION: Xaa = X or \* as defined in Table 2  
US-10-450-763-50690

Query Match 57.3%; Score 51; DB 5; Length 334;  
Best Local Similarity 53.3%; Pred. No. 21;  
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
1 EPPWLWMDRGALDV 15  
Db 263 KPDMSWGPSCWIDV 277

RESULT 9  
US-10-634-548-27  
Sequence 27; Application US/10634548  
Publication No. US20040045051A1  
GENERAL INFORMATION:  
APPLICANT: No. US20040045051A1, Susan R  
APPLICANT: Lincoln, Kim  
APPLICANT: Abad, Mark Scott  
APPLICANT: Ellers, Robert  
APPLICANT: Hartsuyker, Karen Kindle  
APPLICANT: Hirschberg, Joseph  
APPLICANT: Karunanandaa, Balasubramanian  
APPLICANT: Moshiri, Farhad  
APPLICANT: Stein, Joshua C.  
APPLICANT: Valentin, Henry B.  
APPLICANT: Venkatesh, Tyamagondlu V.  
TITLE OF INVENTION: Tocopherol biosynthesis related genes and used thereof  
FILE REFERENCE: Ren-01-125  
CURRENT APPLICATION NUMBER: US/10/634,548  
CURRENT FILING DATE: 2003-08-05  
PRIOR APPLICATION NUMBER: US 60/400,689  
PRIOR FILING DATE: 2002-08-05  
NUMBER OF SEQ ID NOS: 79  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 27  
LENGTH: 201  
TYPE: PRT  
ORGANISM: *Prochlorococcus marinus*-MT9313  
US-10-634-548-27

Query Match 53.9%; Score 48; DB 4; Length 201;  
Best Local Similarity 50.0%; Pred. No. 37;  
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
Qy 2 PDMWLWMDRGAL 13  
Db 123 PNMWLWMDGRKSI 134

RESULT 10  
US-10-159-257A-160  
Sequence 160; Application US/10159257A  
Publication No. US20040161828A1  
GENERAL INFORMATION:  
APPLICANT: SHEN, BEN  
APPLICANT: LIU, WEN  
APPLICANT: CHRISTENSON, STEVEN D.  
APPLICANT: STANDAGE, SCOTT  
TITLE OF INVENTION: GENE CLUSTER FOR PRODUCTION OF THE ENEDIYNE ANTITUMOR

;; TITLE OF INVENTION: ANTIBIOTIC C-1027  
;; FILE REFERENCE: 407T-896020US  
;; CURRENT APPLICATION NUMBER: US/10/159,257A  
;; CURRENT FILING DATE: 2002-05-31  
;; PRIOR APPLICATION NUMBER: 09/478,188  
;; PRIOR FILING DATE: 2000-01-05/115,434  
;; PRIOR APPLICATION NUMBER: 60/115,434  
;; PRIOR FILING DATE: 1999-01-06  
;; NUMBER OF SEQ ID NOS: 207  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO: 160  
;; LENGTH: 775  
;; TYPE: PRT  
;; ORGANISM: Streptomyces globisporus  
;; FEATURE:  
;; OTHER INFORMATION: orf(-1)  
US-10-159-257A-160

Query Match 53.9%; Score 48; DB 4; Length 775;  
Best Local Similarity 53.8%; Pred. No. 1.3e+02;  
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 PDMWLMGDRGALD 14  
DB 195 PDMQIMAKSGRLD 207

## RESULT 11

US-10-437-963-134365  
;; Sequence 134365, Application US/10437963  
;; Publication No. US20040123343A1  
;; GENERAL INFORMATION:  
;; APPLICANT: La Rosa, Thomas J.  
;; APPLICANT: Kovalic, David K.  
;; APPLICANT: Zhou, Yihua  
;; APPLICANT: Cao, Yongwei  
;; APPLICANT: Wu, Wei  
;; APPLICANT: Boukharov, Andrey A.  
;; APPLICANT: Barbazuk, Brad  
;; APPLICANT: Li, Ping  
;; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
;; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
;; FILE REFERENCE: 38-21(53221)B  
;; CURRENT APPLICATION NUMBER: US/10/437,963  
;; CURRENT FILING DATE: 2003-05-14  
;; NUMBER OF SEQ ID NOS: 204966  
;; SEQ ID NO: 134365  
;; LENGTH: 992  
;; TYPE: PRT  
;; ORGANISM: Oryza sativa  
;; FEATURE:  
;; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_36146C.1.pap  
US-10-437-963-134365

Query Match 53.4%; Score 47.5; DB 4; Length 992;  
Best Local Similarity 50.0%; Pred. No. 2e+02;  
Matches 9; Conservative 3; Mismatches 3; Indels 3; Gaps 1;

QY 1 EPDWL---MGDRGALDV 15  
DB 551 EPNWLDWYMGDKGTGTV 568

## RESULT 12

US-10-450-763-52883  
;; Sequence 52883, Application US/10450763  
;; Publication No. US20050196754A1  
;; GENERAL INFORMATION:  
;; APPLICANT: HySeq, Inc  
;; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
;; FILE REFERENCE: 790CIP3/US  
;; CURRENT APPLICATION NUMBER: US/10/450,763  
;; CURRENT FILING DATE: 2003-06-11

;; PRIOR APPLICATION NUMBER: PCT/US01/08631  
;; PRIOR FILING DATE: 2001-03-30  
;; PRIOR APPLICATION NUMBER: 09/540,217  
;; PRIOR FILING DATE: 2000-03-31  
;; PRIOR APPLICATION NUMBER: 09/649,167  
;; PRIOR FILING DATE: 2000-08-23  
;; NUMBER OF SEQ ID NOS: 60736  
;; SOFTWARE: Custom  
;; SEQ ID NO: 52883  
;; LENGTH: 455  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: misc\_feature  
;; LOCATION: (1)...(455)  
;; OTHER INFORMATION: Xaa = X or \* as defined in Table 2  
US-10-450-763-52883

Query Match 52.8%; Score 47; DB 5; Length 455;  
Best Local Similarity 53.8%; Pred. No. 1.1e+02;  
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EPDWLWMDRGAL 13  
DB 93 EQNWLMCRGVM 105

## RESULT 13

US-10-369-493-12420  
;; Sequence 12420, Application US/10369493  
;; Publication No. US20030233675A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Cao, Yongwei  
;; APPLICANT: Hinkle, Gregory J.  
;; APPLICANT: Slater, Steven C.  
;; APPLICANT: Goldman, Barry S.  
;; APPLICANT: Chen, Xianfeng  
;; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
;; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
;; FILE REFERENCE: 38-10(52052)B  
;; CURRENT APPLICATION NUMBER: US/10/369,493  
;; CURRENT FILING DATE: 2003-02-28  
;; PRIOR APPLICATION NUMBER: US 60/360,039  
;; PRIOR FILING DATE: 2002-02-21  
;; NUMBER OF SEQ ID NOS: 47374  
;; SEQ ID NO: 12420  
;; LENGTH: 904  
;; TYPE: PRT  
;; ORGANISM: Aspergillus nidulans  
US-10-369-493-12420

Query Match 52.8%; Score 47; DB 4; Length 904;  
Best Local Similarity 70.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 WLWMDRGAL 13  
DB 460 WLWMDKSTSL 469

## RESULT 14

US-10-425-115-240160  
;; Sequence 240160, Application US/10425115  
;; Publication No. US20040214272A1  
;; GENERAL INFORMATION:  
;; APPLICANT: La Rosa, Thomas J.  
;; APPLICANT: Kovalic, David K.  
;; APPLICANT: Zhou, Yihua  
;; APPLICANT: Cao, Yongwei  
;; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
;; TITLE OF INVENTION: Plants  
;; FILE REFERENCE: 38-21(53222)B  
;; CURRENT APPLICATION NUMBER: US/10/425,115

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; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 240160
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(159)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: clone ID: MRT4577_150607C.1.pep
; US-10-425-115-240160
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Query Match          50.6%; Score 45; DB 4; Length 159;
Best Local Similarity 75.0%; Pred. No. 83;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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OY      2 PDWLLMGDRGAL 13
          |||||
Db      35 PGRLLMGRRGAL 46
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## RESULT 15

US-10-282-122A-68332

; Sequence 68332, Application US/10282122A

; Publication No. US20040029129A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu

; APPLICANT: Zamudio, Carlos

; APPLICANT: Malone, Cheryl

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Kari

; APPLICANT: Zyskind, Judith

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John

; APPLICANT: Carr, Grant

; APPLICANT: Yamamoto, Robert

; APPLICANT: Forsyth, R.

; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: EUTRA.034A

; CURRENT APPLICATION NUMBER: US/10/282,122A

; PRIOR FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/230,335

; PRIOR FILING DATE: 2000-09-06

; PRIOR APPLICATION NUMBER: 60/230,347

; PRIOR FILING DATE: 2000-09-09

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/267,636

; PRIOR FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; Remaining Prior Application data removed - See file wrapper or PALM.

; NUMBER OF SEQ ID NOS: 78614

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 68332

; LENGTH: 372

; TYPE: PRT

; ORGANISM: Pseudomonas putida

US-10-282-122A-68332

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Query Match          50.6%; Score 45; DB 4; Length 372;
Best Local Similarity 70.0%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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OY      2 PDWLLMGDRG 11
          |||||
Db      221 PDWLLMTTPAG 230
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Job time : 121.5 secs
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## OM protein - protein search, using sw model

Run on: December 4, 2005, 04:08:08 ; Search time 4.375 Seconds  
(without alignments)  
16.417 Million cell updates/sec

Title: US-10-632-706-197  
Perfect score: 89  
Sequence: 1 EPDWLWMDRCALDV 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

## Database :

Published Applications AA New:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US06\_NEM\_PUB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEM\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEM\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US08\_NEM\_PUB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US11\_NEM\_PUB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US11\_NEM\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US06\_NEM\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	48.3	383	6	US-10-467-657-5602
2	41	46.1	251	7	US-11-054-515-1084
3	40.5	45.5	125	6	US-10-821-234-1277
4	38.5	43.3	1075	7	US-11-174-150-34
5	38.5	42.3	1114	7	US-11-174-150-35
6	38	42.7	248	7	US-11-054-515-1679
7	38	42.7	251	7	US-11-054-515-944
8	37	41.6	344	6	US-10-967-527A-24
9	36	40.4	225	6	US-10-821-234-1116
10	36	40.4	322	6	US-10-467-657-1006
11	36	40.4	428	6	US-10-793-626-484
12	36	40.4	1857	7	US-11-057-058-60
13	36	40.4	1857	7	US-11-057-058-61
14	35.5	33.9	158	6	US-10-510-386-128
15	35.5	33.9	247	6	US-10-793-626-1466
16	35.5	33.9	344	6	US-10-821-234-923
17	35.5	33.9	380	6	US-10-624-932-20
18	35	33.3	239	6	US-10-957-569-54
19	35	33.3	350	6	US-10-467-657-5524
20	35	33.3	401	6	US-10-510-386-68
21	35	33.3	530	6	US-10-980-388-62
22	35	33.3	551	6	US-10-793-626-1668
23	34.5	38.8	1613	7	US-11-108-528-84
24	34.5	38.8	1613	7	US-11-108-528-86
25	34	38.2	251	7	US-11-054-515-1079

26	34	38.2	251	7	US-11-054-515-1793	Sequence 1793, Ap
27	34	38.2	253	7	US-11-015-546A-2	Sequence 2, Appl
28	34	38.2	253	7	US-11-054-515-1069	Sequence 1069, Ap
29	34	38.2	269	7	US-11-015-546A-10	Sequence 10, Appl
30	34	38.2	274	7	US-11-015-546A-12	Sequence 12, Appl
31	34	38.2	486	6	US-10-821-234-1063	Sequence 1063, Ap
32	34	38.2	613	6	US-10-131-826A-190	Sequence 190, App
33	34	38.2	616	6	US-10-131-826A-206	Sequence 206, App
34	34	38.2	820	7	US-11-147-047-31	Sequence 31, Appl
35	34	38.2	2725	7	US-11-113-424-82	Sequence 52, Appl
36	33.5	37.6	137	6	US-10-821-234-882	Sequence 882, App
37	33.5	37.6	249	7	US-11-054-515-649	Sequence 649, App
38	33	37.1	91	6	US-10-467-657-1052	Sequence 1052, Ap
39	33	37.1	177	6	US-10-980-388-95	Sequence 95, Appl
40	33	37.1	247	7	US-11-054-515-1307	Sequence 1307, Ap
41	33	37.1	248	7	US-11-054-515-877	Sequence 877, App
42	33	37.1	248	7	US-11-054-515-953	Sequence 953, App
43	33	37.1	248	7	US-11-054-515-965	Sequence 965, App
44	33	37.1	248	7	US-11-054-515-980	Sequence 980, App
45	33	37.1	248	7	US-11-054-515-984	Sequence 984, App

## ALIGNMENTS

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RESULT 1
US-10-467-657-5602
; Sequence 5602, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASTIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5602
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5602

Query Match      48.3%  Score 43;  DB 6;  Length 383;
Best Local Similarity 70.0%  Pred. No. 3.8;
Matches          7;  Conservative 2;  Mismatches 1;  Indels 0;  Gaps 0;

Cy      2 PDWLWMDRG 11
Db      181 PFWLFGYRG 190

RESULT 2
US-11-054-515-1084
; Sequence 1084, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
```



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; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23p3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1679
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1679

Query Match          42.7%; Score 38; DB 7; Length 248;
Best Local Similarity 42.9%; Pred. No. 15;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Cy      1  EPDWLWGDRCALD 14
      |||:|:|:|:|
Db      44  EPEWGWINGSGD 57

RESULT 7
US-11-054-515-944
; Sequence 944, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23p3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
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; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 944
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-944

Query Match          42.7%; Score 38; DB 7; Length 251;
Best Local Similarity 42.9%; Pred. No. 15;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Cy      1  EPDWLWGDRCALD 14
      |||:|:|:|:|
Db      44  EPEWGWINGSGD 57

RESULT 8
US-10-967-527A-24
; Sequence 24, Application US/10967527A
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Holloway, James L.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Ztnf14, A Tumor Necrosis Factor
; TITLE OF INVENTION: Receptor
; FILE REFERENCE: 03-17
; CURRENT APPLICATION NUMBER: US/10/967,527A
; CURRENT FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 344
; TYPE: PRT
; ORGANISM: mus musculus
US-10-967-527A-24

Query Match          41.6%; Score 37; DB 6; Length 344;
Best Local Similarity 83.3%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy      2  PDWLLW 7
      |||||
Db      3  PSWLLW 8

RESULT 9
US-10-821-234-1116
; Sequence 1116, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Steache-Crain, Birgit
; APPLICANT: Andarmant, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc seq_genes Version 1.0
; SEQ ID NO 1116
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1116

Query Match          40.4%; Score 36; DB 6; Length 225;
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Best Local Similarity 62.5%; Pred. No. 27;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 WLMGDRG 11  
|:|:|:|  
Db 74 WVRWGRG 81

## RESULT 10

US-10-467-657-1006  
; Sequence 1006, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SPA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 1006  
; LENGTH: 322  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-1006

Query Match 40.4%; Score 36; DB 6; Length 322;  
Best Local Similarity 63.6%; Pred. No. 38;  
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 PDMWLMGDRGA 12  
|:|:|:|  
Db 251 PDMWLMGDRGA 261

## RESULT 11

US-10-793-626-484  
; Sequence 484, Application US/10793626  
; Publication No. US20050255478A1  
; GENERAL INFORMATION:  
; APPLICANT: KIMBERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PU3480US  
; CURRENT APPLICATION NUMBER: US/10/793,626  
; CURRENT FILING DATE: 2004-03-04  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 484  
; LENGTH: 428  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: amino acid sequence  
US-10-793-626-484

Query Match 40.4%; Score 36; DB 6; Length 428;  
Best Local Similarity 62.5%; Pred. No. 50;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 7 WGDGALD 14  
|:|:|:|  
Db 333 WGDGALD 340

RESULT 12  
US-11-057-058-60  
; Sequence 60, Application US/11057058  
; Publication No. US20050244400A1  
; GENERAL INFORMATION:  
; APPLICANT: Lebowitz, Jonathan  
; APPLICANT: Maza, John  
; TITLE OF INVENTION: ACID ALPHA-GLUCOSIDASE AND FRAGMENTS THEREOF  
; FILE REFERENCE: SYM-011  
; CURRENT APPLICATION NUMBER: US/11/057,058  
; CURRENT FILING DATE: 2005-02-10  
; PRIOR APPLICATION NUMBER: US 60/543,812  
; PRIOR FILING DATE: 2004-02-10  
; NUMBER OF SEQ ID NOS: 68  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 60  
; LENGTH: 1857  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-057-058-60

Query Match 40.4%; Score 36; DB 7; Length 1857;  
Best Local Similarity 45.5%; Pred. No. 2.1e+02;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 4 WLMGDRGALD 14  
|:|:|:|  
Db 1749 WLMGDRGALD 1759

## RESULT 13

US-11-057-058-61  
; Sequence 61, Application US/11057058  
; Publication No. US20050244400A1  
; GENERAL INFORMATION:  
; APPLICANT: Lebowitz, Jonathan  
; APPLICANT: Maza, John  
; TITLE OF INVENTION: ACID ALPHA-GLUCOSIDASE AND FRAGMENTS THEREOF  
; FILE REFERENCE: SYM-011  
; CURRENT APPLICATION NUMBER: US/11/057,058  
; CURRENT FILING DATE: 2005-02-10  
; PRIOR APPLICATION NUMBER: US 60/543,812  
; PRIOR FILING DATE: 2004-02-10  
; NUMBER OF SEQ ID NOS: 68  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 61  
; LENGTH: 1857  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-057-058-61

Query Match 40.4%; Score 36; DB 7; Length 1857;  
Best Local Similarity 45.5%; Pred. No. 2.1e+02;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 4 WLMGDRGALD 14  
|:|:|:|  
Db 1749 WLMGDRGALD 1759

## RESULT 14

US-10-510-386-128  
; Sequence 128, Application US/10510386  
; Publication No. US20050244922A1  
; GENERAL INFORMATION:  
; APPLICANT: Andersen, Jens Tonne  
; APPLICANT: Clausen, Ib Groth  
; APPLICANT: Jorgensen, Steen Troels  
; APPLICANT: Olesen, Peter Bjarke  
; APPLICANT: Rasmussen, Michael Dolberg  
; TITLE OF INVENTION: Improved Bacillus Host Cell  
; FILE REFERENCE: 10294.204-US  
; CURRENT APPLICATION NUMBER: US/10/510,386

; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 248  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 128  
; LENGTH: 158  
; TYPE: PRT  
; ORGANISM: Bacillus licheniformis  
US-10-510-386-128

Query Match 39.9%; Score 35.5; DB 6; Length 158;  
Best Local Similarity 72.7%; Pred. No. 23;  
Matches 8; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

OY 5 LWM-GDRGALD 14  
| | | | |  
Db 65 LWMGDRGKLD 75

RESULT 15  
US-10-793-626-1466  
; Sequence 1466, Application US/10793626  
; Publication No. US20050255478A1  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PUS480US  
; CURRENT APPLICATION NUMBER: US/10/793,626  
; CURRENT FILING DATE: 2004-03-04  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1466  
; LENGTH: 247  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: amino acid sequence  
US-10-793-626-1466

Query Match 39.9%; Score 35.5; DB 6; Length 247;  
Best Local Similarity 63.6%; Pred. No. 35;  
Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

OY 4 WLM-LMGDRGAL 13  
| | | | |  
Db 186 WMLMGVNGAL 196

Search completed: December 4, 2005, 04:37:50  
Job time : 5.375 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:31:36 ; Search time 100.375 Seconds

(without alignments)  
77.318 Million cell updates/sec

Title: US-10-632-706-198

Perfect score: 59

Sequence: 1 WGGGTTVTSS 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Uniprot 05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	119	2	Q9GYZ2_MOUSE
2	59	100.0	121	2	Q8CGS2_MOUSE
3	59	100.0	146	1	HY21_HUMAN
4	59	100.0	147	1	HY1C_HUMAN
5	59	100.0	147	2	Q925S3_MOUSE
6	59	100.0	159	2	Q96Q80_HUMAN
7	59	100.0	170	2	Q925S2_MOUSE
8	59	100.0	218	2	Q925S1_MOUSE
9	59	100.0	241	2	Q921A6_MOUSE
10	59	100.0	348	2	Q6PYX1_HUMAN
11	59	100.0	416	2	Q9NP66_HUMAN
12	59	100.0	472	2	Q6N089_HUMAN
13	59	100.0	573	2	Q8WU38_HUMAN
14	59	100.0	575	2	Q6P418_HUMAN
15	59	100.0	595	2	Q8WUX4_HUMAN
16	59	100.0	597	2	Q9BU10_HUMAN
17	59	100.0	597	2	Q9BOB8_HUMAN
18	59	100.0	597	2	Q6GMX5_HUMAN
19	59	100.0	606	2	Q6GMW2_HUMAN
20	59	100.0	625	2	Q96A46_HUMAN
21	59	98.3	465	2	Q6PUB2_MOUSE
22	59	98.3	468	2	Q66W99_MOUSE
23	59	98.3	468	2	Q605N9_MOUSE
24	59	98.3	471	2	Q66K04_MOUSE
25	59	98.3	472	2	Q6PUJ7_MOUSE
26	59	98.3	473	2	Q91Z05_MOUSE
27	59	98.3	476	2	Q669X1_MOUSE
28	59	98.3	477	2	Q68E56_MOUSE
29	59	98.3	486	2	Q91Z07_MOUSE
30	59	98.3	487	2	Q99K44_MOUSE
31	59	94.9	109	2	Q9JL75_MOUSE

32	56	94.9	111	1	HV35_MOUSE	P01804_mus_musculu
33	56	94.9	114	2	Q9JL81_MOUSE	Q9JL81_mus_musculu
34	56	94.9	117	2	Q90KF0_MOUSE	Q90KF0_mus_musculu
35	56	94.9	118	1	HV39_MOUSE	P01809_mus_musculu
36	56	94.9	118	2	Q921C4_MOUSE	Q921C4_mus_musculu
37	56	94.9	120	1	HV03_MOUSE	P01747_mus_musculu
38	56	94.9	121	1	HV01_MOUSE	P01745_mus_musculu
39	56	94.9	134	2	Q65ZK6_MOUSE	Q65ZK6_mus_musculu
40	56	94.9	136	1	HV15_MOUSE	P01759_mus_musculu
41	56	94.9	137	1	HV11_MOUSE	P01755_mus_musculu
42	56	94.9	137	1	HV46_MOUSE	P01822_mus_musculu
43	56	94.9	137	2	Q924R6_MOUSE	Q924R6_mus_musculu
44	56	94.9	139	1	HV07_MOUSE	P01751_mus_musculu
45	56	94.9	140	2	Q924P8_MOUSE	Q924P8_mus_musculu

## ALIGNMENTS

```

RESULT 1
ID Q9GYZ2_MOUSE PRELIMINARY; PRT; 119 AA.
AC Q9GYZ2;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Monoclonal anti-idiotypic Schistosoma japonicum antibody NP30 heavy
DE chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Song X.T., Feng Z.Q., Guan X.H.
RT "Amplification, cloning and sequence analysis of the heavy chain
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT Schistosoma japonicum.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF282622; AAC01452.1; -, mRNA.
DR HSSP; P01751; 1A6W.
DR SMR; Q9GYZ2; 1-119.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003566; IG_v.
DR SMART; SM00406; IGv; 1_v.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13567 MW; BA893873FDSFA6AB CRC64;

Query Match 100.0%; Score 59; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTVTSS 11
Db 109 WGGGTTVTSS 119

RESULT 2
ID Q8CGS2_MOUSE PRELIMINARY; PRT; 121 AA.
AC Q8CGS2;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Anti-deoxyribovalenol scfv lambda heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.

```

OK NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN-BALB/c;  
 RA Wang Z., Munehi K., Osawa F., Pestka J.J., Hart L.P.;  
 RL Submitted (SEP-2002) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AY151140; AA075452.1; -, mRNA.  
 DR HSSP; P01751; INOB.  
 DR Ensemble; ENSMUSG0000021155; Mus musculus.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG-LIKE; 1.  
 FT NON\_TER 1 121  
 FT NON\_TER 121 121  
 SQ SEQUENCE 121 AA; 13475 MW; 84P6CFA8053F5D6 CRC64;

Query Match 100.0%; Score 59; DB 2; Length 121;  
 Best Local Similarity 100.0%; Pred. No. 0.0054;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WGGGTTTVSS 11  
 |||||  
 Db 111 WGGGTTTVSS 121

## RESULT 3

HV21\_HUMAN STANDARD; PRT; 146 AA.  
 AC P06331;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Ig heavy chain V-II region ARH-77 precursor.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
 OC Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=8520532; PubMed=3922855; DOI=10.1016/0378-1119(85)90092-7;  
 RA Kudo A., Ishihara T., Nishimura Y., Watanabe T.;  
 RT "A cloned human immunoglobulin heavy chain gene with a novel direct-  
 RT repeat sequence in 5' flanking region.";  
 RL Gene 33:181-189 (1985).  
 CC CC

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DR PIR; A02101; G1HHR2.  
 DR HSSP; P01825; 7FAB.  
 DR SMR; P06331; 21-146.  
 DR GO; GO:0005576; C:extracellular region; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG-LIKE; 1.  
 KW Immunoglobulin domain; Immunoglobulin V region; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 146 Ig heavy chain V-II region ARH-77.  
 FT REGION 20 117 V segment.  
 FT REGION 118 127 D segment.  
 FT REGION 128 146 J segment.  
 FT DISULFID 42 115 By similarity.  
 FT NON\_TER 146 146  
 SQ SEQUENCE 146 AA; 16228 MW; 8D7FD5B218171F CRC64;

Query Match 100.0%; Score 59; DB 1; Length 146;  
 Best Local Similarity 100.0%; Pred. No. 0.0066;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WGGGTTTVSS 11  
 |||||  
 Db 136 WGGGTTTVSS 146

## RESULT 4

HVIC\_HUMAN STANDARD; PRT; 147 AA.  
 AC P01744;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Ig heavy chain V-I region ND precursor (Fragments).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
 OC Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=83065234; PubMed=6815656;  
 RA Kenten J.H., Moigaard H.V., Houghton M., Derbyshire R.B., Viney J.,  
 RA Bell L.O., Gould H.J.;  
 RT "Cloning and sequence determination of the gene for the human  
 RT immunoglobulin epsilon chain expressed in a myeloma cell line."  
 RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665 (1982).  
 RN [2]  
 RP PROTEIN SEQUENCE OF 20-147.  
 RA Benich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;  
 RA (in) B.H.M. (eds.);  
 RT Immediate hypersensitivity: modern concepts and developments, pp.1-36,  
 RL Marcel Dekker, New York (1978). This epsilon chain was isolated from a myeloma  
 CC protein.  
 CC -----

CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.  
 CC -----  
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 CC -----

DR HSSP; P01751; INOB.  
 DR GO; GO:0005576; C:extracellular region; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG-LIKE; 1.  
 KW Direct protein sequencing; Immunoglobulin domain;  
 KW Immunoglobulin V region; Pyroglutamate carboxylic acid; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 147 Ig heavy chain V-I region ND.  
 FT DOMAIN 20 131 IG-like.  
 FT MOD\_RES 20 20 Pyroglutamate carboxylic acid.  
 FT DISULFID 41 115  
 FT CONFLICT 21 21 T -> V (in Ref. 2).  
 FT CONFLICT 53 54 IH -> HI (in Ref. 2).  
 FT CONFLICT 67 68 VG -> GV (in Ref. 2).  
 FT CONFLICT 125 125 Missing (in Ref. 2).  
 FT NON\_TER 147 147  
 SQ SEQUENCE 147 AA; 16496 MW; 948P9F72A536CC20 CRC64;

Query Match 100.0%; Score 59; DB 1; Length 147;  
 Best Local Similarity 100.0%; Pred. No. 0.0067;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WGGGTTTVSS 11



Db 137 WGGTTVTVSS 147

## RESULT 5

Q92553\_MOUSE PRELIMINARY; PRT; 147 AA.

AC Q92553;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE MRP3.

OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.

RC STRAIN=BALB/c;  
RX PubMed=11819679;  
RA Cui D.X., Zeng G.Y., Wang F., Xu J.R., Ren D.Q., Guo Y.H., Tian F.R.,  
Yan X.J., Hou Y., Su C.Z.,

RT "Mechanism of exogenous nucleic acids and their precursors improving  
the repair of intestinal epithelium after gamma-irradiation in mice."  
RL World J. Gastroenterol. 6:709-717(2000).  
RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=BALB/c;

RA Cui D., Zeng G., Yan X., Li X., Su C.;

RT "Cloning of mouse genes related to repairing of intestinal epithelium  
of the irradiated mice by treatment with the intestinal RNA of mice of  
the same strain."

RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).  
DR EMBL; AF240166; AAK3731.1; -; mRNA.

DR HSP; P01751; IAGW.  
DR SMR; Q92553; 3-139.

DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG\_LIKE; 1.  
DR Immunoglobulin domain.

SO SEQUENCE 147 AA; 16274 MW; 800594A12B97191F CRC64;

Query Match 100.0%; Score 59; DB 2; Length 147;

Best Local Similarity 100.0%; Pred. No. 0.0067;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGTTVTVSS 11

Db 111 WGGTTVTVSS 121

## RESULT 6

Q96QSO\_HUMAN PRELIMINARY; PRT; 159 AA.

AC Q96QSO;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Putative matrix cell adhesion molecule-3.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;

OC Homo.  
OX NCBI\_TaxID=9606;

RP NUCLEOTIDE SEQUENCE.

RA Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY039025; AAK82649.1; -; mRNA.  
DR HSP; P01869; IAGW.  
DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig\_v.

DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin domain.

SO SEQUENCE 159 AA; 17497 MW; 5D29537E881FAF02 CRC64;

Query Match 100.0%; Score 59; DB 2; Length 159;

Best Local Similarity 100.0%; Pred. No. 0.0073;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGTTVTVSS 11

Db 139 WGGTTVTVSS 149

## RESULT 7

Q92552\_MOUSE PRELIMINARY; PRT; 170 AA.

AC Q92552;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE MRP4.

OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.

RC STRAIN=BALB/c;  
RX PubMed=11819679;  
RA Cui D.X., Zeng G.Y., Wang F., Xu J.R., Ren D.Q., Guo Y.H., Tian F.R.,  
Yan X.J., Hou Y., Su C.Z.,

RT "Mechanism of exogenous nucleic acids and their precursors improving  
the repair of intestinal epithelium after gamma-irradiation in mice."  
RL World J. Gastroenterol. 6:709-717(2000).  
RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=BALB/c;

RA Cui D., Zeng G., Yan X., Li X., Su C.;

RT "Cloning of mouse genes related to repairing of intestinal epithelium  
of the irradiated mice by treatment with the intestinal RNA of mice of  
the same strain."

RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).  
DR EMBL; AF240167; AAK43732.1; -; mRNA.

DR HSP; P01751; IAGW.  
DR SMR; Q92552; 3-124.

DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG\_LIKE; 1.  
DR Immunoglobulin domain.

SO SEQUENCE 170 AA; 17978 MW; 5042823CC6C10F38 CRC64;

Query Match 100.0%; Score 59; DB 2; Length 170;

Best Local Similarity 100.0%; Pred. No. 0.0078;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGTTVTVSS 11

Db 113 WGGTTVTVSS 123

## RESULT 8

Q92551\_MOUSE PRELIMINARY; PRT; 218 AA.

AC Q92551;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE MRP5 (Fragment).  
OS Mus musculus (Mouse).



```

OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Aufferay C., Angeorge W., Ballabio A., Escivill X., Gibson K.,
RA Leinrach H., Pousicka A., Lundeberg J.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Pluvinet R., Estivill X., Escarceller M., Sunoy L.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL389978; CAB97534.1; -; mRNA.
DR HSSP; P01876; IOM0.
DR SMR; Q9NPP6; 186-394.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-sec; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
FT NON_TER
SQ SEQUENCE 416 AA; 44786 MW; 8C41708BB8AB4687 CRC64;

Query Match 100.0%; Score 59; DB 2; Length 416;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTVTSS 11
Db 66 WGGGTTVTSS 76

RESULT 12
Q6N089 HUMAN
ID Q6N089 HUMAN PRELIMINARY; PRT; 472 AA.
AC Q6N089;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKFZp686P15220.
GN Name=DKFZp686P15220;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Rectum tumor;
RA Wandut R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640627; CA645781.1; -; mRNA.
DR HSSP; P01861; IAD0.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-sec; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGV; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 100.0%; Score 59; DB 2; Length 472;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 WGGGTTVTSS 11
Db 132 WGGGTTVTSS 142

RESULT 13
Q6WU38 HUMAN
ID Q6WU38 HUMAN PRELIMINARY; PRT; 573 AA.
AC Q6WU38;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGH domain.
GN Name=IGHD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshitsuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Matra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RA Director MGC Project;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP PROTEIN SEQUENCE.
RX PubMed=1555592;
RA Makiya R., Stigbrand T.;
RT "Placental alkaline phosphatase has a binding site for the human
RT immunoglobulin-G Fc portion.";
RL Eur. J. Biochem. 205:341-345(1992).
DR EMBL; BC021276; AA821276.1; -; mRNA.
DR PIR; S21205; S21205.
DR PIR; S30532; S30532.
DR HSSP; P18529; I18K.
DR Ensemble; ENSG00000196122; Homo sapiens.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-sec; 1.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Immunoglobulin domain; Repeat.
SQ SEQUENCE 573 AA; 62967 MW; FD072344033AC530 CRC64;

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Query Match 100.0%; Score 59; DB 2; Length 573;  
Best Local Similarity 100.0%; Pred. No. 0.03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 133 WGCITVTSS 143

1 WGCITVTSS 11  

RESULT 14  
06P418\_HUMAN PRELIMINARY; PRT; 576 AA.  
ID 06P418\_HUMAN PRELIMINARY; PRT; 576 AA.  
AC 06P418\_HUMAN PRELIMINARY; PRT; 576 AA.  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE IGH protein.  
GN IGH protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Primary B-Cells; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Dicicenko L., Marzina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stadelon M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,  
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Paley J., Heltan E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Bikesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences".  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Primary B-Cells;  
RA Strausberg R.L.; PubMed=2497188; Nucleotide sequences of eight human natural antibody VH regions  
RT "Nucleotide sequences of eight human natural antibody VH regions  
RT reveals apparent restricted use of VH families.";  
RL J. Immunol. 142:4054-4061(1989).  
DE EMBL, BC019235; AAH19235.2; mRNA.  
DR PIR, G34964; G34964.  
DR HSSP, P01820; IADQ.  
DR SMR, O8WDX4; 27-256.  
DE Ensembl, ENSG00000130076; Homo sapiens.  
DR InterPro, IPR003599; IG.  
DR InterPro, IPR007110; IG-like.  
DR InterPro, IPR003597; IG-cl.  
DR InterPro, IPR003006; IG\_MHC.  
DR InterPro, IPR003596; IG\_v.  
DR Pfam, PF07654; Cl-sec; 4.  
DR SMART, SM00409; IG; 2.  
DR SMART, SM00407; IG; 1.  
DR SMART, SM00406; IGV; 1.  
DR SMART, SM00405; IGV; 1.  
DR PROSITE, PS00835; IG\_LIKE; 4.  
DR PROSITE, PS00290; IG\_MHC; UNKNOWN\_2.  
SQ SEQUENCE 576 AA; 63364 MW; FB97C949720F1E CRC64;

Query Match 100.0%; Score 59; DB 2; Length 576;  
Best Local Similarity 100.0%; Pred. No. 0.03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 133 WGCITVTSS 143

Query Match 100.0%; Score 59; DB 2; Length 576;  
Best Local Similarity 100.0%; Pred. No. 0.03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 133 WGCITVTSS 146

1 WGCITVTSS 11  

RESULT 15  
08WDX4\_HUMAN PRELIMINARY; PRT; 595 AA.  
ID 08WDX4\_HUMAN PRELIMINARY; PRT; 595 AA.  
AC 08WDX4\_HUMAN PRELIMINARY; PRT; 595 AA.  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein.  
GN Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Lymph;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Dicicenko L., Marzina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stadelon M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,  
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Paley J., Heltan E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Bikesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences".  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Lymph;  
RA Strausberg R.L.; PubMed=2497188; Nucleotide sequences of eight human natural antibody VH regions  
RT "Nucleotide sequences of eight human natural antibody VH regions  
RT reveals apparent restricted use of VH families.";  
RL J. Immunol. 142:4054-4061(1989).  
DE EMBL, BC019235; AAH19235.2; mRNA.  
DR PIR, G34964; G34964.  
DR HSSP, P01820; IADQ.  
DR SMR, O8WDX4; 27-256.  
DE Ensembl, ENSG00000130076; Homo sapiens.  
DR InterPro, IPR003599; IG.  
DR InterPro, IPR007110; IG-like.  
DR InterPro, IPR003597; IG-cl.  
DR InterPro, IPR003006; IG\_MHC.  
DR InterPro, IPR003596; IG\_v.  
DR Pfam, PF07654; Cl-sec; 4.  
DR SMART, SM00409; IG; 2.  
DR SMART, SM00407; IG; 1.  
DR SMART, SM00406; IGV; 1.  
DR SMART, SM00405; IGV; 1.  
DR PROSITE, PS00835; IG\_LIKE; 5.  
DR PROSITE, PS00290; IG\_MHC; UNKNOWN\_3.  
KV Hypothetical protein.  
SQ SEQUENCE 595 AA; 65291 MW; 0D4B5076545714E CRC64;

Query Match 100.0%; Score 59; DB 2; Length 595;  
Best Local Similarity 100.0%; Pred. No. 0.032;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WGGGTTTVSS 11  
|||||  
Db 141 WGGGTTTVSS 151

Search completed: December 4, 2005, 04:52:27  
Job time : 102.375 secs

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GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: December 4, 2005, 04:09:54 ; Search time 95.5625 Seconds  
(without alignments)  
50.576 Million cell updates/sec

Title: US-10-632-706-127

Perfect score: 60

Sequence: 1 LATYYRFGIDV 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_21:\*  
1: geneseqp19808:\*  
2: geneseqp19908:\*  
3: geneseqp20008:\*  
4: geneseqp20018:\*  
5: geneseqp20028:\*  
6: geneseqp20038:\*  
7: geneseqp20048:\*  
8: geneseqp20058:\*  
9: geneseqp20068:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	60	100.0	11	8	ADR38724	AdR38724 Mouse hea
2	60	100.0	11	8	ADR38725	AdR38725 Mouse hea
3	48	80.0	122	9	AEBA45960	AEBA45960 Human mon
4	47	78.3	114	7	ADD28082	ADD28082 Lymphoma
5	47	78.3	129	7	ADD28323	ADD28323 Human het
6	47	78.3	134	7	ADD28237	ADD28237 Human het
7	47	78.3	134	9	ADVB6824	ADVB6824 Bacillus
8	47	78.3	244	8	ADR28082	ADR28082 NPB polyp
9	47	78.3	468	9	AEBA45891	AEBA45891 Human mon
10	47	78.3	468	9	AEBA45853	AEBA45853 Human mon
11	46	76.7	13	8	ADR38712	ADR38712 Mouse hea
12	46	76.7	21	9	ADM04816	ADM04816 PAPP-A im
13	46	76.7	126	9	ADZ41994	ADZ41994 Ig H chat
14	46	76.7	140	9	ADM04810	ADM04810 PAPP-A im
15	45	75.0	16	9	ADM04952	ADM04952 PAPP-A im
16	45	75.0	21	5	ABP47057	ABP47057 Human Bly
17	45	75.0	21	7	ADG97884	ADG97884 scFV VHCD
18	45	75.0	24	9	ADM77426	ADM77426 Human pla
19	45	75.0	117	9	AEBO1019	AEBO1019 Human hea
20	45	75.0	135	9	ADM04946	ADM04946 PAPP-A im
21	45	75.0	256	5	ABP45589	ABP45589 Human Bly
22	45	75.0	256	7	ADG96416	ADG96416 Single ch
23	44	73.3	13	4	AAU02710	AAU02710 CDR regio
24	44	73.3	14	9	ADY70216	ADY70216 Human Mab

25	44	73.3	16	5	ABP46118	ABP46118 Human Bly
26	44	73.3	16	7	ADG96945	ADG96945 scFV VHCD
27	44	73.3	17	5	ABP46865	ABP46865 Human Bly
28	44	73.3	17	7	ADG97692	ADG97692 scFV VHCD
29	44	73.3	18	9	AEA21444	AEA21444 Human ant
30	44	73.3	109	8	ADI05782	ADI05782 Human mon
31	44	73.3	117	7	ADK18782	ADK18782 Anti-huma
32	44	73.3	122	4	AAU02589	AAU02589 Anti-edip
33	44	73.3	123	7	ADP03878	ADP03878 Murine-ex
34	44	73.3	123	7	ADP03878	ADP03878 Murine-ex
35	44	73.3	123	9	ADY70198	ADY70198 Human mon
36	44	73.3	127	5	ABG76565	ABG76565 HCV E1 an
37	44	73.3	127	7	ADK18819	ADK18819 Anti-huma
38	44	73.3	127	7	ADK18901	ADK18901 Anti-huma
39	44	73.3	127	7	ADK18607	ADK18607 Anti-huma
40	44	73.3	127	8	ADL25432	ADL25432 Human mab
41	44	73.3	127	9	AEA21438	AEA21438 Human ant
42	44	73.3	129	7	ADE28407	ADE28407 Human ant
43	44	73.3	134	7	ADD28238	ADD28238 Human het
44	44	73.3	134	7	ADD28332	ADD28332 Human het
45	44	73.3	134	7	ADD28331	ADD28331 Human het

## ALIGNMENTS

RESULT 1  
ADR38724 ADR38724 standard; peptide; 11 AA.  
XX

AC ADR38724;  
XX

DT 02-DEC-2004 (first entry)  
XX

DE Mouse heavy chain variable region CDR3 seq'd 126.  
XX

KW antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;  
KW BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
KW toxin neutralisation; botulinum neurotoxin poisoning; mouse;  
KW heavy chain variable region; complementarily determining region; CDR3.  
XX

OS Mus sp.  
XX

PN US2004175385-A1.  
XX

PD 09-SEP-2004.  
XX

PF 01-AUG-2003; 2003US-00632706.  
XX

PR 31-AUG-1998; 98US-00144886.  
XX

PR 01-AUG-2002; 2002US-0400721P.  
XX

PA (REGC ) UNIV CALIFORNIA.  
XX

PI Marks JD, Amersdorfer P;  
XX

DR WPI; 2004-652009/63.  
XX

XX New isolated antibody that neutralizes botulinum neurotoxin type A,  
XX useful for diagnosing botulism or for treating pathologies associated  
XX with botulinum neurotoxin poisoning.  
PT

PT with botulinum neurotoxin poisoning.  
PT

Example 3; SEQ ID NO 126; 110pp; English.  
XX

The invention describes an isolated antibody (I) that specifically binds  
XX to an epitope specifically bound by an antibody expressed by a specific  
XX clone where (I) binds to and neutralizes botulinum neurotoxin type A  
XX (BoNT/A). An isolated antibody (I) that specifically binds to an epitope  
XX specifically bound by an antibody expressed by a clone chosen from clone  
XX S25, C25, C39, 1C6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1,  
XX 3-8, 3-10 and INGL, where (I) binds to and neutralizes botulinum  
XX neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)  
XX comprising BoNT/A neutralising epitope having an epitope that is

specifically bound by an antibody expressed by clones as mentioned in (I) ; producing (I) ; and a composition (II) comprising several anti-botulinum neurotoxin antibodies, where each antibody is specific for a different epitope of a botulinum neurotoxin and the combination of antibodies shows greater toxin neutralisation than the single antibodies in surplis. The following are disclosed: a pharmaceutical composition comprising (I) ; and a kit comprising (I) . (I) is useful for neutralising BONT/A antibody and for neutralising a botulinum neurotoxin which involves contacting neurotoxin with (I) in surplis, where each of (I) is specific for a different epitope of the botulinum neurotoxin and the combination of antibodies shows greater toxin neutralisation than the single antibodies in surplis. (I) is useful for diagnosing the botulism or for treating pathologies associated with botulinum neurotoxin poisoning. (I) exhibits specificity and affinity towards BONT/A. (I) enables rapid detection or diagnosis of botulism. This is the amino acid sequence of mouse heavy chain variable region complementarity determining region 3 (CDR3) from anti-botulinum neurotoxin antibodies.

XX SQ Sequence 11 AA;

Query Match 100.0%; Score 60; DB 8; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.0017; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LATYYFGSDV 11  
| | | | |  
Db 1 LATYYFGSDV 11

RESULT 2  
ADR38725 standard; peptide; 11 AA.

AC ADR38725;

XX 02-DEC-2004 (first entry)

XX Mouse heavy chain variable region CDR3 seqid 127.

XX antihacterial; antibody; botulinum neurotoxin type A; BONT/A;

XX BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;

XX toxin neutralisation; botulinum neurotoxin poisoning; mouse;

XX heavy chain variable region; complementarity determining region; CDR3.

XX Mus sp.

XX US2004175385-A1.

XX 01-AUG-2003; 2003US-00632706.

XX 31-AUG-1998; 98US-00144886.

XX 01-AUG-2002; 2002US-0400721P.

XX (REGC ) UNIV CALIFORNIA.

XX Marks JD, Amersdorfer P;

XX WPI; 2004-652009/63.

XX New isolated antibody that neutralizes botulinum neurotoxin type A,

XX useful for diagnosing botulism or for treating pathologies associated

XX with botulinum neurotoxin poisoning.

XX Example 3; SEQ ID NO 127; 110pp; English.

XX The invention describes an isolated antibody (I) that specifically binds

3-8, 3-10 and INGI, where (I) binds to and neutralizes botulinum neurotoxin type A (BONT/A). Also described are: a polypeptide (II) comprising BONT/A neutralising epitope having an epitope that is specifically bound by an antibody expressed by clones as mentioned in (I) ; producing (I) ; and a composition (III) comprising several anti-botulinum neurotoxin antibodies, where each antibody is specific for a different epitope of a botulinum neurotoxin and the combination of antibodies shows greater toxin neutralisation than the single antibodies in surplis. The following are disclosed: a pharmaceutical composition comprising (I) ; and a kit comprising (I) . (I) is useful for neutralising BONT/A antibody and for neutralising a botulinum neurotoxin which involves contacting neurotoxin with (I) in surplis, where each of (I) is specific for a different epitope of the botulinum neurotoxin and the combination of antibodies shows greater toxin neutralisation than the single antibodies in surplis. (I) is useful for diagnosing the botulism or for treating pathologies associated with botulinum neurotoxin poisoning. (I) exhibits specificity and affinity towards BONT/A. (I) enables rapid detection or diagnosis of botulism. This is the amino acid sequence of mouse heavy chain variable region complementarity determining region 3 (CDR3) from anti-botulinum neurotoxin antibodies.

XX SQ Sequence 11 AA;

Query Match 100.0%; Score 60; DB 8; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.0017; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LATYYFGSDV 11  
| | | | |  
Db 1 LATYYFGSDV 11

RESULT 3  
AEB45960 standard; protein; 122 AA.

XX AEB45960;

XX 06-OCT-2005 (first entry)

XX Human monoclonal anti-MADCM antibody related protein #4.

XX Monoclonal antibody; mucosal addressin cell adhesion molecule; MADCM;

XX inflammation; inflammatory bowel disease; Crohn's disease;

XX ulcerative colitis; diverticular disease; gastritis; liver disease;

XX primary biliary cirrhosis; primary sclerosing cholangitis;

XX insulin dependent diabetes; graft versus host disease; antidiabetic;

XX immunosuppressive; antibody.

XX Homo sapiens.

XX WO2005067620-A2.

XX 28-JUL-2005.

XX 07-JAN-2005; 2005WO-US000370.

XX 09-JAN-2004; 2004US-0535490P.

XX (Pfizer ) Pfizer INC.

XX (Pfizer ) ABGENIX INC.

XX (Pfizer ) Pfizer LTD.

XX Pullen N, Molloy E, Kellermann S, Green LL, Haek-Frendescho M,

XX WPI; 2005-554958/56.

XX New antibody to Mucosal Addressin Cell Adhesion Molecule, useful for

XX diagnosing and treating an inflammatory disease, e.g. inflammatory bowel

XX disease, ulcerative colitis, gastritis, insulin-dependent diabetes or

XX graft versus host disease.



PS Example 5; Fig 1; 167pp; English.

CC The invention relates to a human monoclonal antibody or its antigen-  
CC binding portion that specifically binds to mucosal addressin cell  
CC adhesion molecule (MacCAM). The invention also relates to a hybridoma  
CC cell line that produces the human monoclonal antibody, a pharmaceutical  
CC composition comprising an amount of the monoclonal antibody or its  
CC antigen-binding portion and a pharmaceutical carrier, a method of  
CC treating inflammatory disease in a subject, an isolated cell line that  
CC produces the monoclonal antibody or its antigen-binding portion or the  
CC heavy chain or light chain of the antibody or of its portion, an isolated  
CC nucleic acid molecule comprising a nucleotide sequence encoding the heavy  
CC chain or its antigen-binding portion or the light chain or its antigen-  
CC binding portion of an antibody described above, a vector comprising the  
CC nucleic acid molecule, where the vector optionally comprises an  
CC expression control sequence operably linked to the nucleic acid molecule,  
CC a host cell comprising the vector or the nucleic acid molecule above, a  
CC method of producing a human monoclonal antibody or its antigen-binding  
CC portion that specifically binds MacCAM, a method of isolating an antibody  
CC or its antigen-binding portion that specifically binds to MacCAM, a  
CC method of treating a subject in need of a human antibody or its antigen-  
CC binding portion that specifically binds to MacCAM and inhibits binding to  
CC alpha4beta7, a method of inhibiting alpha4beta7 binding to cells  
CC expressing human MacCAM, a method of inhibiting MacCAM-mediated leukocyte  
CC endothelial cell adhesion, migration and infiltration into tissues, a  
CC method of inhibiting alpha4beta7/MacCAM-dependent cellular adhesion,  
CC inhibiting the MacCAM-mediated recruitment of lymphocytes to  
CC gastrointestinal lymphoid tissue, a method of diagnosing a disorder  
CC characterized by circulating soluble human MacCAM and detecting  
CC inflammation in a subject. The antibody, composition and methods are  
CC useful for diagnosing and treating inflammatory diseases, e.g.  
CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,  
CC diverticular disease, gastritis, liver disease, primary biliary  
CC cirrhosis, primary sclerosing cholangitis, insulin dependent diabetes and  
CC graft versus host disease. This sequence represents a human monoclonal  
CC anti-MacCAM antibody related protein of the invention.

SO Sequence 122 AA;

Query Match 80.0%; Score 48; DB 9; Length 122;  
Best Local Similarity 63.6%; Pred. No. 2.5;  
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LATYYFGLDV 11  
: ||||: ||  
DB 100 VVTTYYYGMDV 110

RESULT 4  
ADD28082  
ID ADD28082 standard; protein; 114 AA.  
XX  
AC ADD28082;

DT 15-JAN-2004 (first entry)

DE Lymphoma related immunoglobulin variable region.

XX B-cell; malignant; immunoglobulin; immunoglobulin variable region;  
KM Ig variable region; glycosylation site; lymphoma; B cell receptor;  
KW cytostatic; gene therapy; glycosylation inhibitor;  
XX non-Hodgkin's lymphoma.

OS Synthetic.  
OS Homo sapiens.

PN WO2003074059-A2.

PD 12-SEP-2003.

PR 24-FEB-2003; 2003WO-GB000783.

XX 07-MAR-2002; 2002GB-00005395.

XX (CANC-) CANCER RES TECHNOLOGY LTD.  
PA  
XX Zhu D, Stevenson P;  
PI  
XX WPI, 2003-902720/82.  
DR

PT Classifying a B-cell as malignant or normal by isolating a sequence  
PT representing an Ig variable region from the B cell, detecting the  
PT presence of a glycosylation site and classifying the cell as malignant or  
PT normal.

PS Disclosure; Fig 3; 64pp; English.

XX The present invention describes a method for classifying a B-cell as  
XX malignant or normal comprising: (a) isolating a sequence representing an  
XX immunoglobulin (Ig) variable region from the B cell; (b) detecting the  
XX presence of a glycosylation site; and (c) classifying the cell as  
XX malignant or normal on the basis of the presence or absence of a  
XX glycosylation site. Also described: (1) treating a patient suffering from  
XX or at risk of having lymphoma; (2) screening for substances capable of  
XX inhibiting glycosylation of the Ig variable region of the B cell receptor  
XX; and (3) screening for substances (S) capable of inhibiting the  
XX interaction between lectins of the type found in the germinal centre and  
XX N-glycans found on the surface of Ig of lymphoma cells. (S) has  
XX cytostatic activity, and can be used in gene therapy, and as a  
XX glycosylation inhibitor. The method is useful in classifying a B-cell as  
XX malignant or normal. The glycosylation inhibitor is useful in preparing a  
XX medicament for treating non-Hodgkin's lymphoma. The present sequence  
XX represents an Ig variable region sequence which is used in the  
XX exemplification of the present invention.

SO Sequence 114 AA;

Query Match 78.3%; Score 47; DB 7; Length 114;  
Best Local Similarity 77.8%; Pred. No. 3.4;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYTFGLDV 11  
|||: ||  
DB 106 TTYYYGMDV 114

RESULT 5  
ADD28323  
ID ADD28323 standard; protein; 129 AA.  
XX  
AC ADD28323;

DT 15-JAN-2004 (first entry)

DE Human heterodimeric antibody heavy chain variable region SEQ ID NO:101.

XX human heterodimeric antibody; human; antibody; binding affinity;  
KM protective antigen; Bacillus anthracis; anthrax infection; cell receptor;  
KW edema factor; lethal factor; virulence; antibacterial; immunotherapy;  
KM anti-toxin; anti-infective; anthrax; botulinum; smallpox;  
XX Venezuelan equine encephalomyelitis virus; VEEV; West Nile virus; WNV.

OS Synthetic.  
OS Homo sapiens.

PN WO2003076568-A2.

PD 18-SEP-2003.

PR 11-FEB-2003; 2003WO-US004206.

PR 11-FEB-2002; 2002US-0356086P.

PR 29-APR-2002; 2002US-0376408P.

PR 27-SEP-2002; 2002US-0414053P.

PR 25-NOV-2002; 2002US-0428807P.

PA (ALEX-) ALEXION PHARM INC.  
XX  
XX Bowdish KS, Wild MA;  
XX  
DR WPI; 2003-722327/68.  
XX  
PT New human heterodimeric antibodies or their antibody fragments, useful as  
PT anti-toxins or anti-infectives with respect to infective agents, e.g.  
PT anthrax, botulinum, smallpox, Venezuelan equine encephalomyelitis or West  
PT Nile virus.  
XX  
XX Claim 11; SEQ ID NO 101; 67bp; English.  
XX  
XX The present invention describes a human heterodimeric antibody (I)  
CC (fragment) having a binding affinity of at least 1x10<sup>-8</sup> M to the  
CC protective antigen of Bacillus anthracis or a molecule involved in  
CC anthrax infection that blocks binding of the antigen or molecule to cell  
CC receptors, edema factor and lethal factor. (I) has virucide and  
CC antibacterial activities, and can be used in immunotherapy. The  
CC antibodies (I) are useful as anti-toxins or anti-infectives with respect  
CC to infective agents, such as anthrax, botulinum, smallpox, Venezuelan  
CC equine encephalomyelitis virus (VEEV), or West Nile virus (WNV). The  
CC present sequence represents a human heterodimeric antibody heavy chain  
CC variable region amino acid sequence, which is used in the exemplification  
CC of the present invention.  
XX  
SQ Sequence 129 AA;  
XX  
Query Match 78.3%; Score 47; DB 7; Length 129;  
Best Local Similarity 77.8%; Pred. No. 3.9;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 3 TTYVFGLDV 11  
|||:|:|  
105 TTYVGMVDV 113  
DB  
RESULT 6  
ADD28237  
ID ADD28237 standard; protein; 134 AA.  
XX  
AC ADD28237;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Human heterodimeric antibody heavy chain variable region SEQ ID NO:15.  
XX  
XX human heterodimeric antibody; human; antibody; binding affinity;  
KM protective antigen; Bacillus anthracis; anthrax infection; cell receptor;  
KM edema factor; lethal factor; virucide; antibacterial; immunotherapy;  
KM anti-toxin; anti-infective; anthrax; botulinum; smallpox;  
KM Venezuelan equine encephalomyelitis virus; VEEV; West Nile virus; WNV.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
XX MO2003076568-A2.  
XX  
XX PD 18-SEP-2003.  
XX  
XX PF 11-FEB-2003; 2003WO-US004206.  
XX  
XX PR 11-FEB-2002; 2002US-0356086P.  
XX PR 29-APR-2002; 2002US-0376408P.  
XX PR 27-SEP-2002; 2002US-0414053P.  
XX PR 25-NOV-2002; 2002US-0428807P.  
XX  
XX (ALEX-) ALEXION PHARM INC.  
XX  
XX Bowdish KS, Wild MA;  
XX  
XX WPI; 2003-722327/68.  
XX

PT New human heterodimeric antibodies or their antibody fragments, useful as  
PT anti-toxins or anti-infectives with respect to infective agents, e.g.  
PT anthrax, botulinum, smallpox, Venezuelan equine encephalomyelitis or West  
PT Nile virus.  
XX  
XX Claim 6; SEQ ID NO 15; 67bp; English.  
XX  
XX The present invention describes a human heterodimeric antibody (I)  
CC (fragment) having a binding affinity of at least 1x10<sup>-8</sup> M to the  
CC protective antigen of Bacillus anthracis or a molecule involved in  
CC anthrax infection that blocks binding of the antigen or molecule to cell  
CC receptors, edema factor and lethal factor. (I) has virucide and  
CC antibacterial activities, and can be used in immunotherapy. The  
CC antibodies (I) are useful as anti-toxins or anti-infectives with respect  
CC to infective agents, such as anthrax, botulinum, smallpox, Venezuelan  
CC equine encephalomyelitis virus (VEEV), or West Nile virus (WNV). The  
CC present sequence represents a human heterodimeric antibody heavy chain  
CC variable region amino acid sequence, which is used in the exemplification  
CC of the present invention.  
XX  
SQ Sequence 134 AA;  
XX  
Query Match 78.3%; Score 47; DB 7; Length 134;  
Best Local Similarity 77.8%; Pred. No. 4;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 3 TTYVFGLDV 11  
|||:|:|  
110 TTYVGMVDV 118  
DB  
RESULT 7  
ADV66824  
ID ADV66824 standard; protein; 134 AA.  
XX  
XX ADV66824;  
XX  
DT 10-MAR-2005 (first entry)  
XX  
DE Bacillus anthracis toxin Fab 9 K 2e G pro heavy chain variable region.  
XX  
XX Bioterrorism; Bacillus anthracis infection; vaccine; diagnosis;  
KM antibacterial; antibody; heavy chain variable region.  
XX  
OS Homo sapiens.  
XX  
XX MO2004110362-A2.  
XX  
XX PD 23-DEC-2004.  
XX  
XX PF 26-MAY-2004; 2004WO-US016557.  
XX  
XX PR 02-JUN-2003; 2003US-00452593.  
XX  
XX (ALEX-) ALEXION PHARM INC.  
XX  
XX Bowdish KS, Frederickson S, Wild MA, Maruyama T, Nolan MJ;  
XX  
XX WPI; 2005-057715/06.  
XX  
XX DR  
XX  
XX PT Treating an animal with anthrax infection by administering an antibody to  
PT the protective antigen of Bacillus anthracis, and blocking binding to  
PT cell receptors, edema factor or lethal factor.  
XX  
XX Claim 7; SEQ ID NO 15; 87bp; English.  
XX  
XX A claimed method for treating an animal infected with Bacillus anthracis  
CC comprises administering an antibody or antibody fragment that binds to a  
CC molecule involved in anthrax infection and which has the ability to block  
CC the binding of the molecule to at least one of a cell receptor, PA63,  
CC PA63 heptamer, PA83, edema factor and lethal factor. A claimed method for  
CC determining exposure to B. anthracis comprises assaying a sample for the  
CC presence of a molecule selected from cell receptors, PA63, PA63 heptamer,

CC PA83, edema factor or lethal factor with an antibody that has binding  
CC affinity for the molecule, where the presence of elevated levels of the  
CC antibody correlates with the presence of a disease associated with B.  
CC anthrax. Alternatively, the method involves assaying for the presence  
CC of an antibody to a cell receptor, PA63, PA63 heptamer, PA83, edema  
CC factor or lethal factor with a secondary antibody having binding affinity  
CC for the antibody, where the presence of elevated levels of the secondary  
CC antibody correlates with the presence of B. anthrax in a subject. In  
CC all cases, the antibody (full-length or functional fragment) may comprise  
CC a heavy chain variable region selected from a group of sequences ADV86810  
CC -ADV86827, a light chain kappa region selected from a group of sequences  
CC ADV86828-ADV86835 and a light chain lambda region selected from a group  
CC of sequences ADV86836-ADV86847. Diagnostic kits are provided. A claimed  
CC vaccine comprises a multimer of anthrax toxin PA63. The methods and  
CC compositions of the present invention are also useful for producing anti-  
CC toxins or anti-infectives to infective agents such as anthrax, botulinum,  
CC smallpox, Venezuelan equine encephalomyelitis and West Nile virus. The  
CC present sequence is that of the heavy chain variable region of a human  
CC Fab (designated 9 K 2e G pro) with positive reactivity to anthrax  
CC proteins PA63 and PA83. Phage libraries were developed from mRNA isolated  
CC from blood and bone marrow samples of donors who had been vaccinated  
CC against anthrax. The libraries were panned against PA83 and PA63, and  
CC sequence analysis was performed on positive responders. Neutralization of  
CC anthrax toxin activity by purified Fabs was demonstrated.

SQ Sequence 134 AA;

Query Match 78.3%; Score 47; DB 9; Length 134;

Best Local Similarity 77.8%; Pred. No. 4;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;Qy 3 TTYFGLDV 11  
|||:|:|

Db 110 TTYYYGMDV 118

RESULT 8  
ADR28082  
ID ADR28082 standard; protein; 244 AA.

XX ADR28082;

XX 07-OCT-2004 (first entry)

XX NPB polypeptide scfv27, seq id 29.

XX DE Cytostatic; metastasis inhibitor; neuropilin binder; NPB; scFv;  
XX KW single chain antibody; neuropilin-1; NP-1; angiogenesis; tumour; cancer.XX Mus sp.  
XX OS Synthetic.XX Key Location/Qualifiers  
XX FM 87.103XX FT /note="complementary determining region claimed under  
XX PT claim 5"

XX MO2004056874-AA.

XX PD 08-JUL-2004.

XX PF 22-DEC-2003; 2003WO-EP014756.

XX PR 20-DEC-2002; 2002US-0435893P.

XX PR 15-JAN-2003; 2003EP-00000615.

XX PA (XERT-) XERION PHARM AG.

XX PA (TUFT) UNIV TUFTS.

XX PI Unger CM, Beste G, Zehetmayer C, Jain B, Torella C, Niewoehner J;  
XX PI Jay DG, Eustace BK, Knauer R, Jensen KH;

XX WPI; 2004-507700/48.

DR N-P8DB; ADR28116.

XX Novel neuropilin binder which is scFv, antibody fragment or bioconjugate,  
XX PT that modulates neuropilin-1 function or inhibits NP-1 dependent  
XX PT angiogenesis of endothelial cells and/or invasion of tumor cells useful  
XX for treating cancer.

PS Claim 3; SEQ ID NO 29; 120pp; English.

XX The invention relates to a neuropilin binder (NPB) (I) which is a  
XX polypeptide, antibody, scFv, antibody fragment or bioconjugate, that  
XX modulates neuropilin-1 (NP-1) function or inhibits NP-1 dependent  
XX angiogenesis of endothelial cells and/or invasion of tumor cells,  
XX whereby the NPB binds to NP-1 and modulates NP-1 function. Further  
XX disclosed is an ex vivo method of determining the dependency of the  
XX invasiveness of a naturally occurring invasive cancer cell on the  
XX functionality of NP-1. The NPB of the invention is an inhibitor of  
XX metastasis of NP-1 mediated invasion and/or adhesion and an inhibitor of  
XX tumour-associated NP-1 dependent angiogenesis. The NPB of the invention  
XX is useful for detecting NP-1 expression, modulation of NP-1 function,  
XX particularly for detecting NP-1 expression of NP-dependent invasion or  
XX adhesion of cells, preferably tumour cells. It is useful in the  
XX manufacture of medicament for the treatment or prevention of NP-dependent  
XX angiogenesis and non-physiological blood vessel growth, particularly  
XX correlated with a tumour. It is also useful for treatment or prevention  
XX of cancer and/or metastasis of tumour cells. The current sequence  
XX represents a single chain antibody neuropilin binder (NPB) polypeptide.

SQ Sequence 244 AA;

Query Match 78.3%; Score 47; DB 8; Length 244;

Best Local Similarity 77.8%; Pred. No. 7.7;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;Qy 3 TTYFGLDV 11  
|||:|:|

Db 95 TTYYYGMDV 103

RESULT 9  
AEB45891  
ID AEB45891 standard; protein; 468 AA.

XX AEB45891;

XX 06-OCT-2005 (first entry)

XX DE Human monoclonal anti-MAdCAM antibody #27.

XX Monoclonal antibody; mucosal addressin cell adhesion molecule; MAdCAM;  
XX inflammation; inflammatory bowel disease; Crohn disease;  
XX ulcerative colitis; diverticular disease; gastritis; liver disease;  
XX primary biliary cirrhosis; primary sclerosing cholangitis;  
XX insulin dependent diabetes; graft versus host disease; antiinflammatory;  
XX gastrointestinal gen.; anticancer; hepatotropic; antidiabetic;  
XX immunosuppressive; antibody.

XX Homo sapiens.

XX MO2005067620-AA.

XX PD 28-JUL-2005.

XX PF 07-JAN-2005; 2005WO-US000370.

XX PR 09-JAN-2004; 2004US-0535490P.

XX PA (PFIZ) PFIZER INC.

XX PA (ABGE-) ABGENIX INC.

XX PA (PFIZ) PFIZER LTD.

XX PI Pullen N, Molloy E, Kellermann S, Green LL, Haak-Frendschio M;

DR WPI, 2005-554958/56.  
DR N-PSDB; AEB45890.  
PT New antibody to Mucosal Adhesin Cell Adhesion Molecule, useful for  
PT diagnosing and treating an inflammatory disease, e.g. inflammatory bowel  
PT disease, ulcerative colitis, gastritis, insulin-dependent diabetes or  
PT graft versus host disease.  
XX  
XX  
XX Claim 8; SEQ ID NO 56; 167pp; English.  
XX  
XX The invention relates to a human monoclonal antibody or its antigen-  
XX binding portion that specifically binds to mucosal adhesin cell  
XX adhesion molecule (MadCAM). The invention also relates to a hybridoma  
XX cell line that produces the human monoclonal antibody, a pharmaceutical  
XX composition comprising an amount of the monoclonal antibody or its  
XX antigen-binding portion and a pharmaceutical carrier, a method of  
XX treating inflammatory disease in a subject, an isolated cell line that  
XX produces the monoclonal antibody or its antigen-binding portion or the  
XX heavy chain or light chain of the antibody or of its portion, an isolated  
XX nucleic acid molecule comprising a nucleotide sequence encoding the heavy  
XX chain or its antigen-binding portion or the light chain or its antigen-  
XX binding portion of an antibody described above, a vector comprising the  
XX nucleic acid molecule, where the vector optionally comprises an  
XX expression control sequence operably linked to the nucleic acid molecule,  
XX a host cell comprising the vector or the nucleic acid molecule above,  
XX a method of producing a human monoclonal antibody or its antigen-binding  
XX portion that specifically binds MadCAM, a method of isolating an antibody  
XX or its antigen-binding portion that specifically binds to MadCAM, a  
XX method of treating a subject in need of a human antibody or its antigen-  
XX binding portion that specifically binds to MadCAM and inhibits binding to  
XX alpha4beta7, a method of inhibiting alpha4beta7 binding to cells  
XX expressing human MadCAM, a method of inhibiting MadCAM-mediated leukocyte  
XX -endothelial cell adhesion, migration and infiltration into tissues, a  
XX method of inhibiting alpha4beta7/MadCAM-dependent cellular adhesion,  
XX inhibiting the MadCAM-mediated recruitment of lymphocytes to  
XX gastrointestinal lymphoid tissue, a method of diagnosing a disorder  
XX characterized by circulating soluble human MadCAM and detecting  
XX inflammation in a subject. The antibody, composition and methods are  
XX useful for diagnosing and treating inflammatory disease, e.g.  
XX inflammatory bowel disease, Crohn's disease, ulcerative colitis,  
XX diverticular disease, gastritis, liver disease, primary biliary  
XX cirrhosis, primary sclerosing cholangitis, insulin dependent diabetes and  
XX graft versus host disease. This sequence represents a human monoclonal  
XX anti-MadCAM antibody of the invention.  
SQ Sequence 468 AA;  
Query Match 78.3%; Score 47; DB 9; Length 468;  
Best Local Similarity 77.8%; Pred. No. 15;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 3 TYYFGLDV 11  
DB 123 TYYFGMDV 131  
RESULT 10  
AEB45853  
ID AEB45853 standard; protein; 469 AA.  
XX  
XX AEB45853;  
AC  
XX  
XX 06-OCT-2005 (first entry)  
XX  
XX Human monoclonal anti-MadCAM antibody #9.  
XX  
XX Monoclonal antibody; mucosal adhesin cell adhesion molecule; MadCAM;  
XX inflammation; inflammatory bowel disease; Crohn disease;  
XX ulcerative colitis; diverticular disease; gastritis; liver disease;  
XX primary biliary cirrhosis; primary sclerosing cholangitis;  
XX insulin dependent diabetes; graft versus host disease; anti-inflammatory;  
XX gastrointestinal-gen.; antidiabetic; hepatotropic; antidiabetic;  
XX immunosuppressive; antibody.

XX  
XX Homo sapiens.  
OS  
XX  
XX MO2005067620-A2.  
PN  
XX  
XX 28-JUL-2005.  
PD  
XX  
XX  
XX 07-JAN-2005; 2005WO-US000370.  
PF  
XX  
XX 09-JAN-2004; 2004US-0535490P.  
PR  
XX  
XX (PFIZ ) PFIZER INC.  
PA (ABGE-) ABGENIX INC.  
PA (PFIZ ) PFIZER LTD.  
XX  
XX Pullen N, Molloy E, Kellermann S, Green LL, Haak-Frendescho M;  
PI  
XX  
XX WPI, 2005-554958/56.  
DR  
XX  
XX N-PSDB; AEB45852.  
DR  
XX  
XX New antibody to Mucosal Adhesin Cell Adhesion Molecule, useful for  
PT diagnosing and treating an inflammatory disease, e.g. inflammatory bowel  
PT disease, ulcerative colitis, gastritis, insulin-dependent diabetes or  
PT graft versus host disease.  
XX  
XX  
XX Claim 8; SEQ ID NO 18; 167pp; English.  
XX  
XX The invention relates to a human monoclonal antibody or its antigen-  
XX binding portion that specifically binds to mucosal adhesin cell  
XX adhesion molecule (MadCAM). The invention also relates to a hybridoma  
XX cell line that produces the human monoclonal antibody, a pharmaceutical  
XX composition comprising an amount of the monoclonal antibody or its  
XX antigen-binding portion and a pharmaceutical carrier, a method of  
XX treating inflammatory disease in a subject, an isolated cell line that  
XX produces the monoclonal antibody or its antigen-binding portion or the  
XX heavy chain or light chain of the antibody or of its portion, an isolated  
XX nucleic acid molecule comprising a nucleotide sequence encoding the heavy  
XX chain or its antigen-binding portion or the light chain or its antigen-  
XX binding portion of an antibody described above, a vector comprising the  
XX nucleic acid molecule, where the vector optionally comprises an  
XX expression control sequence operably linked to the nucleic acid molecule,  
XX a host cell comprising the vector or the nucleic acid molecule above,  
XX a method of producing a human monoclonal antibody or its antigen-binding  
XX portion that specifically binds MadCAM, a method of isolating an antibody  
XX or its antigen-binding portion that specifically binds to MadCAM, a  
XX method of treating a subject in need of a human antibody or its antigen-  
XX binding portion that specifically binds to MadCAM and inhibits binding to  
XX alpha4beta7, a method of inhibiting alpha4beta7 binding to cells  
XX expressing human MadCAM, a method of inhibiting MadCAM-mediated leukocyte  
XX -endothelial cell adhesion, migration and infiltration into tissues, a  
XX method of inhibiting alpha4beta7/MadCAM-dependent cellular adhesion,  
XX inhibiting the MadCAM-mediated recruitment of lymphocytes to  
XX gastrointestinal lymphoid tissue, a method of diagnosing a disorder  
XX characterized by circulating soluble human MadCAM and detecting  
XX inflammation in a subject. The antibody, composition and methods are  
XX useful for diagnosing and treating inflammatory disease, e.g.  
XX inflammatory bowel disease, Crohn's disease, ulcerative colitis,  
XX diverticular disease, gastritis, liver disease, primary biliary  
XX cirrhosis, primary sclerosing cholangitis, insulin dependent diabetes and  
XX graft versus host disease. This sequence represents a human monoclonal  
XX anti-MadCAM antibody of the invention.  
SQ Sequence 469 AA;  
Query Match 78.3%; Score 47; DB 9; Length 469;  
Best Local Similarity 77.8%; Pred. No. 15;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 3 TYYFGLDV 11  
DB 123 TYYFGMDV 131

D8		4	ANYYYGMDV 13
RESULT 12			
ID	ADW04816		
XX	ADW04816 standard; peptide; 21 AA.		
AC	ADW04816;		
DT	07-APR-2005 (first entry)		
DE	PAPP-A immunoglobulin variable domain AB b03 heavy chain CDR3 SEQ ID 141.		
XX			
KM	Cytosolic; Vasotropic; heavy chain variable domain;		
XX	proliferative disorder; restenosis; glioblastoma; osteosarcoma.		
OS	Unidentified.		
PN	US2005009136-A1.		
XX			
PD	13-JAN-2005.		
XX			
PF	19-FEB-2004; 2004US-00783311.		
XX			
PR	19-FEB-2003; 2003US-0448515P.		
XX			
PA	(DYAX-) DYAX CORP.		
PI	Nixon A, Hogan S;		
DR	WPI; 2005-080519/09.		
PT	New pregnancy-associated plasma protein-A (PAPP-A) binding proteins		
PT	comprising immunoglobulin variable domain sequences, useful for		
PT	diagnosing, preventing or treating diseases such as cancer.		
PS	Example; SEQ ID NO 141; 168pp; English.		
CC	The present invention relates to novel proteins (I) that bind to		
CC	pregnancy-associated plasma protein A (PAPP-A ADW04676). (I) comprises a		
CC	first and second immunoglobulin variable domain sequence which binds to		
CC	PAPP-A. Also claimed are proteins (II) which comprise light chain (Lc)		
CC	and heavy chain immunoglobulin variable domain sequences which binds to		
CC	PAPP-A. The proteins are useful for diagnosing, preventing or treating		
CC	proliferative diseases such as glioblastoma, osteosarcoma and overgrowth		
CC	of vascular smooth muscle cells following e.g., balloon angioplasty		
CC	(which may cause restenosis). The proteins are especially useful for		
CC	useful for treating diseases involving IGF regulated growth.The present		
CC	sequence is one such immunoglobulin variable domain sequence.		
SQ	Sequence 21 AA;		
Query Match	76.7%; Score 46; DB 9; Length 21;		
Best Local Similarity	63.6%; Pred. No. 0.83; Mismatches	2; Indels	0; Gaps
Matches	7; Conservative	2; Mismatches	0; Gaps
OY	1 LATYYFGIDV 11       :     Db 11 LGNTYYGMDV 21		
RESULT 13			
ID	ADZ41994		
XX	ADZ41994 standard; peptide; 126 AA.		
AC	ADZ41994;		
XX			
DT	30-JUN-2005 (first entry)		
XX			
DE	Ig H chain variable region, B-CLL set II peptide #4.		
KM	Antibody; antibody engineering; antibody therapy;		
KM	light chain variable region; heavy chain variable region;		

KM chronic lymphocytic leukemia; cytostatic; Hodgkins disease; lymphoma;  
 KM Burkitts lymphoma; multiple myeloma; systemic lupus erythematosus;  
 KM antinflammatory; dermatological; immunosuppressive; myasthenia gravis;  
 KM muscular-gen.; neuroprotective; Graves disease; antithyroid;  
 KM insulin dependent diabetes; diabetes mellitus; antidiabetic;  
 KM autoimmune hemolytic anemia; antianemic.  
 XX  
 OS Homo sapiens.  
 PN WO2005034733-A2.  
 XX  
 XX 21-APR-2005.  
 XX  
 XX 08-OCT-2004; 2004WO-US033176.  
 XX  
 XX 08-OCT-2003; 2003US-0509473P.  
 XX  
 PA (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.  
 PI Messner BT, Chlorazzi N, Albesiano E;  
 DR WPI; 2005-306220/31.  
 XX  
 PT New isolated and purified preparation of light chain and heavy chain  
 PT antibody genes, useful for diagnosing, preventing or treating B cell  
 PT chronic lymphocytic leukemia, or in screening for agents that may treat  
 PT such disease.  
 PS Disclosure; Fig 2; 58pp; English.  
 XX  
 CC The new invention relates to combinations of light chain antibody genes  
 CC and heavy chain antibody genes, useful for treating B cell chronic  
 CC lymphocytic leukemia (B-CLL). B-CLL is a disease of slowly proliferating  
 CC CD5+ B lymphocytes. These cells express low levels of surface membrane Ig  
 CC that serves as the receptor for antigen (BCR). Analysis of V region gene  
 CC cassette usage has shown that distribution of variable region gene  
 CC cassettes used by B-CLL clones differs from that in normal cells, with an  
 CC increased frequency of VH3-07, VH4-34, and VH1-69 genes. This implies  
 CC that the structure of the antibody molecule, and antigen specificity,  
 CC play a role in the leukemic transformation of particular B cells. The  
 CC present invention discloses that a significant proportion of VH, D, JH, VL  
 CC patients with aggressive disease share the same classes of VH, D, JH, VL  
 CC and JH antibody genes, forming sets of patients with highly homologous B  
 CC cell receptors. Alternatively, the patients have a disorder selected from  
 CC Hodgkin's disease, non-Hodgkin's lymphoma, Burkitt's lymphoma, myeloma or  
 CC systemic lupus erythematosus, myasthenia gravis, Graves' disease, type I  
 CC diabetes mellitus, autoimmune peripheral neuropathy, and autoimmune  
 CC hemolytic anemia. The new members of the antibody genes are: VH4-39/D6-  
 CC 13/JH5/VLkappa012/2/JLkappa1/kappa2 (Set I); VH4-34/D5-  
 CC 5/JH6/VLkappa012/2/JLkappa1/kappa2 (Set II); VH3-  
 CC 21/JH6/VLkappa012/2/JLkappa1/kappa2 (Set III); VH1-69/D3-  
 CC 16/JH3/VLkappa012/2/JLkappa1/kappa2 (Set IV); VH1-02/D6-  
 CC 10/JH6/VLkappa012/2/JLkappa1/kappa2 (Set V); VH1-03/D6-  
 CC 19/JH4/VLkappa012/2/JLkappa1/kappa2 (Set VI); VH1-18/D6-  
 CC 19/JH4/VLkappa012/2/JLkappa1/kappa2 (Set VII); VH1-18/D6-  
 CC 19/JH4/VLkappa012/2/JLkappa1/kappa2 (Set VIII); VH1-18/D6-  
 CC 31/JH6-19/JH4/VLkappa012/2/JLkappa1/kappa2 (Set IX); VH1-69/D3-  
 CC 3/JH4/VLkappa012/2/JLkappa1/kappa2 (Set X); and VH1-69/D2-  
 CC 2/JH6/VLkappa012/2/JLkappa1/kappa2 (Set XI).  
 CC with the above genes comprises administering an agent that binds to the  
 CC antigen-binding region of an antibody encoded by the antibody genes. The  
 CC agent is an anti-idiotypic antibody, a peptide antigen, or an aptamer. The  
 CC present sequence is an Ig H chain variable region, B-CLL set II peptide.  
 XX  
 SO Sequence 126 AA;  
 Query Match 76.7%; Score 46; DB 9; Length 126;  
 Best Local Similarity 72.7%; Pred. No. 5.6;  
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 LATYYFGIDV 11  
 DB 105 LKRYYYGLDV 115

RESULT 14  
 ADW04810  
 ID ADW04810 standard; protein; 140 AA.  
 XX  
 AC ADW04810;  
 XX  
 DT 07-APR-2005 (first entry)  
 XX  
 DE PAPP-A immunoglobulin variable domain AB b03 heavy chain SEQ ID 135.  
 XX  
 XX Cytostatic; Vasotropic; heavy chain variable domain;  
 KM proliferative disorder; restenosis; glioblastoma; osteosarcoma.  
 XX  
 OS Undefined.  
 XX  
 PN US2005009136-A1.  
 XX  
 PD 13-JAN-2005.  
 XX  
 PF 19-FEB-2004; 2004US-00763311.  
 XX  
 PR 19-FEB-2003; 2003US-0448515P.  
 XX  
 PA (DYAX-) DYAX CORP.  
 XX  
 PI Nixon A, Hogan S;  
 DR WPI; 2005-080519/09.  
 XX  
 PT New pregnancy-associated plasma protein-A (PAPP-A) binding proteins  
 PT comprising immunoglobulin variable domain sequences, useful for  
 PT diagnosing, preventing or treating diseases such as cancer.  
 PS Example; SEQ ID NO 135, 168pp; English.  
 XX  
 CC The present invention relates to novel proteins (I) that bind to  
 CC pregnancy-associated plasma protein A (PAPP-A ADW04676). (I) comprises a  
 CC first and second immunoglobulin variable domain sequence which binds to  
 CC PAPP-A. Also claimed are proteins (II) which comprise light chain (LC)  
 CC and heavy chain immunoglobulin variable domain sequences which binds to  
 CC PAPP-A. The proteins are useful for diagnosing, preventing or treating  
 CC proliferative diseases such as glioblastoma, osteosarcoma and overgrowth  
 CC of vascular smooth muscle cells following e.g., balloon angioplasty  
 CC (which may cause restenosis). The proteins are especially useful for  
 CC useful for treating diseases involving IGF regulated growth. The present  
 CC sequence is one such immunoglobulin variable domain sequence.  
 XX  
 SO Sequence 140 AA;  
 Query Match 76.7%; Score 46; DB 9; Length 140;  
 Best Local Similarity 63.6%; Pred. No. 6.3;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 LATYYFGIDV 11  
 DB 109 LGNTYYGMDV 119  
 RESULT 15  
 ADW04952  
 ID ADW04952 standard; peptide; 16 AA.  
 XX  
 AC ADW04952;  
 XX  
 DT 07-APR-2005 (first entry)  
 XX  
 DE PAPP-A immunoglobulin variable domain AB f03 heavy chain CDR3 SEQ ID 277.  
 XX  
 KM Cytostatic; Vasotropic; heavy chain variable domain;  
 KM proliferative disorder; restenosis; glioblastoma; osteosarcoma.  
 XX

OS Unidentified.

PN US2005009136-A1.

PD 13-JAN-2005.

PF 19-FEB-2004; 2004US-00783311.

PR 19-FEB-2003; 2003US-0448515P.

PA (DYAX-) DYAX CORP.

PI Nixon A, Hogan S;

DR WPI; 2005-080519/09.

PT New pregnancy-associated plasma protein-A (PAPP-A) binding proteins  
PT comprising immunoglobulin variable domain sequences, useful for  
PT diagnosing, preventing or treating diseases such as cancer.

PS Example; SEQ ID NO 277; 168bp; English.

CC The present invention relates to novel proteins (I) that bind to  
CC pregnancy-associated plasma protein A (PAP-A; AOM04676). (I) comprises a  
CC first and second immunoglobulin variable domain sequence which binds to  
CC PAP-A. Also claimed are proteins (II) which comprise light chain (LC)  
CC and heavy chain immunoglobulin variable domain sequences which bind to  
CC PAP-A. The proteins are useful for diagnosing, preventing or treating  
CC proliferative diseases such as glioblastoma, osteosarcoma and overgrowth  
CC of vascular smooth muscle cells following e.g., balloon angioplasty  
CC (which may cause restenosis). The proteins are especially useful for  
CC useful for treating diseases involving IGF regulated growth. The present  
CC sequence is one such immunoglobulin variable domain sequence.

**SQ Sequence 16 AA;**

### Query Match

## Matches

QY 1 LATYYFGLDV 11

Db 6 VAGY<sup>+</sup>Y<sup>+</sup>YGMDV 16

Db 6 VAGYTYYGMDV 16

Db 6 VAGYTYYGMDV 16

Search completed: December 4, 2005, 04:44:54  
Job time : 98.5625 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:31:45, Search time 15.583 Seconds  
(without alignments)  
67.918 Million cell updates/sec

Title: US-10-632-706-127

Sequence: 1 LATYYRGLDV 11

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 80:\*

1: PIR1:\*

2: PIR2:\*

3: PIR3:\*

4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	71.7	19	2	PH1307
2	43	71.7	23	2	PH1361
3	43	71.7	29	2	PH1328
4	43	71.7	160	2	D70189
5	43	71.7	160	2	S05271
6	43	71.7	408	2	E70380
7	42	70.0	19	2	PH1304
8	42	70.0	19	2	S43960
9	42	70.0	23	2	PH1364
10	42	70.0	24	2	PT0258
11	42	70.0	27	2	PH1371
12	42	70.0	27	2	PH1355
13	42	70.0	74	2	S26793
14	42	70.0	118	2	PH1666
15	42	70.0	119	2	PH0961
16	42	70.0	120	2	PH1650
17	42	70.0	125	2	S24686
18	42	70.0	128	2	S48797
19	42	70.0	132	2	PH0954
20	42	70.0	133	2	C33548
21	42	70.0	136	2	A49047
22	42	70.0	147	2	I37780
23	42	70.0	627	2	S14683
24	40	66.7	22	2	PH1325
25	39.5	65.8	581	2	E83729
26	39	65.0	126	2	S44107
27	39	65.0	375	2	A83788
28	38	63.3	22	2	PH1359
29	38	63.3	45	2	PL0094

30	38	63.3	287	2	T27056	hypothetical prote
31	38	63.3	473	2	H86240	hypothetical prote
32	38	63.3	979	2	A39792	transcription acti
33	37	61.7	14	2	PH1601	Ig H chain V-D-J r
34	37	61.7	126	1	MHRUOU	Ig heavy chain V-I
35	37	61.7	276	2	S16892	probable transpos
36	37	61.7	447	2	T09809	NADH2 dehydrogen
37	37	61.7	448	2	T12006	NADH2 dehydrogen
38	37	61.7	527	2	C70130	glycerol-3-phospha
39	37	61.7	571	2	A42138	conditioned medium
40	37	61.7	571	2	S24482	conditioned medium
41	37	61.7	685	2	T22223	sel-1 protein - Ca
42	36.5	60.8	120	2	R49590	Ig heavy chain V r
43	36.5	60.8	316	2	C75205	hypothetical prote
44	36	60.0	18	2	PH1368	Ig heavy chain DJ
45	36	60.0	145	2	H97707	30S ribosomal prot

#### ALIGNMENTS

##### RESULT 1

PH1307  
Ig heavy chain DJ region (clone C96-119) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C:Accession: PH1307  
R:Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
J. Exp. Med. 176, 1577-1581, 1992  
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph  
A:Reference number: PH1302; MUID:93094761; PMID:1460419  
A:Accession: PH1307  
A:Molecule type: DNA  
A:Residues: 1-19 <WAS>  
A:Cross-references: UNIPARC:UPI0000176935  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

Query Match 71.7%; Score 43; DB 2; Length 19;  
Best Local Similarity 66.7%; Pred. No. 0.23;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 TYYRGLDV 11  
DB 6 STYYRGLDV 14

##### RESULT 2

PH1361  
Ig heavy chain DJ region (clone C178-122B) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C:Accession: PH1361  
R:Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
J. Exp. Med. 176, 1577-1581, 1992  
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph  
A:Reference number: PH1302; MUID:93094761; PMID:1460419  
A:Accession: PH1361  
A:Molecule type: DNA  
A:Residues: 1-23 <WAS>  
A:Cross-references: UNIPARC:UPI0000176948  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

Query Match 71.7%; Score 43; DB 2; Length 23;  
Best Local Similarity 63.6%; Pred. No. 0.28;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LATYYRGLDV 11  
DB 8 LFPYYRGLDV 18

RESULT 3  
PH1328  
Ig heavy chain DJ region (clone C113-148) - human (fragment)  
A:Residues: 1-144 <KIS2>  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C:Accession: PH1328  
R:Masserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
J. Exp. Med. 176, 1577-1581, 1992  
A:Title: Predominance of fetal type DH joining in young children with B precursor lymph  
A:Reference number: PH1302; MUID:93094761; PMID:1460419  
A:Accession: PH1328  
A:Molecule type: DNA  
A:Residues: 1-29 <MAS>  
A:Cross-references: UNIPARC:UPI0000176939  
C:Superfamily: immunoglobulin V region; immunoglobulin  
C:Keywords: heterotrimer; immunoglobulin

Query Match 71.7%; Score 43; DB 2; Length 29;  
Best Local Similarity 66.7%; Pred. No. 0.36;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYTFFGLDV 11  
:||||:|  
Db 16 STYYGMDV 24

RESULT 4  
D70189  
conserved hypothetical integral membrane protein B90717 - Lyme disease spirochete  
C:Species: Borrelia burgdorferi (Lyme disease spirochete)  
C:Date: 13-Feb-1998 #sequence\_revision 13-Feb-1998 #text\_change 09-Jul-2004  
C:Accession: D70189  
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White  
son, D.; Peterson, J.; Kirlavaga, A.R.; Quackenbush, J.; Salberg, S.; Hanson, M.; Vugt,  
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.  
Nature 390, 580-586, 1997  
A:Authors: Smith, H.O.; Venter, J.C.  
A:Title: Genomic sequence of a Lyme disease spirochete, *Borrelia burgdorferi*.  
A:Reference number: A70100; MUID:98055943; PMID:9403685  
A:Accession: D70189  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-160 <KLB>  
A:Cross-references: UNIPROT:O51659; UNIPARC:UPI0000575B2; GB:AE001171; GB:AE000783; NID  
A:Experimental source: strain B31

Query Match 71.7%; Score 43; DB 2; Length 160;  
Best Local Similarity 60.0%; Pred. No. 2;  
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATYYTFFGLDV 11  
:||||:|  
Db 23 ATYYTFFGLDV 32

RESULT 5  
S05271  
Ig heavy chain precursor - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 31-Dec-2004  
C:Accession: S05271; S04602  
R:Kishimoto, T.  
submitted to the EMBL Data Library, March 1989  
A:Reference number: S05270  
A:Accession: S05271  
A:Molecule type: mRNA  
A:Residues: 1-160 <KIS1>  
A:Cross-references: UNIPROT:Q96B89; UNIPARC:UPI0000176B50; EMBL:X14584  
R:Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.  
Nucleic Acids Res. 17, 4385, 1989  
A:Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of  
A:Reference number: S04601; MUID:89296497; PMID:2500644  
A:Accession: S04602

A:Molecule type: mRNA  
A:Residues: 1-144 <KIS2>  
A:Cross-references: UNIPARC:UPI0000176B51; EMBL:X14584  
C:Superfamily: immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-160/Product: Ig heavy chain (fragment) #status predicted <MAT>  
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 71.7%; Score 43; DB 2; Length 160;  
Best Local Similarity 66.7%; Pred. No. 2;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYTFFGLDV 11  
:||||:|  
Db 125 STYYGMDV 133

RESULT 6  
E70380  
Na+/H+-exchanging protein - Aquifex aeolicus  
N:Alternate names: Na+/H+ antiporter  
C:Species: Aquifex aeolicus  
C:Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 09-Jul-2004  
C:Accession: E70380  
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ove  
V.  
Nature 392, 353-358, 1998  
A:Title: The complete genome of the hyperthermophilic bacterium *Aquifex aeolicus*.  
A:Reference number: A70300; MUID:98196666; PMID:9537320  
A:Accession: E70380  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-408 <AQF>  
A:Cross-references: UNIPROT:O67072; UNIPARC:UPI00000564AB; GB:AE000714; NID:G2983446; PIR  
A:Experimental source: strain VFS  
A:Genetics:  
A:Gene: napA2  
C:Superfamily: Aquifex aeolicus Na+/H+-exchanging protein napA1

Query Match 71.7%; Score 43; DB 2; Length 408;  
Best Local Similarity 54.5%; Pred. No. 5.2;  
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 LATYYTFFGLDV 11  
:||||:|  
Db 116 IVSYTFFGLDV 126

RESULT 7  
PH1304  
Ig heavy chain DJ region (clone C439-111) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C:Accession: PH1304  
R:Masserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
J. Exp. Med. 176, 1577-1581, 1992  
A:Title: Predominance of fetal type DH joining in young children with B precursor lymph  
A:Reference number: PH1302; MUID:93094761; PMID:1460419  
A:Accession: PH1304  
A:Molecule type: DNA  
A:Residues: 1-19 <MAS>  
A:Cross-references: UNIPARC:UPI0000176934  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin

Query Match 70.0%; Score 42; DB 2; Length 19;  
Best Local Similarity 75.0%; Pred. No. 0.35;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYTFFGLDV 11  
:||||:|  
Db 7 YYYTFFGLDV 14

## RESULT 8

S43960  
Ig mu chain V region (clone 18) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 20-Oct-1994 #sequence\_revision 26-Jul-1996 #text\_change 17-Mar-1999  
C:Accession: S43960  
R:Wagner, S.D.; Williams, G.T.; Larson, T.; Neuberger, M.S.; Kitamura, D.; Rajewsky, K.;  
Nucleic Acids Res. 22, 1389-1393, 1994  
A:Title: Antibodies generated from human immunoglobulin miniloci in transgenic mice.  
A:Reference number: S43956; MUID:94248036; PMID:8190629  
A:Accession: S43960  
A:Molecule type: DNA  
A:Residues: 1-19 <WAS>  
A:Cross-references: UNIPARC:UPI000017690D  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: immunoglobulin

Query Match 70.0%; Score 42; DB 2; Length 19;  
Best Local Similarity 75.0%; Pred. No. 0.35;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11  
|||:|:  
DB 10 YYYGMDV 17

## RESULT 9

PH1364  
Ig heavy chain DJ region (clone C178-136A) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C:Accession: PH1364  
R:Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
J. Exp. Med. 176, 1577-1581, 1992  
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph  
A:Reference number: PH1302; MUID:93094761; PMID:1460419  
A:Accession: PH1364  
A:Molecule type: DNA  
A:Residues: 1-23 <WAS>  
A:Cross-references: UNIPARC:UPI0000176949  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

Query Match 70.0%; Score 42; DB 2; Length 23;  
Best Local Similarity 75.0%; Pred. No. 0.42;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11  
|||:|:  
DB 11 YYYGMDV 18

## RESULT 10

PT0258  
Ig heavy chain CDR3 region (clone 2-118B) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 30-May-1997  
C:Accession: PT0258  
R:Itamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.V.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and  
A:Reference number: PT0222; MUID:91108337; PMID:1899102  
A:Accession: PT0258  
A:Molecule type: DNA  
A:Residues: 1-24 <WAS>  
A:Cross-references: UNIPARC:UPI0000176940  
A:Experimental source: B lymphocyte  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

Query Match 70.0%; Score 42; DB 2; Length 24;

Best Local Similarity 75.0%; Pred. No. 0.44;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11  
|||:|:  
DB 12 YYYGMDV 19

## RESULT 11

PH1371  
Ig heavy chain DJ region (clone C111-145) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C:Accession: PH1371  
R:Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
J. Exp. Med. 176, 1577-1581, 1992  
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph  
A:Reference number: PH1302; MUID:93094761; PMID:1460419  
A:Accession: PH1371  
A:Molecule type: DNA  
A:Residues: 1-27 <WAS>  
A:Cross-references: UNIPARC:UPI000017694B  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

Query Match 70.0%; Score 42; DB 2; Length 27;  
Best Local Similarity 75.0%; Pred. No. 0.5;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11  
|||:|:  
DB 15 YYYGMDV 22

## RESULT 12

PH1355  
Ig heavy chain DJ region (clone C100-136) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C:Accession: PH1355  
R:Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
J. Exp. Med. 176, 1577-1581, 1992  
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph  
A:Reference number: PH1302; MUID:93094761; PMID:1460419  
A:Accession: PH1355  
A:Molecule type: DNA  
A:Residues: 1-27 <WAS>  
A:Cross-references: UNIPARC:UPI0000176945  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

Query Match 70.0%; Score 42; DB 2; Length 27;  
Best Local Similarity 75.0%; Pred. No. 0.5;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11  
|||:|:  
DB 15 YYYGMDV 22

## RESULT 13

S26793  
Ig heavy chain V region - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Jun-2000  
C:Accession: S26793  
R:Morcari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.  
Eur. J. Immunol. 22, 241-245, 1992  
A:Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene fam  
A:Reference number: S26786; MUID:92111632; PMID:1730251  
A:Accession: S26793  
A>Status: preliminary  
A:Molecule type: mRNA

A:Residues: 1-74 <MOR>  
 A:Cross-references: UNIPARC:UPI0000115FCA; EMBL:X61019; NID:g32787; PIDN:CAA43353.1; PID  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin

Query Match 70.0%; Score 42; DB 2; Length 74;  
 Best Local Similarity 75.0%; Pred. No. 1.4;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 4 YYYFGLDV 11  
 |||:|:|  
 Db 56 YYYGMDV 63

## RESULT 14

PH1666  
 Ig heavy chain V region (clone 6C9) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 16-Aug-1996  
 C:Accession: PH1666  
 R:Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.  
 J. Exp. Med. 178, 331-336, 1993  
 A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylo  
 A:Reference number: PH1642; MUID:93301610; PMID:8315388  
 A:Accession: PH1666  
 A:Molecule type: mRNA  
 A:Residues: 1-118 <HIL>  
 A:Cross-references: UNIPARC:UPI0000176BE7  
 A:Experimental source: B cell  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 70.0%; Score 42; DB 2; Length 118;  
 Best Local Similarity 75.0%; Pred. No. 2.2;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 4 YYYFGLDV 11  
 |||:|:|  
 Db 100 YYYGMDV 107

## RESULT 15

PH0961  
 Ig heavy chain V region (G6+ T-133) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996  
 C:Accession: PH0961  
 R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.  
 J. Exp. Med. 175, 983-991, 1992  
 A:Title: Evidence for somatic selection of natural autoantibodies.  
 A:Reference number: PH0952; MUID:92202860; PMID:1552291  
 A:Accession: PH0961  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: DNA  
 A:Residues: 1-119 <MAR>  
 A:Cross-references: UNIPARC:UPI0000176CE5  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:1-30/Region: framework 1  
 F:15-98/Domain: immunoglobulin homology <IMM>  
 F:31-35/Region: complementarity-determining 1  
 F:36-50/Region: framework 2  
 F:51-67/Region: complementarity-determining 2  
 F:68-98/Region: framework 3  
 F:99-107/Region: complementarity-determining 3

Query Match 70.0%; Score 42; DB 2; Length 119;  
 Best Local Similarity 75.0%; Pred. No. 2.2;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 4 YYYFGLDV 11  
 |||:|:|

Db 101 YYYGMDV 108

Search completed: December 4, 2005, 04:53:32  
 Job time : 17.5833 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:31:36 ; Search time 100.375 Seconds  
(without alignments)  
77.318 Million cell updates/sec

Title: US-10-632-706-127  
Perfect score: 60  
Sequence: 1 LATYTFGLDV 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot 05.80: \*  
1: uniprot\_sprot: \*  
2: uniprot\_crembl: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	44	73.3	1348	2	Q4N9V2_THEPA	Q4N9V2 thelteria p
2	44	73.3	2262	2	Q4U9Y8_THEPA	Q4U9Y8 thelteria a
3	43	71.7	160	2	O51659_BORBU	O51659 borrelia bu
4	43	71.7	160	2	O660F6_BORGA	O660F6 borrelia ga
5	43	71.7	408	2	O67072_AOUAE	O67072 aquifex aeo
6	42	70.0	364	2	O7VY71_BORBP	O7VY71 borrelia
7	42	70.0	364	2	O7W926_BORBP	O7W926 borrelia
8	42	70.0	364	2	O7W926_BORBP	O7W926 borrelia
9	42	70.0	364	2	O7W926_BORBP	O7W926 borrelia
10	42	70.0	378	2	O4QAI0_LEIMA	O4QAI0 leishmania
11	42	70.0	382	2	O89NT9_BRAJA	O89NT9 bradyrhizob
12	42	70.0	594	2	O74N07_NAMEO	O74N07 nanoarchaeu
13	42	70.0	606	2	O6GMY2_HUMAN	O6GMY2 homo sapien
14	42	70.0	1062	2	O96X97_SUITO	O96X97 sulfolobus
15	42	70.0	3212	2	O4FWX4_LEIMA	O4FWX4 leishmania
16	41	68.3	716	2	O6A021_DESPS	O6A021 desulfocale
17	40	66.7	288	2	O6F6N6_ACIAD	O6F6N6 acinetobact
18	40	66.7	291	2	O4RUB1_PSEBY	O4RUB1 pseudomonas
19	40	66.7	293	2	O6D023_ERWCT	O6D023 erwina car
20	40	66.7	447	2	O8EU78_OCRTH	O8EU78 oceanobacil
21	40	66.7	702	2	O8C3X8_MOUSE	O8C3X8 mus musculu
22	40	66.7	978	2	O5AAV6_CANAL	O5AAV6 candida alb
23	40	66.7	1113	2	O6WE05_ARALY	O6WE05 arabidopsis
24	40	66.7	3964	2	O4OBV4_LEIMA	O4OBV4 leishmania
25	39	65.0	581	1	Y637_BRCHD	O9K449 bacillus ha
26	39	65.0	188	2	O52G31_MAGGR	O52G31 magnaporthe
27	39	65.0	215	2	O51X02_NOCFA	O51X02 nocardia fa
28	39	65.0	317	2	O97BK3_THERVO	O97BK3 thermoplaem
29	39	65.0	375	2	O9KDV6_BACDH	O9KDV6 bacillus ha
30	39	65.0	419	2	O82700_MEDTR	O82700 medicago tr
31	39	65.0	423	2	O9S7A5_MEDTR	O9S7A5 medicago tr
			434	2	O6ZBX7_ORISA	O6ZBX7 oryza sativ

32	39	65.0	451	2	O6ZBX6_ORISA	O6ZBX6 oryza sativ
33	39	65.0	478	2	O6F181_HUMAN	O6F181 homo sapien
34	39	65.0	662	2	O88RT5_LACPL	O88RT5 lactobacill
35	39	65.0	701	1	LSP2_DROME	O24388 drosophila
36	39	65.0	779	2	O65821_MANSM	O65821 mantheimia
37	39	65.0	780	2	O7VOH6_CANBF	O7VOH6 candidatus
38	38	63.3	116	2	O723Y6_HUMAN	O723Y6 homo sapien
39	38	63.3	148	2	O5TMX6_HUMAN	O5TMX6 anophelis g
40	38	63.3	159	2	O96QSO_HUMAN	O96QSO homo sapien
41	38	63.3	239	2	O5X0G3_LEGPL	O5X0G3 legionella
42	38	63.3	243	2	O5Z2F4_LEGPH	O5Z2F4 legionella
43	38	63.3	307	2	O6NSD3_RHOPA	O6NSD3 rhodospseudo
44	38	63.3	350	2	O8TVT5_METKA	O8TVT5 methanopyru
45	38	63.3	366	2	O9XTT1_CABEL	O9XTT1 caenorhabdi

## ALIGNMENTS

```
RESULT 1
Q4N9V2_THEPA PRELIMINARY; PRT; 1348 AA.
AC Q4N9V2;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=TP01_0021;
OS Theileria parva.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
OC Theileria.
OX NCBI_Taxid=5875;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RP STRAIN=Muguga;
RA Gardner M.J., Bishop R., Shah T., de Villiers E.P., Carlton J.M.,
RA Hall N., Ren O., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M.,
RA Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J.,
RA Jiang L., Lynn J., Weaver B., Shoib A., Masawo D., Crabtree J.,
RA Wortman J.R., Haas B., Angiuoli S.V., Creasy T.H., Lu C., Suh B.,
RA Silva J.C., Utecherback T.R., Feldblyum T.H., Pertea M., Allen J.,
RA Taracha E.L.N., Salzberg S.L., White O.R., Fitzhugh H.A., Morzaria S.,
RA Venter J.C., Frazer C.M., Nene V.;
RA "Genome sequence of Theileria parva, a bovine pathogen that transforms
RT lymphocytes.";
RL Science 309:134-137(2005).
RN [2]
RC NUCLEOTIDE SEQUENCE.
RP STRAIN=Muguga;
RA Gardner M., Bishop R., Shah T., de Villiers E., Carlton J.M., Hall N.,
RA Ren O., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,
RA Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J., Jiang L.,
RA Lynn J., Weaver B., Shoib A., Masawo D., Crabtree J., Wortman J.R.,
RA Haas B., Angiuoli S., Creasy T.H., Lu C., Suh B., Silva J.C.,
RA Utecherback T., Feldblyum T., Pertea M., Allen J., Taracha E.L.,
RA Salzberg S.L., Nene V., White O., Fitzhugh H.A., Morzaria S., Venter J.C.,
RA Frazer C.M., Nene V.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAGK0100001; EMBL3265.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 1348 AA; 155635 MW; 474C3A40C23E8C5F CRC64;

Query Match 73.3%; Score 44; DB 2; Length 1348;
Best Local Similarity 87.5%; Pred. No. 60;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
RESULT 2
Q4UFY8 THEAN
ID Q4UFY8 THEAN PRELIMINARY; PRT; 2262 AA.
AC Q4UFY8
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=TA19710;
OS Theileria annulata.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
OC Theileria.
OX NCBI_TaxID=5874;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ankara isolate clone C9;
RA Pain A., Renaud H., Murphy L., Harris D.A., Quail M.A., Berriman M.,
RA Hall N., Barrett B.G.;
RT "The chromosome 1 sequence of Theileria annulata."
RL Submitted (Apr-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR940347; CA174001.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ
SEQUENCE 2262 AA; 262068 MW; FD9E8915243EF512 CRC64;

Query Match
Best Local Similarity 73.3%; Score 44; DB 2; Length 2262;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTYFFGLD 10
Db 1244 SYTYFFGLD 1251

RESULT 3
O51659 BORBU
ID O51659 BORBU PRELIMINARY; PRT; 160 AA.
AC O51659;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Conserved hypothetical integral membrane protein.
GN OrderedLocustNames=B80711;
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia;
OC Borrelia burgdorferi group.
OX NCBI_TaxID=139;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 35210 / B31;
RA MEDLINE=98065943; PubMed=9403685; DOI=10.1038/37551;
RA Fraser C.M., Castles S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Lathigra R., White O., Ketchum K.A., Dodson R.J., Hickey E.K.,
RA Gwinn M.L., Dougherty B.A., Tomb J.-F., Fleischmann R.D.,
RA Richardson D.L., Peterson J.D., Kertland A.R., Quackenbush J.,
RA Salzberg S.L., Hanson M., Van Vugt R., Palmer N., Adams M.D.,
RA Gocayne J.D., Weidman J.F., Utterback T.R., Matthews L., McDonald L.A.,
RA Artach P., Bowman C., Garland S.A., Fujii C., Cotton M.D., Horek K.,
RA Roberts K.W., Hatch B., Smith H.O., Venter J.C.;
RT "Genomic sequence of a Lyme disease spirochaete, Borrelia
burgdorferi."
RL Nature 390:580-586(1997).
DR EMBL; AE001171; AAC67057.1; -; Genomic_DNA.
DR PIR; D70189; D70189.
KW Complete proteome; Hypothetical protein.
SQ
SEQUENCE 160 AA; 19300 MW; 9DE28A497C0F5737 CRC64;

Query Match
Best Local Similarity 71.7%; Score 43; DB 2; Length 160;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ATYYFGLDV 11
Db 23 ATYYFGLDV 11
```

```
Db 23 ATYYFSDI 32

RESULT 4
O660F6 BORGA
ID O660F6 BORGA PRELIMINARY; PRT; 160 AA.
AC O660F6;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Conserved hypothetical integral membrane protein.
GN OrderedLocustNames=BG0739;
OS Borrelia garinii.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia;
OC Borrelia burgdorferi group.
OX NCBI_TaxID=29519;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PB1;
RA Gloeckner G., Lehmann R., Romualdi A., Pradella S.,
RA Schulte-Spechtel U., Wilske B., Suenkel J., Platzer M.;
RT "Comparative analysis of the Borrelia garinii genome."
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000013; AAU07565.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ
SEQUENCE 160 AA; 19293 MW; B5B15C5197FB89 CRC64;

Query Match
Best Local Similarity 71.7%; Score 43; DB 2; Length 160;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ATYYFGLDV 11
Db 23 ATYYFSDI 32

RESULT 5
O67072 AQUAE
ID O67072 AQUAE PRELIMINARY; PRT; 408 AA.
AC O67072;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Na(+)/H(+) antiporter.
GN Name=npa2; OrderedLocustNames=AQ_929;
OS Aquifex aeolicus.
OC Aquifex; Aquificae; Aquificales; Aquificaceae; Aquifex.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VF5;
RA MEDLINE=98196666; PubMed=9537320; DOI=10.1038/32831;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Gehlman D.E., Overbeek R., Sneed M.A., Kallier M., Aujay M., Huber R.,
RA Feldman R.A., Short J.M., Olsen G.J., Sanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
aeolicus."
RL Nature 392:353-358(1998).
DR EMBL; AE000714; AAC07034.1; -; Genomic_DNA.
DR PIR; E70380; E70380.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0015299; F:isolate;hydrogen antiporter activity; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006153; Na_H_porter.
DR Pfam; PF00999; Na_H_Exchange; 1.
KW Complete proteome; Transmembrane; Transport.
SQ
SEQUENCE 408 AA; 43582 MW; 7E05B4B387A6C506 CRC64;

Query Match
Best Local Similarity 71.7%; Score 43; DB 2; Length 408;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 LATYVFGADV 11
    : : : : :
Db 116 IVSYVFGDL 126

RESULT 6
Q7VY71 BORPE PRELIMINARY; PRT; 364 AA.
ID Q7VY71 BORPE PRELIMINARY; PRT; 364 AA.
AC Q7VY71;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, last annotation update)
DE Putative periplasmic solute-binding protein.
GN Name=sbmw; OrderedLocNames=Bp1487;
OS Bordetella pertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=520;
KW [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebathia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Felwell T., Goble A., Hamlin N., Hauser H., Holtroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640415; CAB37248.1; -; Genomic DNA.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006311; Tat.
DR InterPro; IPR004682; TRAP_transpDctP.
DR Pfam; PF03480; SBP_bac_7_1.
DR TIGRFAMs; TIGR01409; TAT_signal_seq; 1.
KW Complete proteome.
SQ SEQUENCE 364 AA; 40021 MW; 03F1C2B6FCS1D502 CRC64;

Query Match 70.0%; Score 42; DB 2; Length 364;
Best Local Similarity 77.8%; Pred. No. 38;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATYVYFGDL 10
    : : : : :
Db 98 ASYVYFGKD 106

RESULT 7
Q7W926 BORPA PRELIMINARY; PRT; 364 AA.
ID Q7W926 BORPA PRELIMINARY; PRT; 364 AA.
AC Q7W926;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, last annotation update)
DE Putative periplasmic solute-binding protein.
GN Name=sbmw; OrderedLocNames=Bp1948;
OS Bordetella parapertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=519;
KW [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=12822 / ATCC BAA-587;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebathia M., Preston A., Murphy L.D., Thomson N.R.,
```

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RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Felwell T., Goble A., Hamlin N., Hauser H., Holtroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640428; CAB37248.1; -; Genomic DNA.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006311; Tat.
DR InterPro; IPR004682; TRAP_transpDctP.
DR Pfam; PF03480; SBP_bac_7_1.
DR TIGRFAMs; TIGR01409; TAT_signal_seq; 1.
KW Complete proteome.
SQ SEQUENCE 364 AA; 39967 MW; 9700BC4608CFID8 CRC64;

Query Match 70.0%; Score 42; DB 2; Length 364;
Best Local Similarity 77.8%; Pred. No. 38;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATYVYFGDL 10
    : : : : :
Db 98 ASYVYFGKD 106

RESULT 8
Q7WKH1 BORBR PRELIMINARY; PRT; 364 AA.
ID Q7WKH1 BORBR PRELIMINARY; PRT; 364 AA.
AC Q7WKH1;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, last annotation update)
DE Putative periplasmic solute-binding protein.
GN Name=sbmw; OrderedLocNames=BB2116;
OS Bordetella bronchiseptica (Alcaligenes bronchiseptica).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=518;
KW [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=RB50 / ATCC BAA-588;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebathia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Felwell T., Goble A., Hamlin N., Hauser H., Holtroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640443; CAB37248.1; -; Genomic DNA.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006311; Tat.
DR InterPro; IPR004682; TRAP_transpDctP.
DR Pfam; PF03480; SBP_bac_7_1.
DR TIGRFAMs; TIGR01409; TAT_signal_seq; 1.
KW Complete proteome.
SQ SEQUENCE 364 AA; 39997 MW; 8AB672BA3BF09AD CRC64;

Query Match 70.0%; Score 42; DB 2; Length 364;
Best Local Similarity 77.8%; Pred. No. 38;
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Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 Qy 2 ATYYFGLD 10  
 |:|||||  
 Db 98 ASYYFGKD 106

## RESULT 9

Q4QA10 LEIMA  
 ID Q4QA10 LEIMA PRELIMINARY; PRT; 378 AA.

AC Q4QA10 13-SEP-2005 (TREMBLrel. 31, Created)  
 DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)  
 DE Hypothetical protein.  
 DE Hypothetical protein.  
 CN ORFNames=LmjF25.0840;  
 OS Leishmania major.  
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.  
 OX NCBI\_TaxID=5664;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Friedlin;  
 RA Pearce C.S., Murphy L., Ivens A.C., Berriman M., Blackwell J.,  
 RA Smith D., Collins M., Foster N., Harris D., Oliver K., O'Neill S.,  
 RA Saunders D., Seeger K., Warren T., Rajandream M., and Barrell B.G.;  
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; CTO05264; CAJ04989.1; -; Genomic\_DNA.  
 KW Hypothetical protein.  
 SQ SEQUENCE 378 AA; 41605 MW; 9EBBF7C1CF04833 CRC64;

Query Match 70.0%; Score 42; DB 2; Length 378;  
 Best Local Similarity 100.0%; Pred. No. 40;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTYRFG 9  
 |||||  
 Db 112 TTYRFG 118

## RESULT 10

Q89NT9 BRAJA  
 ID Q89NT9 BRAJA PRELIMINARY; PRT; 382 AA.

AC Q89NT9 01-JUN-2003 (TREMBLrel. 24, Created)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
 DE Periplasmic mannitol-binding protein.  
 DE Periplasmic mannitol-binding protein.  
 GN Ordered locus names=blj3745;  
 OS Bradyrhizobium japonicum.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Bradyrhizobiales; Bradyrhizobium.  
 OX NCBI\_TaxID=375;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=USDA 110;  
 RX MEDLINE=2248498; PubMed=12597275;

RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiyama T.,  
 RA Saenomo S., Matsunaga A., Ideasa K., Iritoguchi M., Kawashima K.,  
 RA Kohara M., Watanabe M., Shimo S., Tsunokawa H., Wada T., Yamada M.,  
 RA Tabata S.;  
 RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium  
 RT Bradyrhizobium japonicum USDA110.";  
 RL DNA Res. 9:189-197 (2002).

DR EMBL; BA000040; BAC49010.1; -; Genomic\_DNA.  
 DR GO; GO:0003288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR006311; Tac.  
 DR InterPro; IPR004682; TRAP\_transpDctP.  
 DR Pfam; PF03480; SBP\_bac 7.1.

DR TIGRfam; TIGR01405; TAT\_signal\_seq; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 382 AA; 42090 MW; 23C26498A9F9B8D CRC64;

Query Match 70.0%; Score 42; DB 2; Length 382;  
 Best Local Similarity 77.8%; Pred. No. 40;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ATYYFGLD 10  
 |:|||||  
 Db 117 ASYYFGKD 125

## RESULT 11

Q7AN07 NANEQ  
 ID Q7AN07 NANEQ PRELIMINARY; PRT; 594 AA.

AC Q7AN07 05-JUL-2004 (TREMBLrel. 27, Created)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DE NEQ353.  
 DE NEQ353.  
 GN Ordered locus names=NEQ353;  
 OS Nanoarchaeum equitans.  
 OC Archaea; Nanoarchaeota; Nanoarchaeum.  
 OX NCBI\_TaxID=160232;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=Kin4-M;  
 RX PubMed=1456062; DOI=10.1073/pnas.1735403100;  
 RA Waters E., Hohn M.J., Abel I., Graham D.E., Adams M.D., Barnstead M.,  
 RA Beeson K.Y., Bibbs L., Bolanos R., Keller M., Kretz K., Lin X.,  
 RA Mathur E., Ni J., Podar M., Richardson T., Sutton G.G., Simon M.,  
 RA Soell D., Stetter K.O., Short J.M., Noordvliet M.;  
 RT "The genome of Nanoarchaeum equitans: insights into early archaeal  
 RT evolution and derived parasitism."  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:12984-12988 (2003).  
 DR EMBL; AE017199; AAR39202.1; -; Genomic\_DNA.  
 KW Complete proteome.  
 SQ SEQUENCE 594 AA; 69673 MW; FD2E60ACF00CD9F4 CRC64;

Query Match 70.0%; Score 42; DB 2; Length 594;  
 Best Local Similarity 54.5%; Pred. No. 62;  
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LATYYFGLDV 11  
 |:|||||  
 Db 569 LSRHYFGVDI 579

## RESULT 12

Q6GMV2 HUMAN  
 ID Q6GMV2 HUMAN PRELIMINARY; PRT; 606 AA.

AC Q6GMV2 05-JUL-2004 (TREMBLrel. 27, Created)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DE IGHM protein.  
 DE IGHM protein.  
 GN Name=IGHM;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;

DR Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 DR Klausner R.D., Collins F.S., Wagner L., Schein C.M., Schuler G.D.,  
 DR Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usslin T.B., Toshikiyuki S., Carinici P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,



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RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallue D.E.,
RA Scherach A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073758; AAH73758.1; -; mRNA.
DR SMR; O6GM2; 20-256.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 606 AA; 66185 MW; B6B3B51114E4C55 CRC64;

Query Match 70.0%; Score 42; DB 2; Length 606;
Best Local Similarity 75.0%; Pred. No. 63;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Cy 4 YYYEGLDV 11
Db 135 YYYGMDV 142

RESULT 13
O96X97.SULTO PRELIMINARY; PRT; 1062 AA.
ID O96X97;
AC O96X97;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 1062aa long hypothetical thermopsin.
GN OrderedLocustNames=ST72615;
OS Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=111955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JCM 10545 / ?;
RX MEDLINE=21456156; PubMed=11572479;
RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
RA Nagai Y., Nishijima K., Otuka R., Nakazawa J., Takamiya M., Kato Y.,
RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
RA Oshima T., Kikuchi H.;
RT "Complete genome sequence of an aerobic thermophilic
RT Crenarchaeon, Sulfolobus tokodaii strain7."
RL DNA Res. 8:123-140(2001).
DR EMBL; BA000023; BAB67731.1; -; Genomic_DNA.
DR InterPro; IPR007961; Peptidase_A5.
DR Pfam; PF05317; Thermopsin; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 1062 AA; 118024 MW; 16FAED60A040DB4 CRC64;

Query Match 70.0%; Score 42; DB 2; Length 1062;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 3 TYYFGGL 9
Db 623 TYYFGGL 629

RESULT 14
O4FMX4.LEIMA PRELIMINARY; PRT; 3212 AA.
ID O4FMX4;
AC O4FMX4;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=LMU_1075;
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Friedlin; DOI=10.1126/science.1112660;
RX PubMed=16020728; DOI=10.1126/science.1112660;
RA Ivens A.C., Peacock C.S., Worthey E.A., Murphy L., Aggarwal G.,
RA Berriman M., Siak E., Rajandream M.A., Adlem E., Aert R., Anupama A.,
RA Apostolou Z., Attipoe P., Baeson N., Bauser C., Beck A., Beverley S.M.,
RA Bianchetti G., Borzym K., Bothe G., Brusch C.V., Collins M.,
RA Cadag E., Clarion L., Clayton C., Coulson R.M., Cronin A., Cruz A.K.,
RA Davies R.M., De Gaudenzi J., Dobson D.E., Duesterhoeft A.,
RA Fazelina G., Foster N., Frasch A.C., Fraser A., Fuchs M., Gabel C.,
RA Goble A., Goffeau A., Harris D., Hertz-Fowler C., Hilbert H., Horn D.,
RA Huang Y., Klages S., Knights A., Kube M., Larke N., Livy L.,
RA Lord A., Louie T., Marra M., Masuy D., Mathews K., Michael S.,
RA Mottier J.C., Muller-Auer S., Munden H., Nelson S., Norbertczak H.,
RA Olliver K., O'Neill S., Pentony M., Pohl T.M., Price C., Purnelle B.,
RA Quail M.A., Rabinowitch E., Reinhardt R., Rieger M., Rinta J.,
RA Robben J., Robertson L., Ruiz J.C., Rutter S., Saunders D.,
RA Schaefer M., Schein J., Schwartz D.C., Seeger K., Seyler A., Sharp S.,
RA Shin H., Sivan D., Squares R., Squares S., Toato V., Vogt C.,
RA Voickaert G., Wambut R., Warren T., Wedler H., Woodward J., Zhou S.,
RA Zimmermann W., Smith D.F., Blackwell J.M., Stuart K.D., Barrell B.,
RA Myler P.J.;
RT "The genome of the Kinetoplastid Parasite, Leishmania major."
RL Science 309:436-442(2005).
DR EMBL; CP000081; AA214369.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 3212 AA; 342958 MW; E26EA125060F8A6B CRC64;

Query Match 70.0%; Score 42; DB 2; Length 3212;
Best Local Similarity 70.0%; Pred. No. 3.3e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Cy 1 LATYYFGLD 10
Db 164 LAGYYFGVE 173

RESULT 15
O6AQZ1.DESPS PRELIMINARY; PRT; 716 AA.
ID O6AQZ1;
AC O6AQZ1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Related to mercuric reductase.
GN OrderedLocustNames=DP0504;
OS Desulfotalea psychrophila.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacterales;
OC Desulfobulbaceae; Desulfotalea.
OX NCBI_TaxID=84980;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=LSV54 / DSM 12343;
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RX PubMed=15305914; DOI=10.1111/j.1462-2920.2004.00665.x;  
RA Rabus R., Ruepp A., Frickey T., Rattei T., Fartmann B., Stark M.,  
RA Bauer M., Zibat A., Lombardot T., Becker I., Amann U., Gellner K.,  
RA Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R.,  
RA Klenk H.-P.,  
RT "The genome of Desulfocala psychrophila, a sulfate-reducing bacterium  
from permanently cold Arctic sediments.";  
RL Environ. Microbiol. 6:887-902(2004).  
DR EMBL: CR522870; CAC35233.1; -; Genomic DNA.  
DR GO: GO:0005737; C:cytoplasm; IEA.  
DR GO: GO:0015036; F:disulfide oxidoreductase activity; IEA.  
DR GO: GO:0050660; F:FAD binding; IEA.  
DR GO: GO:0006118; P:electron transport; IEA.  
DR InterPro: IPR001327; FAD\_pyr\_redox.  
DR InterPro: IPR000815; Hg\_reductase.  
DR InterPro: IPR006162; Ppantc S.  
DR InterPro: IPR001100; Pyr\_redox.  
DR InterPro: IPR004093; Pyr\_redox\_dim.  
DR Pfam: PF00070; Pyr\_redox; 2.  
DR Pfam: PF02852; Pyr\_redox\_dim; 1.  
DR PRINTS: PR00368; FADPNR.  
DR PRINTS: PR00945; HGRDTRASE.  
DR PRINTS: PR00411; PNDRTASEI.  
DR ProDom: PD000139; FAD\_pyr\_redox; 1.  
DR PROSITE: PS00012; PHOSPHOPANTETHEINE; UNKNOWN\_1.  
DR PROSITE: PS00076; PYRIDINE\_REDOX\_1; 1.  
KM Complete proteome.  
SQ SEQUENCE 716 AA; 78725 MW; 68EFC0600DE44094 CRC64;

Query Match 68.3%; Score 41; DB 2; Length 716;  
Best Local Similarity 60.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 LATYVFGLD 10  
Db 14 VSATYFGLD 23

Search completed: December 4, 2005, 04:52:20  
Job time : 104.375 secs

GenCore version 5.1.6  
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## OM protein - protein search, using SW model

Run on: December 4, 2005, 03:59:51 ; Search time 23.6042 Seconds  
(without alignments)  
38.528 Million cell updates/sec

Title: US-10-632-706-127

Perfect score: 60

Sequence: 1 LATYYFGIDV 11

## Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

## Database :

Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/aa/5 COMB.pep:\*  
2: /cgn2\_6/prodata/1/aa/6 COMB.pep:\*  
3: /cgn2\_6/prodata/1/aa/H COMB.pep:\*  
4: /cgn2\_6/prodata/1/aa/PCTUS COMB.pep:\*  
5: /cgn2\_6/prodata/1/aa/RE COMB.pep:\*  
6: /cgn2\_6/prodata/1/aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	71.7	33	1 US-08-053-131-78	Sequence 78, Appl
2	43	71.7	33	1 US-08-645-641-78	Sequence 78, Appl
3	43	71.7	33	1 US-07-853-408B-78	Sequence 78, Appl
4	43	71.7	33	1 US-08-096-762-78	Sequence 78, Appl
5	43	71.7	33	1 US-08-308-865-78	Sequence 78, Appl
6	43	71.7	33	2 US-09-042-353-275	Sequence 275, App
7	43	71.7	33	2 US-08-758-417A-123	Sequence 123, App
8	43	71.7	33	4 PCT-US92-10983-78	Sequence 78, Appl
9	43	71.7	125	2 US-08-840-459-84	Sequence 84, Appl
10	43	71.7	125	2 US-09-497-625A-84	Sequence 84, Appl
11	42	70.0	29	1 US-08-053-131-73	Sequence 73, Appl
12	42	70.0	29	1 US-08-645-641-73	Sequence 73, Appl
13	42	70.0	29	1 US-07-853-408B-73	Sequence 73, Appl
14	42	70.0	29	1 US-08-096-762-73	Sequence 73, Appl
15	42	70.0	29	1 US-08-308-865-73	Sequence 73, Appl
16	42	70.0	29	2 US-09-042-353-270	Sequence 270, App
17	42	70.0	29	2 US-08-758-417A-118	Sequence 118, App
18	42	70.0	29	4 PCT-US92-10983-73	Sequence 73, Appl
19	42	70.0	31	1 US-08-053-131-83	Sequence 83, Appl
20	42	70.0	31	1 US-08-645-641-83	Sequence 83, Appl
21	42	70.0	31	1 US-07-853-408B-83	Sequence 83, Appl
22	42	70.0	31	1 US-08-096-762-83	Sequence 83, Appl
23	42	70.0	31	1 US-08-308-865-83	Sequence 83, Appl
24	42	70.0	31	2 US-09-042-353-280	Sequence 280, App
25	42	70.0	31	2 US-08-758-417A-128	Sequence 128, App
26	42	70.0	31	4 PCT-US92-10983-83	Sequence 83, Appl
27	42	70.0	36	1 US-08-053-131-84	Sequence 84, Appl

28	42	70.0	36	1 US-08-645-641-84	Sequence 84, Appl
29	42	70.0	36	1 US-07-853-408B-84	Sequence 84, Appl
30	42	70.0	36	1 US-08-096-762-84	Sequence 84, Appl
31	42	70.0	36	1 US-08-308-865-84	Sequence 84, Appl
32	42	70.0	36	2 US-09-042-353-281	Sequence 281, App
33	42	70.0	36	2 US-08-758-417A-129	Sequence 129, App
34	42	70.0	36	4 PCT-US92-10983-84	Sequence 84, Appl
35	42	70.0	119	2 US-08-840-459-88	Sequence 88, Appl
36	42	70.0	119	2 US-09-497-625A-88	Sequence 88, Appl
37	42	70.0	128	2 US-09-840-459-77	Sequence 77, Appl
38	42	70.0	128	2 US-09-840-459-79	Sequence 79, Appl
39	42	70.0	128	2 US-09-497-625A-77	Sequence 79, Appl
40	42	70.0	128	2 US-09-497-625A-79	Sequence 80, Appl
41	42	70.0	167	2 US-09-472-087-80	Sequence 80, Appl
42	42	70.0	236	2 US-09-456-090A-64	Sequence 64, Appl
43	42	70.0	236	2 US-09-456-090A-104	Sequence 104, App
44	42	70.0	236	2 US-09-453-234-64	Sequence 64, Appl
45	42	70.0	236	2 US-09-453-234-104	Sequence 104, App

## ALIGNMENTS

RESULT 1  
US-08-053-131-78  
; Sequence 78, Application US/08053131  
; Patent No. 5661016  
; GENERAL INFORMATION:  
; APPLICANT: Lonberg, Nils  
; APPLICANT: Kay, Robert M.  
; TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for  
; TITLE OF INVENTION: Producing Heterologous Antibodies  
; NUMBER OF SEQUENCES: 197  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Townsend and Townsend Klourie and Crew  
; STREET: One Market Plaza, Stewart Tower, Suite 200  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/053,131  
; FILING DATE: 26-Apr-1993  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/990,860  
; FILING DATE: 16-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/810,279  
; FILING DATE: 17-DEC-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/853,408  
; FILING DATE: 18-MAR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 14643-9-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 78:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 33 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-053-131-78

Query Match 71.7%; Score 43; DB 1; Length 33;  
Best Local Similarity 66.7%; Pred. No. 1.6;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTYFGLDV 11  
:||||:|  
Db 10 SYTYGMDV 18

## RESULT 2

US-08-645-641-78  
; Sequence 78, Application US/08645641  
; Patent No. 5719032  
; GENERAL INFORMATION:  
; APPLICANT: Lonberg, Nils  
; TITLE OF INVENTION: Transgenic No. 5719032-Human Animals for  
; NUMBER OF SEQUENCES: 150  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: William M. Smith  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/645,641  
; FILING DATE: 20-MAY-1996  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/904,068  
; FILING DATE: 23-JUN-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 14643-000913  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 78:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 33 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-645-641-78

Query Match 71.7%; Score 43; DB 1; Length 33;  
Best Local Similarity 66.7%; Pred. No. 1.6;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTYFGLDV 11  
:||||:|  
Db 10 SYTYGMDV 18

## RESULT 3

US-07-853-408B-78  
; Sequence 78, Application US/07853408B  
; Patent No. 5789650  
; GENERAL INFORMATION:  
; APPLICANT: Lonberg, Nils  
; TITLE OF INVENTION: Transgenic No. 5789650-Human Animals for  
; TITLE OF INVENTION: Producing Heterologous Antibodies

; NUMBER OF SEQUENCES: 150  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: William M. Smith  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/853,408B  
; FILING DATE: 19920318  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 14643-9  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 78:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 33 amino acids  
; TYPE: AMINO ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-07-853-408B-78

Query Match 71.7%; Score 43; DB 1; Length 33;  
Best Local Similarity 66.7%; Pred. No. 1.6;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTYFGLDV 11  
:||||:|  
Db 10 SYTYGMDV 18

## RESULT 4

US-08-096-762-78  
; Sequence 78, Application US/08096762  
; Patent No. 5814318  
; GENERAL INFORMATION:  
; APPLICANT: Lonberg, Nils  
; TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for  
; TITLE OF INVENTION: Producing Heterologous Antibodies  
; NUMBER OF SEQUENCES: 210  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: One Market Plaza, Steuart Tower, Suite 200  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/096,762  
; FILING DATE: 22-JUL-1993  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/053,131  
; FILING DATE: 26-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/990,860

FILING DATE: 16-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/904,068  
FILING DATE: 23-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/853,408  
FILING DATE: 18-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/810,279  
FILING DATE: 17-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 14643-9-4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 78:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-096-762-78

Query Match 71.7% Score 43; DB 1; Length 33;  
Best Local Similarity 66.7% Pred. No. 1.6;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYTREGLDV 11  
:||||:|  
DB 10 SYTYGMDV 18

RESULT 5  
US-08-308-865-78  
Sequence 78, Application US/08308865  
Patent No. 5877397  
GENERAL INFORMATION:  
APPLICANT: Lomborg, Nils  
TITLE OF INVENTION: Transgenic No. 5877397-Human Animals for  
NUMBER OF SEQUENCES: 150  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: William M. Smith  
STREET: One Market Plaza, Stewart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/308,865  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/145,707  
FILING DATE:  
APPLICATION NUMBER: US 07/904,068  
FILING DATE: 23-JUN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 14643-9-1-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 78:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-308-865-78

Query Match 71.7% Score 43; DB 1; Length 33;  
Best Local Similarity 66.7% Pred. No. 1.6;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYTREGLDV 11  
:||||:|  
DB 10 SYTYGMDV 18

RESULT 6  
US-09-042-353-275  
Sequence 275, Application US/09042353  
Patent No. 6255458  
GENERAL INFORMATION:  
APPLICANT: Lomborg, Nils  
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for  
NUMBER OF SEQUENCES: 421  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/042,353  
FILING DATE: 13-MAR-1998  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/810,279  
FILING DATE: 17-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/853,408  
FILING DATE: 18-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/904,068  
FILING DATE: 23-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/990,860  
FILING DATE: 16-DEC-1992  
PRIOR APPLICATION NUMBER: US 08/053,131  
FILING DATE: 26-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/096,762  
FILING DATE: 22-JUL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/155,301  
FILING DATE: 18-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/161,739  
FILING DATE: 03-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/165,699  
FILING DATE: 10-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/209,741

FILING DATE: 09-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/352,322  
FILING DATE: 07-DEC-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/544,404  
FILING DATE: 10-OCT-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/728,463  
FILING DATE: 10-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US96/16433  
FILING DATE: 10-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/758,417  
FILING DATE: 02-DEC-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/21803  
FILING DATE: 01-DEC-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 014643-009040US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 275:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 amino acids  
TYPE: amino acid  
STRANDEDNESS: linear  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-042-353-275

Query Match 71.7% Score 43; DB 2; Length 33;  
Best Local Similarity 66.7%; Pred. No. 1.6;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYRFGDLY 11  
:||||:|  
DB 10 SYTYGMDV 18

RESULT 7  
US-08-758-417A-123  
Sequence 123, Application US/08758417A  
Patent No. 6300129  
GENERAL INFORMATION:  
APPLICANT: Lomborg, Nils  
Kay, Robert M.  
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for  
Producing Heterologous Antibodies  
NUMBER OF SEQUENCES: 417  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/758,417A  
FILING DATE: 02-DEC-1996  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/728,463  
FILING DATE: 10-OCT-1996

APPLICATION NUMBER: US 08/544,404  
FILING DATE: 10-OCT-1995  
APPLICATION NUMBER: US 08/352,322  
FILING DATE: 07-DEC-1994  
APPLICATION NUMBER: US 08/209,741  
FILING DATE: 09-MAR-1994  
APPLICATION NUMBER: US 08/165,699  
FILING DATE: 10-DEC-1993  
APPLICATION NUMBER: US 08/161,739  
FILING DATE: 03-DEC-1993  
APPLICATION NUMBER: US 08/155,301  
FILING DATE: 18-NOV-1993  
APPLICATION NUMBER: US 08/096,762  
FILING DATE: 22-JUL-1993  
APPLICATION NUMBER: US 08/053,131  
FILING DATE: 26-APR-1993  
APPLICATION NUMBER: US 07/990,860  
FILING DATE: 16-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Serfati, Andrew T.  
REGISTRATION NUMBER: 41,303  
REFERENCE/DOCKET NUMBER: 014643-009030US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 123:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 123:  
US-08-758-417A-123

Query Match 71.7% Score 43; DB 2; Length 33;  
Best Local Similarity 66.7%; Pred. No. 1.6;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYRFGDLY 11  
:||||:|  
DB 10 SYTYGMDV 18

RESULT 8  
PCT-US92-10983-78  
Sequence 78, Application PC/TUS9210983  
GENERAL INFORMATION:  
APPLICANT: Lomborg, Nils  
Kay, Robert M.  
TITLE OF INVENTION: Transgenic Non-Human Animals for  
Producing Heterologous Antibodies  
NUMBER OF SEQUENCES: 152  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: William M. Smith  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10983  
FILING DATE: 19921217  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 14643-9-2

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 78:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US92-10983-78

Query Match 71.7%; Score 43; DB 4; Length 33;  
Best Local Similarity 66.7%; Pred. No. 1.6;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYTFFGLDV 11  
:||||:|  
Db 10 SYTYGMDV 18

RESULT 9  
US-09-840-459-84  
Sequence 84, Application US/09840459  
Patent No. 6696350  
GENERAL INFORMATION:  
APPLICANT: Larosa, Gregory J.  
APPLICANT: Horvath, Christopher  
APPLICANT: Newman, Walter  
APPLICANT: Jones, S. Tarran H.  
APPLICANT: O'Keefe, Theresa  
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
FILE REFERENCE: 1855.1052-012  
CURRENT APPLICATION NUMBER: US/09/840,459  
CURRENT FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: PCT/US01/03537  
PRIOR FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: 09/497,625  
PRIOR FILING DATE: 2000-02-03  
PRIOR FILING DATE: 1999-07-22  
PRIOR FILING DATE: 1999-07-22  
PRIOR APPLICATION NUMBER: 09/121,781  
PRIOR FILING DATE: 1998-07-23  
NUMBER OF SEQ ID NOS: 107  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 84  
LENGTH: 125  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-840-459-84

Query Match 71.7%; Score 43; DB 2; Length 125;  
Best Local Similarity 66.7%; Pred. No. 6.4;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYTFFGLDV 11  
:||||:|  
Db 106 SYTYGMDV 114

RESULT 10  
US-09-497-625A-84  
Sequence 84, Application US/09497625A  
Patent No. 6727349  
GENERAL INFORMATION:  
APPLICANT: Larosa, Gregory J.  
APPLICANT: Horvath, Christopher  
APPLICANT: Newman, Walter  
APPLICANT: Jones, S. Tarran H.  
APPLICANT: O'Brien, Siobhan H.  
APPLICANT: O'Keefe, Theresa

TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
FILE REFERENCE: 1855.1052-004  
CURRENT APPLICATION NUMBER: US/09/497,625A  
CURRENT FILING DATE: 2000-02-03  
PRIOR APPLICATION NUMBER: 09/359,193  
PRIOR FILING DATE: 1999-07-22  
PRIOR APPLICATION NUMBER: 09/121,781  
PRIOR FILING DATE: 1998-07-23  
NUMBER OF SEQ ID NOS: 106  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 84  
LENGTH: 125  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-497-625A-84

Query Match 71.7%; Score 43; DB 2; Length 125;  
Best Local Similarity 66.7%; Pred. No. 6.4;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYTFFGLDV 11  
:||||:|  
Db 106 SYTYGMDV 114

RESULT 11  
US-08-053-131-73  
Sequence 73, Application US/08053131  
Patent No. 5661016  
GENERAL INFORMATION:  
APPLICANT: Lomborg, Nils  
APPLICANT: Kay, Robert M.  
TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for  
TITLE OF INVENTION: Producing Heterologous Antibodies  
NUMBER OF SEQUENCES: 197  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Stewart Tower, Suite 200  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/053,131  
FILING DATE: 26-APR-1993  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/990,860  
FILING DATE: 16-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/810,279  
FILING DATE: 17-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/853,408  
FILING DATE: 18-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 14643-9-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 73:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 29 amino acids  
TYPE: amino acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-053-131-73

Query Match 70.0%; Score 42; DB 1; Length 29;  
Best Local Similarity 75.0%; Pred. No. 2.1;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11  
|||:|:|  
DB 7 YYYGMDV 14

RESULT 12  
US-08-645-641-73  
Sequence 73, Application US/08645641  
Patent No. 5719032  
GENERAL INFORMATION:  
APPLICANT: Lonberg, Nils  
APPLICANT: Kay, Robert M.  
TITLE OF INVENTION: Transgenic No. 5719032-Human Animals for  
TITLE OF INVENTION: Producing Heterologous Antibodies  
NUMBER OF SEQUENCES: 150  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: William M. Smith  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/645,641  
FILING DATE: 20-MAY-1996  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/904,068  
FILING DATE: 23-JUN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 14643-000913  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
FAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 73:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 29 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-645-641-73

Query Match 70.0%; Score 42; DB 1; Length 29;  
Best Local Similarity 75.0%; Pred. No. 2.1;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11  
|||:|:|  
DB 7 YYYGMDV 14

RESULT 13  
US-07-853-408B-73  
Sequence 73, Application US/07853408B  
Patent No. 5789650  
GENERAL INFORMATION:  
APPLICANT: Lonberg, Nils

APPLICANT: Kay, Robert M.  
TITLE OF INVENTION: Transgenic No. 5789650-Human Animals for  
TITLE OF INVENTION: Producing Heterologous Antibodies  
NUMBER OF SEQUENCES: 150  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: William M. Smith  
STREET: One Market Plaza, Stuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/853,408B  
FILING DATE: 19920318  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 14643-9  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
FAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 73:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 29 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-853-408B-73

Query Match 70.0%; Score 42; DB 1; Length 29;  
Best Local Similarity 75.0%; Pred. No. 2.1;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11  
|||:|:|  
DB 7 YYYGMDV 14

RESULT 14  
US-08-096-762-73  
Sequence 73, Application US/08096762  
Patent No. 5814318  
GENERAL INFORMATION:  
APPLICANT: Lonberg, Nils  
APPLICANT: Kay, Robert M.  
TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for  
TITLE OF INVENTION: Producing Heterologous Antibodies  
NUMBER OF SEQUENCES: 210  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Stuart Tower, Suite 200  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/096,762  
FILING DATE: 22-JUL-1993  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/053,131



FILING DATE: 26-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/990,860  
FILING DATE: 16-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/904,068  
FILING DATE: 23-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/853,408  
FILING DATE: 18-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/810,279  
FILING DATE: 17-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 14643-9-4  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 73:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 29 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-096-762-73

Query Match 70.0%; Score 42; DB 1; Length 29;  
Best Local Similarity 75.0%; Pred. No. 2.1;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11  
|||:|:|  
DB 7 YYYGMDV 14

RESULT 15  
US-08-308-865-73  
Sequence 73, Application US/0830865  
Patent No. 5877397  
GENERAL INFORMATION:  
APPLICANT: Lomborg, Nils  
APPLICANT: Kay, Robert M.  
TITLE OF INVENTION: Transgenic No. 5877397-Human Animals for  
TITLE OF INVENTION: Producing Heterologous Antibodies  
NUMBER OF SEQUENCES: 150  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: William M. Smith  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/308,865  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/145,707  
FILING DATE:  
APPLICATION NUMBER: US 07/904,068  
FILING DATE: 23-JUN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 14643-9-1-1

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 73:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 29 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-308-865-73

Query Match 70.0%; Score 42; DB 1; Length 29;  
Best Local Similarity 75.0%; Pred. No. 2.1;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11  
|||:|:|  
DB 7 YYYGMDV 14

Search completed: December 4, 2005, 04:09:43  
Job time : 24.6042 secs

**This Page Blank (uspto)**

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## OM protein - protein search, using sw model

Run on: December 4, 2005, 04:07:28 ; Search time 78.8333 Seconds  
(without alignments)  
58.302 Million cell updates/sec

Title: US-10-632-706-127

Perfect score: 60

Sequence: 1 LATYYFGLDV 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	100.0	11	4	US-10-632-706-126
2	60	100.0	11	4	US-10-632-706-127
3	48	80.0	122	6	US-11-031-485-116
4	47	78.3	129	4	US-10-364-743-101
5	47	78.3	129	5	US-10-452-593-101
6	47	78.3	134	4	US-10-364-743-101
7	47	78.3	134	5	US-10-452-593-101
8	47	78.3	134	5	US-10-452-593-101
9	47	78.3	134	5	US-10-452-593-101
10	46	76.7	134	5	US-10-452-593-101
11	46	76.7	134	5	US-10-452-593-101
12	46	76.7	134	5	US-10-452-593-101
13	45	75.0	16	5	US-10-783-311-135
14	45	75.0	16	5	US-10-783-311-135
15	45	75.0	21	3	US-09-880-748-3068
16	45	75.0	21	3	US-09-880-748-3068
17	45	75.0	21	3	US-09-880-748-3068
18	45	75.0	21	3	US-09-880-748-3068
19	45	75.0	21	3	US-09-880-748-3068
20	45	75.0	21	3	US-09-880-748-3068
21	44	73.3	16	4	US-10-293-418-2129
22	44	73.3	17	3	US-09-880-748-2129
23	44	73.3	17	3	US-09-880-748-2129
24	44	73.3	18	5	US-10-984-960A-8
25	44	73.3	117	4	US-10-041-860-206
26	44	73.3	123	4	US-10-309-762-18
27	44	73.3	123	4	US-10-309-762-18

28	44	73.3	124	4	US-10-292-088-106	Sequence 106, App
29	44	73.3	127	4	US-10-041-860-31	Sequence 31, App1
30	44	73.3	127	4	US-10-041-860-243	Sequence 243, App
31	44	73.3	127	4	US-10-041-860-325	Sequence 325, App
32	44	73.3	127	4	US-10-665-383-42	Sequence 42, App1
33	44	73.3	127	4	US-10-466-242-53	Sequence 53, App1
34	44	73.3	127	5	US-10-984-960A-2	Sequence 2, App11
35	44	73.3	129	4	US-10-292-088-10	Sequence 10, App1
36	44	73.3	134	4	US-10-364-743-109	Sequence 109, App
37	44	73.3	134	4	US-10-364-743-110	Sequence 110, App
38	44	73.3	134	5	US-10-452-593-16	Sequence 16, App1
39	44	73.3	134	5	US-10-452-593-109	Sequence 109, App
40	44	73.3	134	5	US-10-452-593-110	Sequence 110, App
41	44	73.3	145	5	US-10-644-277-146	Sequence 146, App
42	44	73.3	157	5	US-10-473-287-34	Sequence 34, App1
43	44	73.3	157	5	US-10-473-287-63	Sequence 63, App1
44	44	73.3	249	5	US-10-935-290-61	Sequence 61, App1

## ALIGNMENTS

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RESULT 1
US-10-632-706-126
; Sequence 126, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: AMERSDORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 126
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-126
Query Match 100.0%; Score 60; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 LATYYFGLDV 11
Db 1 LATYYFGLDV 11
RESULT 2
US-10-632-706-127
; Sequence 127, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: AMERSDORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
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;; PRIOR FILING DATE: 1998-08-31  
;; NUMBER OF SEQ ID NOS: 278  
;; SOFTWARE: PatentIn version 3.2  
;; SEQ ID NO 127  
;; LENGTH: 11  
;; TYPE: PRT  
;; ORGANISM: Artificial  
;; FEATURE:  
;; OTHER INFORMATION: single chain antibody fragment  
US-10-632-706-127

Query Match 100.0%; Score 60; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0027;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LATYYFGLDV 11  
Db 1 LATYYFGLDV 11

RESULT 3  
US-11-031-485-116  
;; Sequence 116, Application US/11031485  
;; Publication No. US20050232917A1  
;; GENERAL INFORMATION:  
;; APPLICANT: PULLEN, NICHOLAS  
;; APPLICANT: MOLLOY, ELIZABETH  
;; APPLICANT: KELLERMAN, SIRIO-AIMEE  
;; APPLICANT: GREEN, LARRY L.  
;; APPLICANT: HAAK-FREDSCHO, MARY  
;; TITLE OF INVENTION: ANTIBODIES TO MADCAM  
;; FILE REFERENCE: ABX-PP6  
;; CURRENT APPLICATION NUMBER: US/11/031,485  
;; PRIOR FILING DATE: 2005-01-07  
;; PRIOR APPLICATION NUMBER: 60/535,490  
;; PRIOR FILING DATE: 2004-01-09  
;; NUMBER OF SEQ ID NOS: 147  
;; SOFTWARE: PatentIn Ver. 3.3  
;; SEQ ID NO 116  
;; LENGTH: 122  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-11-031-485-116

Query Match 80.0%; Score 48; DB 6; Length 122;  
Best Local Similarity 63.6%; Pred. No. 2.8;  
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LATYYFGLDV 11  
Db 100 VVYYYYGMDV 110

RESULT 4  
US-10-364-743-101  
;; Sequence 101, Application US/10364743  
;; Publication No. US20040009178A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Bowdish, Katherine S.  
;; APPLICANT: Frederickson, Shana  
;; APPLICANT: Wild, Martha A.  
;; APPLICANT: Maruyama, Toshiaki  
;; APPLICANT: No. US20040009178A1an, Mary Jean  
;; TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE  
;; FILE REFERENCE: 84 (1087-73)  
;; CURRENT APPLICATION NUMBER: US/10/364,743  
;; PRIOR FILING DATE: 2003-02-11  
;; PRIOR APPLICATION NUMBER: US 60/428,807  
;; PRIOR FILING DATE: 2002-11-25  
;; NUMBER OF SEQ ID NOS: 118  
;; SOFTWARE: PatentIn version 3.2  
;; SEQ ID NO 101  
;; LENGTH: 129

;; TYPE: PRT  
;; ORGANISM: human  
US-10-364-743-101

Query Match 78.3%; Score 47; DB 4; Length 129;  
Best Local Similarity 77.8%; Pred. No. 4.4;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TYYFGLDV 11  
Db 105 TYYYYGMDV 113

RESULT 5  
US-10-452-593-101  
;; Sequence 101, Application US/10452593  
;; Publication No. US20040258699A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Bowdish, Katherine S.  
;; APPLICANT: Frederickson, Shana  
;; APPLICANT: Wild, Martha A.  
;; APPLICANT: Maruyama, Toshiaki  
;; APPLICANT: Nolan, Mary Jean  
;; TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE  
;; FILE REFERENCE: 98 CIP (1087-73 CIP)  
;; CURRENT APPLICATION NUMBER: US/10/452,593  
;; PRIOR FILING DATE: 2003-06-02  
;; PRIOR APPLICATION NUMBER: US 10/364,743  
;; PRIOR FILING DATE: 2003-02-11  
;; PRIOR APPLICATION NUMBER: US 60/356,086  
;; PRIOR FILING DATE: 2002-02-11  
;; PRIOR APPLICATION NUMBER: US 60/376,408  
;; PRIOR FILING DATE: 2002-04-29  
;; PRIOR APPLICATION NUMBER: US 60/428,807  
;; PRIOR FILING DATE: 2002-11-25  
;; NUMBER OF SEQ ID NOS: 118  
;; SOFTWARE: PatentIn version 3.2  
;; SEQ ID NO 101  
;; LENGTH: 129  
;; TYPE: PRT  
;; ORGANISM: human  
US-10-452-593-101

Query Match 78.3%; Score 47; DB 5; Length 129;  
Best Local Similarity 77.8%; Pred. No. 4.4;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TYYFGLDV 11  
Db 105 TYYYYGMDV 113

RESULT 6  
US-10-364-743-15  
;; Sequence 15, Application US/10364743  
;; Publication No. US20040009178A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Bowdish, Katherine S.  
;; APPLICANT: Frederickson, Shana  
;; APPLICANT: Wild, Martha A.  
;; APPLICANT: Maruyama, Toshiaki  
;; APPLICANT: No. US20040009178A1an, Mary Jean  
;; TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE  
;; FILE REFERENCE: 84 (1087-73)  
;; CURRENT APPLICATION NUMBER: US/10/364,743  
;; PRIOR FILING DATE: 2003-02-11  
;; PRIOR APPLICATION NUMBER: US 60/428,807  
;; PRIOR FILING DATE: 2002-11-25  
;; NUMBER OF SEQ ID NOS: 118  
;; SOFTWARE: PatentIn version 3.2  
;; SEQ ID NO 15  
;; LENGTH: 134  
;; TYPE: PRT

ORGANISM: human  
US-10-364-743-15

Query Match 78.3%; Score 47; DB 4; Length 134;  
Best Local Similarity 77.8%; Pred. No. 4.5;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYYPGLDV 11  
| | | | | | | | | |  
Db 110 TTYYYGMDV 118

RESULT 7  
US-10-452-593-15

; Sequence 15, Application US/10452593  
; Publication No. US20040258699A1  
; GENERAL INFORMATION:  
; APPLICANT: Bowdish, Katherine S.  
; APPLICANT: Frederickson, Shana  
; APPLICANT: Wild, Martha A.  
; APPLICANT: Maruyama, Toshiaki  
; APPLICANT: Nolan, Mary Jean  
; TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE  
; FILE REFERENCE: 98 CIP (1087-73 CIP)  
; CURRENT APPLICATION NUMBER: US/10/452,593  
; CURRENT FILING DATE: 2003-06-02  
; PRIOR APPLICATION NUMBER: US 10/364,743  
; PRIOR FILING DATE: 2003-02-11  
; PRIOR APPLICATION NUMBER: US 60/356,086  
; PRIOR FILING DATE: 2002-02-11  
; PRIOR APPLICATION NUMBER: US 60/376,408  
; PRIOR FILING DATE: 2002-04-29  
; PRIOR APPLICATION NUMBER: US 60/428,807  
; PRIOR FILING DATE: 2002-11-25  
; NUMBER OF SEQ ID NOS: 118  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 15  
; LENGTH: 134  
; TYPE: PRT  
; ORGANISM: human  
US-10-452-593-15

Query Match 78.3%; Score 47; DB 5; Length 134;  
Best Local Similarity 77.8%; Pred. No. 4.5;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYYPGLDV 11  
| | | | | | | | | |  
Db 110 TTYYYGMDV 118

RESULT 8

US-11-031-485-56  
; Sequence 56, Application US/11031485  
; Publication No. US20050232917A1  
; GENERAL INFORMATION:  
; APPLICANT: PULLEN, NICHOLAS  
; APPLICANT: MOLLOY, ELIZABETH  
; APPLICANT: KELLERMANN, SIRID-AIMEE  
; APPLICANT: GREEN, LARRY L.  
; APPLICANT: HAAR-FRENDSCHO, MARY  
; TITLE OF INVENTION: ANTIBODIES TO MADCAM  
; FILE REFERENCE: ABX-PF6  
; CURRENT APPLICATION NUMBER: US/11/031,485  
; CURRENT FILING DATE: 2005-01-07  
; PRIOR APPLICATION NUMBER: 60/535,490  
; PRIOR FILING DATE: 2004-01-09  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 56  
; LENGTH: 468  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-11-031-485-56

Query Match 78.3%; Score 47; DB 6; Length 468;  
Best Local Similarity 77.8%; Pred. No. 16;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYYPGLDV 11  
| | | | | | | | | |  
Db 123 TTYYYGMDV 131

RESULT 9

US-11-031-485-18  
; Sequence 18, Application US/11031485  
; Publication No. US20050232917A1  
; GENERAL INFORMATION:  
; APPLICANT: PULLEN, NICHOLAS  
; APPLICANT: MOLLOY, ELIZABETH  
; APPLICANT: KELLERMANN, SIRID-AIMEE  
; APPLICANT: GREEN, LARRY L.  
; APPLICANT: HAAR-FRENDSCHO, MARY  
; TITLE OF INVENTION: ANTIBODIES TO MADCAM  
; FILE REFERENCE: ABX-PF6  
; CURRENT APPLICATION NUMBER: US/11/031,485  
; CURRENT FILING DATE: 2005-01-07  
; PRIOR APPLICATION NUMBER: 60/535,490  
; PRIOR FILING DATE: 2004-01-09  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 18  
; LENGTH: 469  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-031-485-18

Query Match 78.3%; Score 47; DB 6; Length 469;  
Best Local Similarity 77.8%; Pred. No. 16;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYYPGLDV 11  
| | | | | | | | | |  
Db 123 TTYYYGMDV 131

RESULT 10

US-10-632-706-114  
; Sequence 114, Application US/10632706  
; Publication No. US20040175385A1  
; GENERAL INFORMATION:  
; APPLICANT: MARKS, JAMES D.  
; APPLICANT: AMERSDORFER, PETER  
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM  
; FILE REFERENCE: 407T-895120US  
; CURRENT APPLICATION NUMBER: US/10/632,706  
; CURRENT FILING DATE: 2003-08-01  
; PRIOR APPLICATION NUMBER: US 60/400,721  
; PRIOR FILING DATE: 2002-08-01  
; PRIOR APPLICATION NUMBER: US 09/144,806  
; PRIOR FILING DATE: 1998-08-31  
; NUMBER OF SEQ ID NOS: 278  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 114  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial  
; OTHER INFORMATION: single chain antibody fragment  
US-10-632-706-114

Query Match 76.7%; Score 46; DB 4; Length 13;  
Best Local Similarity 70.0%; Pred. No. 0.64;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 ATYYFGLDV 11  
| | | | |  
DB 4 ANYYYGMDV 13

RESULT 11

US-10-783-311-141  
; Sequence 141, Application US/10783311  
; Publication No. US20050009136A1  
; GENERAL INFORMATION:  
; APPLICANT: Nixon, Andrew  
; APPLICANT: Hogan, Shannon  
; TITLE OF INVENTION: PAPP-A LIGANDS  
; FILE REFERENCE: 10280-059001  
; CURRENT APPLICATION NUMBER: US/10/783,311  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: US 60/448,515  
; PRIOR FILING DATE: 2003-02-19  
; NUMBER OF SEQ ID NOS: 394  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 141  
; LENGTH: 21  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Heavy Chain amino acid sequence  
US-10-783-311-141

Query Match 76.7%; Score 46; DB 5; Length 21;  
Best Local Similarity 63.6%; Pred. No. 1;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 ATYYFGLDV 11  
| | | | |  
DB 11 LGNYYYGMDV 21

RESULT 12

US-10-783-311-135  
; Sequence 135, Application US/10783311  
; Publication No. US20050009136A1  
; GENERAL INFORMATION:  
; APPLICANT: Nixon, Andrew  
; APPLICANT: Hogan, Shannon  
; TITLE OF INVENTION: PAPP-A LIGANDS  
; FILE REFERENCE: 10280-059001  
; CURRENT APPLICATION NUMBER: US/10/783,311  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: US 60/448,515  
; PRIOR FILING DATE: 2003-02-19  
; NUMBER OF SEQ ID NOS: 394  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 135  
; LENGTH: 140  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Heavy Chain amino acid sequence  
US-10-783-311-135

Query Match 76.7%; Score 46; DB 5; Length 140;  
Best Local Similarity 63.6%; Pred. No. 6.9;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

US-10-783-311-277  
; Sequence 277, Application US/10783311

Publication No. US20050009136A1

; GENERAL INFORMATION:  
; APPLICANT: Nixon, Andrew  
; APPLICANT: Hogan, Shannon  
; TITLE OF INVENTION: PAPP-A LIGANDS  
; FILE REFERENCE: 10280-059001  
; CURRENT APPLICATION NUMBER: US/10/783,311  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: US 60/448,515  
; PRIOR FILING DATE: 2003-02-19  
; NUMBER OF SEQ ID NOS: 394  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 277  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Heavy Chain amino acid sequence  
US-10-783-311-277

Query Match 75.0%; Score 45; DB 5; Length 16;  
Best Local Similarity 63.6%; Pred. No. 1.2;  
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 ATYYFGLDV 11  
| | | | |  
DB 6 VAGYYGMDV 16

RESULT 14

US-09-880-748-3068  
; Sequence 3068, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3068  
; LENGTH: 21  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-3068

Query Match 75.0%; Score 45; DB 3; Length 21;  
Best Local Similarity 70.0%; Pred. No. 1.5;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

US-10-293-418-3068  
; Sequence 3068, Application US/10293418  
; Publication No. US2003022396A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

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; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3068
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-3068

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Query Match 75.0%; Score 45; DB 4; Length 21;
Best Local Similarity 70.0%; Pred. No. 1.5;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY 2 ATYYRGLDV 11
Db 12 APYYYGMDV 21

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Search completed: December 4, 2005, 04:37:28  
 Job time : 80.8333 secs

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US-11-054-515-1600
; Sequence 1600, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIORITY FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1600
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1600

Query Match          75.0% Score 45; DB 7; Length 256;
Best Local Similarity 70.0%; Pred. No. 0.19;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      2 ATYYFGLDV 11
| |||:|:|
Db      110 APYYYGMDV 119

RESULT 3
US-11-054-515-2129
; Sequence 2129, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIORITY FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
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; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2129
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2129

Query Match          73.3% Score 44; DB 7; Length 16;
Best Local Similarity 63.6%; Pred. No. 0.02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 LATYYFGLDV 11
| |||:|:|
Db      6 LTGYYYGMDV 16

RESULT 4
US-11-054-515-2876
; Sequence 2876, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIORITY FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2876
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2876

Query Match          73.3% Score 44; DB 7; Length 17;
Best Local Similarity 63.6%; Pred. No. 0.02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 LATYYFGLDV 11
| |||:|:|
Db      7 LTGYYYGMDV 17

RESULT 5
US-11-054-515-1431
; Sequence 1431, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
```

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; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1431
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1431

Query Match          73.3%; Score 44; DB 7; Length 252;
Best Local Similarity 63.6%; Pred. No. 0.28;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 LATYYFGADV 11
Db      105 LTGYYYGMDV 115

RESULT 6
US-11-054-515-3
; Sequence 3, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
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; SEQ ID NO 3
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-3

Query Match          73.3%; Score 44; DB 7; Length 254;
Best Local Similarity 63.6%; Pred. No. 0.28;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 LATYYFGADV 11
Db      107 LTGYYYGMDV 117

RESULT 7
US-11-054-515-838
; Sequence 838, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 838
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-838

Query Match          73.3%; Score 44; DB 7; Length 254;
Best Local Similarity 63.6%; Pred. No. 0.28;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 LATYYFGADV 11
Db      107 LTGYYYGMDV 117

RESULT 8
US-11-054-515-870
; Sequence 870, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
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PRIOR FILING DATE: 2004-02-11  
PRIOR APPLICATION NUMBER: 60/580,347  
PRIOR FILING DATE: 2004-06-18  
PRIOR APPLICATION NUMBER: 10/293,418  
PRIOR FILING DATE: 2002-11-14  
PRIOR APPLICATION NUMBER: 60/331,469  
PRIOR FILING DATE: 2001-11-16  
PRIOR APPLICATION NUMBER: 60/340,817  
PRIOR FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: 09/880,748  
PRIOR FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/293,499  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: 60/277,379  
PRIOR FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/276,248  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/240,816  
PRIOR FILING DATE: 2000-10-17  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 3247  
SEQ ID NO 870  
LENGTH: 254  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: Site  
LOCATION: (42)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
FEATURE:  
NAME/KEY: Site  
LOCATION: (45)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
FEATURE:  
NAME/KEY: Site  
LOCATION: (51)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
FEATURE:  
NAME/KEY: Site  
LOCATION: (57)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
FEATURE:  
NAME/KEY: Site  
LOCATION: (65)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
FEATURE:  
NAME/KEY: Site  
LOCATION: (67)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
FEATURE:  
NAME/KEY: Site  
LOCATION: (70)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
FEATURE:  
NAME/KEY: Site  
LOCATION: (170)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
FEATURE:  
NAME/KEY: Site  
LOCATION: (176)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
FEATURE:  
NAME/KEY: Site  
LOCATION: (192)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
FEATURE:  
NAME/KEY: Site  
LOCATION: (235)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
FEATURE:  
NAME/KEY: Site  
LOCATION: (239)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

FEATURE:  
NAME/KEY: Site  
LOCATION: (240)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-11-054-515-870  
Query Match 73.3%; Score 44; DB 7; Length 254;  
Best Local Similarity 63.6%; Pred. No. 0.28;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 1 LATYYRGLDV 11  
DB 107 LTGYYYGMDV 117  
RESULT 9  
US-11-054-515-1287  
Sequence 1287, Application US/11054515  
Publication No. US20050255532A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
FILE REFERENCE: PFS23P3  
CURRENT FILING DATE: 2005-02-10  
PRIOR APPLICATION NUMBER: 60/543,296  
PRIOR FILING DATE: 2004-02-11  
PRIOR APPLICATION NUMBER: 60/580,347  
PRIOR FILING DATE: 2004-06-18  
PRIOR APPLICATION NUMBER: 10/293,418  
PRIOR FILING DATE: 2002-11-14  
PRIOR APPLICATION NUMBER: 60/331,469  
PRIOR FILING DATE: 2001-11-16  
PRIOR APPLICATION NUMBER: 60/340,817  
PRIOR FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: 09/880,748  
PRIOR FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/293,499  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: 60/277,379  
PRIOR FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/276,248  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/240,816  
PRIOR FILING DATE: 2000-10-17  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 3247  
SEQ ID NO 1287  
LENGTH: 254  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-054-515-1287  
Query Match 73.3%; Score 44; DB 7; Length 254;  
Best Local Similarity 63.6%; Pred. No. 0.28;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 1 LATYYRGLDV 11  
DB 107 LTGYYYGMDV 117  
RESULT 10  
US-11-054-515-1288  
Sequence 1288, Application US/11054515  
Publication No. US20050255532A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
FILE REFERENCE: PFS23P3  
CURRENT FILING DATE: 2005-02-10  
PRIOR APPLICATION NUMBER: 60/543,296  
PRIOR FILING DATE: 2004-02-11  
PRIOR APPLICATION NUMBER: 60/580,347  
PRIOR FILING DATE: 2004-06-18  
PRIOR APPLICATION NUMBER: 10/293,418  
PRIOR FILING DATE: 2002-11-14  
PRIOR APPLICATION NUMBER: 60/331,469  
PRIOR FILING DATE: 2001-11-16  
PRIOR APPLICATION NUMBER: 60/340,817  
PRIOR FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: 09/880,748  
PRIOR FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/293,499  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: 60/277,379  
PRIOR FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/276,248  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/240,816  
PRIOR FILING DATE: 2000-10-17  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 3247  
SEQ ID NO 1287  
LENGTH: 254  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-054-515-1287

PRIOR FILING DATE: 2004-02-11  
PRIOR APPLICATION NUMBER: 60/580,347  
PRIOR FILING DATE: 2004-06-18  
PRIOR APPLICATION NUMBER: 10/293,418  
PRIOR FILING DATE: 2002-11-14  
PRIOR APPLICATION NUMBER: 60/331,469  
PRIOR FILING DATE: 2001-11-16  
PRIOR APPLICATION NUMBER: 60/340,817  
PRIOR FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: 09/880,748  
PRIOR FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/293,499  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: 60/277,379  
PRIOR FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/276,248  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/240,816  
PRIOR FILING DATE: 2000-10-17  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 3247  
SEQ ID NO 1288  
LENGTH: 254  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-054-515-1288

Query Match 73.3% Score 44; DB 7; Length 254;  
Best Local Similarity 63.6% Pred. No. 0.28;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTYTFFGLDV 11  
Db 107 LTGYTGYGMDV 117

RESULT 11  
US-11-017-550-47  
Sequence 47, Application US/11017550  
Publication No. US20050250183A1  
GENERAL INFORMATION:  
APPLICANT: The Scripps Research Institute  
APPLICANT: Schultz, Peter G  
APPLICANT: Wang, Lei  
APPLICANT: Anderson, John C  
APPLICANT: Chin, Jason  
APPLICANT: Liu, David R  
APPLICANT: Magliery, Thomas  
APPLICANT: Meggers, Eric L  
APPLICANT: Mehl, Ryan A  
APPLICANT: Pasternak, Mirol  
APPLICANT: Santoro, Stephen W  
APPLICANT: Zhang, Zhiwen  
TITLE OF INVENTION: In Vivo Incorporation of Unnatural Amino Acids  
FILE REFERENCE: 54-000120US  
CURRENT APPLICATION NUMBER: US/11/017,550  
CURRENT FILING DATE: 2004-12-17  
PRIOR APPLICATION NUMBER: US/10/126,927  
PRIOR FILING DATE: 2002-04-19  
PRIOR APPLICATION NUMBER: US 60/285,030  
PRIOR FILING DATE: 2001-04-19  
PRIOR APPLICATION NUMBER: US 60/355,514  
PRIOR FILING DATE: 2002-02-06  
NUMBER OF SEQ ID NOS: 79  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 47  
LENGTH: 306  
TYPE: PRT  
ORGANISM: Methanococcus jannaschii  
US-11-017-550-47

Query Match 71.7% Score 43; DB 7; Length 306;  
Best Local Similarity 77.8% Pred. No. 0.5;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 3 TTYTFFGLDV 11  
Db 158 TTYTFFGLDV 166

RESULT 12  
US-11-054-515-3091  
Sequence 3091, Application US/11054515  
Publication No. US20050255532A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
FILE REFERENCE: PFS23P3  
CURRENT APPLICATION NUMBER: US/11/054,515  
CURRENT FILING DATE: 2005-02-10  
PRIOR APPLICATION NUMBER: 60/543,296  
PRIOR FILING DATE: 2004-02-11  
PRIOR APPLICATION NUMBER: 60/580,347  
PRIOR FILING DATE: 2004-06-18  
PRIOR APPLICATION NUMBER: 10/293,418  
PRIOR FILING DATE: 2002-11-14  
PRIOR APPLICATION NUMBER: 60/331,469  
PRIOR FILING DATE: 2001-11-16  
PRIOR APPLICATION NUMBER: 60/340,817  
PRIOR FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: 09/880,748  
PRIOR FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/293,499  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: 60/277,379  
PRIOR FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/276,248  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/240,816  
PRIOR FILING DATE: 2000-10-17  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 3247  
SEQ ID NO 3091  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-054-515-3091

Query Match 70.0% Score 42; DB 7; Length 13;  
Best Local Similarity 75.0% Pred. No. 0.035;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTYTFFGLDV 11  
Db 6 TTYTFFGLDV 13

RESULT 13  
US-11-054-515-2817  
Sequence 2817, Application US/11054515  
Publication No. US20050255532A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
FILE REFERENCE: PFS23P3  
CURRENT APPLICATION NUMBER: US/11/054,515  
CURRENT FILING DATE: 2005-02-10  
PRIOR APPLICATION NUMBER: 60/543,296  
PRIOR FILING DATE: 2004-02-11  
PRIOR APPLICATION NUMBER: 60/580,347  
PRIOR FILING DATE: 2004-06-18  
PRIOR APPLICATION NUMBER: 10/293,418  
PRIOR FILING DATE: 2002-11-14  
PRIOR APPLICATION NUMBER: 60/331,469  
PRIOR FILING DATE: 2001-11-16  
PRIOR APPLICATION NUMBER: 60/340,817

```
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2817
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2817
```

```
Query Match          70.0%; Score 42; DB 7; Length 17;
Best Local Similarity 75.0%; Pred. No. 0.046;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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```
QY      4 YYYFGLDV 11
        |||:|:|
Db      10 YYYGMDV 17
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```
RESULT 14
US-11-054-515-2735
; Sequence 2735, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2735
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2735
```

```
Query Match          70.0%; Score 42; DB 7; Length 19;
Best Local Similarity 75.0%; Pred. No. 0.051;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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```
QY      4 YYYFGLDV 11
        |||:|:|
Db      12 YYYGMDV 19
```

```
RESULT 15
US-11-054-515-2899
; Sequence 2899, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2899
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2899
```

```
Query Match          70.0%; Score 42; DB 7; Length 19;
Best Local Similarity 75.0%; Pred. No. 0.051;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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```
QY      4 YYYFGLDV 11
        |||:|:|
Db      12 YYYGMDV 19
```

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Search completed: December 4, 2005, 04:37:48
Job time : 3.20833 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 4, 2005, 04:07:28 ; Search time 78.8333 Seconds  
(without alignments)  
58.302 Million cell updates/sec

Title: US-10-632-706-128

Perfect score: 66

Sequence: 1 GPMELVGYFDS 11

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :  
1: /cgn2\_6/prodata/1/pubppaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/prodata/1/pubppaa/US08\_PUBCOMB.pep.\*  
3: /cgn2\_6/prodata/1/pubppaa/US09\_PUBCOMB.pep.\*  
4: /cgn2\_6/prodata/1/pubppaa/US10\_PUBCOMB.pep.\*  
5: /cgn2\_6/prodata/1/pubppaa/US10B\_PUBCOMB.pep.\*  
6: /cgn2\_6/prodata/1/pubppaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	66	100.0	11	4	US-10-632-706-128
2	45	68.2	230	4	US-10-156-761-9341
3	44	66.7	306	4	US-10-282-122A-73455
4	44	66.7	367	4	US-10-282-122A-74966
5	44	66.7	367	4	US-10-282-122A-75801
6	42	63.6	381	4	US-10-437-963-192224
7	41	62.1	125	4	US-10-425-115-253365
8	41	62.1	171	4	US-10-424-599-185545
9	41	62.1	475	4	US-10-282-122A-48377
10	41	62.1	475	4	US-10-437-963-187947
11	41	62.1	792	5	US-10-481-032A-252
12	41	62.1	1352	6	US-11-097-143-29418
13	40	60.6	50	4	US-10-424-599-182764
14	40	60.6	78	4	US-10-425-115-315649
15	40	60.6	146	4	US-10-477-527-21
16	40	60.6	160	4	US-10-425-115-333207
17	40	60.6	477	4	US-10-425-114-70098
18	40	60.6	507	4	US-10-424-599-229226
19	40	60.6	891	4	US-10-425-115-229314
20	40	60.6	931	5	US-10-732-923-22388
21	40	60.6	949	5	US-10-732-923-22387
22	40	60.6	1355	4	US-10-437-963-110486
23	39.5	59.8	511	4	US-10-425-114-52508
24	39	59.1	118	4	US-10-424-599-197468
25	39	59.1	207	4	US-10-424-599-163986
26	39	59.1	235	5	US-10-732-923-22418
27	39	59.1	460	4	US-10-424-599-224678

28	39	59.1	522	4	US-10-437-963-194057	Sequence 194057,
29	39	59.1	537	5	US-10-732-923-10546	Sequence 10546, A
30	39	59.1	658	4	US-10-437-963-121136	Sequence 121136,
31	39	59.1	670	4	US-10-282-122A-46814	Sequence 46814, A
32	39	59.1	696	5	US-10-450-763-50763	Sequence 50763, A
33	39	59.1	949	5	US-10-732-923-22382	Sequence 22382, A
34	39	59.1	949	5	US-10-732-923-22383	Sequence 22383, A
35	39	59.1	954	4	US-10-437-963-204079	Sequence 204079,
36	39	59.1	1199	4	US-10-437-963-121132	Sequence 121132,
37	39	59.1	1441	4	US-10-437-963-111662	Sequence 111662,
38	38	57.6	48	3	US-09-764-891-3713	Sequence 3713, Ap
39	38	57.6	71	4	US-10-425-115-277808	Sequence 277808,
40	38	57.6	84	4	US-10-437-963-150254	Sequence 150254,
41	38	57.6	96	4	US-10-437-963-119111	Sequence 119111,
42	38	57.6	135	4	US-10-424-599-205846	Sequence 205846,
43	38	57.6	167	4	US-10-767-701-60011	Sequence 60011, A
44	38	57.6	185	4	US-10-424-599-230098	Sequence 230098,
45	38	57.6	207	4	US-10-425-114-53925	Sequence 53925, A

## ALIGNMENTS

```

RESULT 1
US-10-632-706-128
; Sequence 128, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: AMERSDORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT FILING DATE: 2003-08-01
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 128
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-128

Query Match      100.0%; Score 66; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00072;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GPMELVGYFDS 11
Db      1 GPMELVGYFDS 11

RESULT 2
US-10-156-761-9341
; Sequence 9341, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10156,761

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; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 9341
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9341
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Query Match      68.2% Score 45; DB 4; Length 290;
Best Local Similarity 77.8% Pred. No. 38;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```

Qy      3  WELVGFPS 11
Db      171 WMLIGYFDS 179
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```

RESULT 3
US-10-282-122A-73455
; Sequence 73455, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zykkind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 73455
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Salmonella paratyphi A
US-10-282-122A-73455
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```

Query Match      66.7% Score 44; DB 4; Length 306;
Best Local Similarity 69.2% Pred. No. 58;
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```

Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
Qy      1  GPWELV----GYF 9
Db      66  GPWELVIGPFGYF 78
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```

RESULT 4
US-10-282-122A-74966
; Sequence 74966, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zykkind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 74966
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Salmonella typhimurium
US-10-282-122A-74966
```

```

Query Match      66.7% Score 44; DB 4; Length 367;
Best Local Similarity 69.2% Pred. No. 69;
Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
```

```

Qy      1  GPWELV----GYF 9
Db      127 GPWELVIGPFGYF 139
```

```

RESULT 5
US-10-282-122A-75801
; Sequence 75801, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
```



```

; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forey, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034
; CURRENT APPLICATION NUMBER: US/10/282,122A
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patent version 3.1
; SEQ ID NO 75801
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Salmonella typhi
; US-10-282-122A-75801

Query Match          66.7%; Score 44; DB 4; Length 367;
Best Local Similarity 69.2%; Pred. No. 69;
Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY      1 GPELVY---GYF 9
DB      127 GPELVYLGPFYF 139

RESULT 6
US-10-437-963-192224
; Sequence 192224, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221) B
; CURRENT APPLICATION NUMBER: US/10/437,963
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 192224
; LENGTH: 381
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; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_88472C.1.pep
; US-10-437-963-192224

Query Match          63.6%; Score 42; DB 4; Length 381;
Best Local Similarity 75.0%; Pred. No. 15+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GPELVGY 8
DB      176 GPELVGYF 183

RESULT 7
US-10-425-115-253365
; Sequence 253365, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53222) B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 253365
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_16264C.1.pep
; US-10-425-115-253365

Query Match          62.1%; Score 41; DB 4; Length 125;
Best Local Similarity 66.7%; Pred. No. 78;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 GPELVGYF 9
DB      75 GPELVGYF 83

RESULT 8
US-10-424-599-186545
; Sequence 186545, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223) B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 186545
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_139463C.1.pep
; US-10-424-599-186545

Query Match          62.1%; Score 41; DB 4; Length 171;
Best Local Similarity 60.0%; Pred. No. 16+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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Qy 1 GPMELVGYFD 10
|||: |||
Db 14 GPMDEMKYFD 23

RESULT 9
US-10-282-122A-48377
; Sequence 48377, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Ziekind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48377
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Bacteroides fragilis
US-10-282-122A-48377

Query Match 62.1%; Score 41; DB 4; Length 475;
Best Local Similarity 54.5%; Pred. No. 2.7e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GPMELVGYFD 11
|||: |||
Db 404 GPMKLIYYDS 414

RESULT 10
US-10-437-963-187947
; Sequence 187947, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua

Qy 1 GPMELVGYFD 10
|||: |||
Db 115 GPMWKGXYHD 124

RESULT 11
US-10-481-032A-252
; Sequence 252, Application US/10481032A
; Publication No. US2005017901A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Tong
; APPLICANT: Cheng, Menglong
; APPLICANT: Briggs, Steven
; APPLICANT: Cooper, Bret
; APPLICANT: Goff, Stephen A.
; APPLICANT: Moushaher, Todd
; APPLICANT: Glazebrook, Jane
; APPLICANT: Katagiri, Fumitaki
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicolas
; APPLICANT: Rieke, Darrell
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
; FILE REFERENCE: 60148USPCT
; CURRENT APPLICATION NUMBER: US/10/481,032A
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 60/300,112
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/342,327
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: PCT/IB02/02450
; NUMBER OF SEQ ID NOS: 1201
; SOFTWARE: PatentIn Ver. 2.2
; SEQ ID NO 252
; LENGTH: 792
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (12)-(14)
; OTHER INFORMATION: Xaa = any naturally occurring amino acid
; NAME/KEY: misc feature
; LOCATION: (16)-(16)
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OTHER INFORMATION: Xaa = any naturally occurring amino acid  
FEATURE: misc feature  
NAME/KEY: (399)..  
LOCATION: (399)..  
OTHER INFORMATION: Xaa = any naturally occurring amino acid  
FEATURE: misc feature  
NAME/KEY: (493)..  
LOCATION: (493)..  
OTHER INFORMATION: Xaa = any naturally occurring amino acid  
FEATURE: misc feature  
NAME/KEY: (669)..  
LOCATION: (669)..  
OTHER INFORMATION: Xaa = any naturally occurring amino acid  
FEATURE: misc feature  
NAME/KEY: (671)..  
LOCATION: (671)..  
OTHER INFORMATION: Xaa = any naturally occurring amino acid  
FEATURE: misc feature  
NAME/KEY: (673)..  
LOCATION: (673)..  
OTHER INFORMATION: Xaa = any naturally occurring amino acid  
US-10-481-032A-252

Query Match 62.1%; Score 41; DB 5; Length 792;  
Best Local Similarity 66.7%; Pred. No. 4.3e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 PWELVGYFD 10  
DB 245 PWQLGTYCD 253

RESULT 12  
US-11-097-143-29418  
; Sequence 29418, Application US/11097143  
; Publication No. US20050208558A1  
; GENERAL INFORMATION:  
; APPLICANT: Venter, J. Craig  
; APPLICANT: et al.  
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID  
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE  
; FILE REFERENCE: CL000728  
; CURRENT APPLICATION NUMBER: US/11/097,143  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: 60/157,832  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: 60/160,191  
; PRIOR FILING DATE: 1999-10-19  
; PRIOR APPLICATION NUMBER: 60/161,932  
; PRIOR FILING DATE: 1999-10-28  
; PRIOR APPLICATION NUMBER: 60/164,769  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: 60/173,383  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: 60/175,693  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: 60/184,831  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/191,637  
; PRIOR FILING DATE: 2000-03-23  
; NUMBER OF SEQ ID NOS: 4308  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 29418  
; LENGTH: 1352  
; TYPE: PRT  
; ORGANISM: DROSOPHILA  
US-11-097-143-29418

Query Match 62.1%; Score 41; DB 6; Length 1352;  
Best Local Similarity 77.8%; Pred. No. 7.2e+02;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 WELVGFPS 11  
DB 161 WKNVGFPS 169

RESULT 13  
US-10-424-599-182764  
; Sequence 182764, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 182764  
; LENGTH: 50  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_13604C.1.pep  
US-10-424-599-182764

Query Match 60.6%; Score 40; DB 4; Length 50;  
Best Local Similarity 66.7%; Pred. No. 48;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 GPELVGYF 9  
DB 32 GKMKLVGYF 40

RESULT 14  
US-10-425-115-319649  
; Sequence 319649, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 319649  
; LENGTH: 78  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_54590C.1.pep  
US-10-425-115-319649

Query Match 60.6%; Score 40; DB 4; Length 78;  
Best Local Similarity 66.7%; Pred. No. 73;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 GPELVGYF 9  
DB 21 GPEVLAAGWF 29

RESULT 15  
US-10-477-527-21  
; Sequence 21, Application US/10477527  
; Publication No. US20040171807A1

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; GENERAL INFORMATION:
; APPLICANT: The Trustees of the University of Pennsylvania
; APPLICANT: Gao, Guangping
; APPLICANT: Mieson, James M.
; TITLE OF INVENTION: Method for Rapid Screening of Bacterial Transformants and Novel S
; FILE REFERENCE: UPN-N2630PCT
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US/10/477,527
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/300,501
; PRIOR FILING DATE: 2002-06-04
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 146
; TYPE: PRT
; ORGANISM: chimpanzee C68 adenovirus protein
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (62) .. (62)
; OTHER INFORMATION: Xaa can be any amino acid
US-10-477-527-21

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Query Match          60.6%; Score 40; DB 4; Length 146;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      1 GPWEIVG 7
        |||:|
Db      101 GPWEIVG 107

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Search completed: December 4, 2005, 04:37:29  
 Job time : 79.8333 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 4, 2005, 03:59:51 ; Search time 23.6042 Seconds  
(without alignments)  
38.528 Million cell updates/sec

Title: US-10-632-706-128  
Perfect score: 66  
Sequence: 1 GPMELVGYFDS 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
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2: /cgn2\_6/prodata/1/1aa/6/COMB.pep:\*  
3: /cgn2\_6/prodata/1/1aa/H/COMB.pep:\*  
4: /cgn2\_6/prodata/1/1aa/PCUS/COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/RE/COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/backfil1a1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	62.1	12	1	US-08-264-093-17
2	41	62.1	121	1	US-08-264-093-3
3	39	59.1	274	2	US-09-502-540-14253
4	38	57.6	332	2	US-09-561-763-5
5	38	57.6	332	2	US-09-431-367B-5
6	38	57.6	493	2	US-09-949-016-10836
7	38	57.6	1207	2	US-09-976-594-4
8	37	56.1	427	2	US-09-902-540-15261
9	37	56.1	464	2	US-09-543-681A-6615
10	36	54.5	132	2	US-09-311-021-162
11	36	54.5	140	2	US-09-698-341-29
12	36	54.5	174	2	US-09-902-540-13916
13	36	54.5	194	1	US-08-260-202A-15
14	36	54.5	194	1	US-08-260-202A-24
15	36	54.5	194	1	US-08-017-114-15
16	36	54.5	194	1	US-08-017-114-15
17	36	54.5	194	1	US-08-017-114-15
18	36	54.5	194	2	US-08-505-307-15
19	36	54.5	194	2	US-08-505-307-17
20	36	54.5	194	2	US-09-609-151A-15
21	36	54.5	194	2	US-09-609-151A-15
22	36	54.5	194	4	PCT-US94-02034-15
23	36	54.5	194	4	PCT-US94-02034-17
24	36	54.5	235	2	US-09-902-540-16467
25	36	54.5	235	2	US-09-252-991A-29814
26	36	54.5	266	2	US-09-252-991A-21116
27	36	54.5	500	2	US-09-134-000C-3783

28	36	54.5	521	2	US-09-221-294-2	Sequence 2, Appl1
29	36	54.5	589	2	US-09-489-039A-8395	Sequence 8395, Ap
30	36	54.5	710	2	US-09-518-550-28	Sequence 28, Appl
31	36	54.5	729	2	US-10-104-047-3450	Sequence 3450, Ap
32	36	54.5	751	2	US-09-252-991A-22770	Sequence 22770, A
33	36	54.5	792	2	US-09-994-192-2	Sequence 4, Appl1
34	36	54.5	797	2	US-09-994-192-4	Sequence 4, Appl1
35	36	54.5	1542	2	US-09-949-016-9215	Sequence 9215, Ap
36	36	54.5	3177	1	US-08-477-451-4	Sequence 4, Appl1
37	36	54.5	5332	2	US-09-914-286-6	Sequence 6, Appl1
38	36	53.0	61	2	US-08-978-741-3	Sequence 3, Appl1
39	35	53.0	61	2	US-09-333-729A-5	Sequence 45, Appl1
40	35	53.0	99	2	US-09-390-134B-45	Sequence 45, Appl1
41	35	53.0	142	2	US-09-902-540-13948	Sequence 13948, A
42	35	53.0	160	2	US-09-668-672B-7	Sequence 7, Appl1
43	35	53.0	160	2	US-10-389-532-7	Sequence 7, Appl1
44	35	53.0	166	2	US-09-302-626B-52	Sequence 52, Appl
45	35	53.0	166	2	US-09-303-518D-886	Sequence 886, App

## ALIGNMENTS

RESULT 1  
US-08-264-093-17  
Sequence 17, Application US/08264093  
Patent No. 5639863  
GENERAL INFORMATION:  
APPLICANT: Michael D. Dan  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO  
TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Ridout & Maybee  
STREET: 2300 Richmond-Adelaide Centre  
STREET: 101 Richmond Street West  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5H 2J7  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: MS-DOS 6.00  
SOFTWARE: ASCII Editor  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/264,093  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA: No. 5639863 applicable  
ATTORNEY/AGENT INFORMATION:  
NAME: Lake, James R.  
REGISTRATION NUMBER: 31081  
REFERENCE/DOCKET NUMBER: NOVOP/106A/7551  
TELEPHONE: (416) 868-1482  
TELEFAX: (416) 362-0823  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: not applicable  
TOPOLOGY: linear  
US-08-264-093-17  
Query Match  
Best Local Similarity 62.1%; Score 41; DB 1; Length 12;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 GPMELVGYFD 10  
Db 2 GWMIDLNYFD 11

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RESULT 2
US-08-264-093-3
; Sequence 3, Application US/08264093
; Patent No. 5639863
; GENERAL INFORMATION:
; APPLICANT: Michael D. Dan
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
; TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
; TITLE OF INVENTION: ANTIGEN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ridout & Maybee
; STREET: 2300 Richmond-Adelaide Centre
; STREET: 101 Richmond Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 2J7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS-DOS 6.00
; SOFTWARE: ASCII Editor
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/264,093
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA: No. 5639863 applicable
; ATTORNEY/AGENT INFORMATION:
; NAME: Lake, James R.
; REGISTRATION NUMBER: 31081
; REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 868-1482
; TELEFAX: (416) 362-0823
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: amino acid
; STRANDEDNESS: not applicable
; TOPOLOGY: linear
US-08-264-093-3

Query Match          62.1%; Score 41; DB 1; Length 121;
Best Local Similarity 60.0%; Pred. No. 6.7;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 GPMELVGYFD 10
DB      100 GVMDLNLYFD 109

RESULT 3
US-09-902-540-14253
; Sequence 14253, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 14253
; LENGTH: 274
; TYPE: PRT
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; ORGANISM: Myxococcus xanthus
US-09-902-540-14253

Query Match          59.1%; Score 39; DB 2; Length 274;
Best Local Similarity 66.7%; Pred. No. 38;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      3 MELVGYFDS 11
DB      153 MNKGYFPT 161

RESULT 4
US-09-561-763-5
; Sequence 5, Application US/09561763
; Patent No. 6664373
; GENERAL INFORMATION:
; APPLICANT: Curtiss, Rory A.J. et al.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: NMI-074CP2
; CURRENT APPLICATION NUMBER: US/09/561,763
; PRIOR FILING DATE: 2000-04-29
; PRIOR APPLICATION NUMBER: 09/431,367
; PRIOR FILING DATE: 01-11-1999
; PRIOR APPLICATION NUMBER: US 09/259,951
; PRIOR FILING DATE: 01-03-1999
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-763-5

Query Match          57.6%; Score 38; DB 2; Length 332;
Best Local Similarity 77.8%; Pred. No. 72;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GPMELVGYF 9
DB      99 GRMELVGSF 107

RESULT 5
US-09-431-367B-5
; Sequence 5, Application US/09431367B
; Patent No. 6670149
; GENERAL INFORMATION:
; APPLICANT: Curtiss, Rory A.J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: NMI-074CP
; CURRENT APPLICATION NUMBER: US/09/431,367B
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: 09/259,951
; PRIOR FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-431-367B-5

Query Match          57.6%; Score 38; DB 2; Length 332;
Best Local Similarity 77.8%; Pred. No. 72;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GPMELVGYF 9
DB      99 GRMELVGSF 107

RESULT 6
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US-09-949-016-10836
; Sequence 10836, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10836
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10836

Query Match      57.6%; Score 38; DB 2; Length 493;
Best Local Similarity 60.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2  PWEVGYFDS 11
Db      69  PWTXYDFDN 78

RESULT 7
US-09-976-594-4
; Sequence 4, Application US/0976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 1207
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6673549 1863336CD1
US-09-976-594-4

Query Match      57.6%; Score 38; DB 2; Length 1207;
Best Local Similarity 77.8%; Pred. No. 3.1e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  GPWEVGYGF 9
Db      389  GPTEAVGYGF 397

RESULT 8
US-09-902-540-15261
; Sequence 15261, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
US-09-902-540-15261

APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 15261
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-15261

Query Match      56.1%; Score 37; DB 2; Length 427;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1  GPWEVGYGF 9
Db      82  GPFSEVGYGF 90

RESULT 9
US-09-543-681A-6615
; Sequence 6615, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 6615
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-6615

Query Match      56.1%; Score 37; DB 2; Length 484;
Best Local Similarity 55.6%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      3  WELVGYFDS 11
Db      155  WALIGYQS 163

RESULT 10
US-09-311-021-162
; Sequence 162, Application US/09311021
; Patent No. 6706869
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Reichel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI 6300-11A
; CURRENT APPLICATION NUMBER: US/09/311,021
; CURRENT FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 162
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-09-311-021-162

Query Match 54.5%; Score 36; DB 2; Length 132;  
Best Local Similarity 55.6%; Pred. No. 59;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GPMELVGYF 9  
|||: |||  
Db 121 GPMQDLPLPF 129

RESULT 11

US-09-698-341-29  
; Sequence 29, Application US/09698341  
; Patent No. 6946273  
; GENERAL INFORMATION:  
; APPLICANT: Sorge, Joseph  
; APPLICANT: Huribut Hogrefe, Holly  
; APPLICANT: Connie, Hansen  
; TITLE OF INVENTION: Compositions and Methods Utilizing DNA Polymerases  
; FILE REFERENCE: 25436/1560  
; CURRENT APPLICATION NUMBER: US/09/698,341  
; PRIOR FILING DATE: 2000-10-27  
; PRIOR APPLICATION NUMBER: 60/162,600  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 29  
; LENGTH: 140  
; TYPE: PRT  
; ORGANISM: Thermococcus sp. JDF-3  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (92)..(92)  
; OTHER INFORMATION: X = Unknown  
US-09-698-341-29

Query Match 54.5%; Score 36; DB 2; Length 140;  
Best Local Similarity 50.0%; Pred. No. 63;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GPMELVGYF 10  
|||: |||  
Db 55 GPMQDLVYLD 64

RESULT 12

US-09-902-540-13916  
; Sequence 13916, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 13916  
; LENGTH: 174  
; TYPE: PRT  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-13916

Query Match 54.5%; Score 36; DB 2; Length 174;  
Best Local Similarity 85.7%; Pred. No. 81;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LVGYFDS 11

Db 6 LVGYFDS 12  
|:|||||

RESULT 13

US-08-260-202A-15  
; Sequence 15, Application US/08260202A  
; Patent No. 5573910  
; GENERAL INFORMATION:  
; APPLICANT: Derecic, Vojo  
; APPLICANT: Martin, Daniel W.  
; TITLE OF INVENTION: DETECTION OF CONVERSION TO MUCOIDY IN  
; TITLE OF INVENTION: PSEUDOMONAS AERUGINOSA INFECTING CYSTIC FIBROSIS PATIENTS  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P. O. Box 4433  
; CITY: Houston  
; STATE: TX  
; COUNTRY: USA  
; ZIP: 77210-4433  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/260,202A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/260,202  
; FILING DATE: 15-JUN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/017,114  
; FILING DATE: 12-FEB-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hodgins, Daniel S.  
; REGISTRATION NUMBER: 31,026  
; REFERENCE/DOCKET NUMBER: UTsk:221\HOD  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (512) 474-7577  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 194 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-260-202A-15

Query Match 54.5%; Score 36; DB 1; Length 194;  
Best Local Similarity 71.4%; Pred. No. 91;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GPMELVGY 7  
|||: |||  
Db 81 GPMRWVG 87

RESULT 14

US-08-260-202A-24  
; Sequence 24, Application US/08260202A  
; Patent No. 5573910  
; GENERAL INFORMATION:  
; APPLICANT: Derecic, Vojo  
; APPLICANT: Martin, Daniel W.  
; TITLE OF INVENTION: DETECTION OF CONVERSION TO MUCOIDY IN  
; TITLE OF INVENTION: PSEUDOMONAS AERUGINOSA INFECTING CYSTIC FIBROSIS PATIENTS  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P. O. Box 4433



CITY: Houston  
STATE: TX  
COUNTRY: USA  
ZIP: 77210-4433  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/260,202A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/260,202  
FILING DATE: 15-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/017,114  
FILING DATE: 12-FEB-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Hodgins, Daniel S.  
REGISTRATION NUMBER: 31,026  
REFERENCE/DOCKET NUMBER: UTSK:221\HOD  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 194 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-260-202A-24

Query Match 54.5%; Score 36; DB 1; Length 194;  
Best Local Similarity 71.4%; Pred. No. 91;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPMELVG 7  
|||:|  
DB 81 GPMRWVG 87

RESULT 15  
US-08-017-114-15  
Sequence 15, Application US/08017114  
Patent No. 5591838  
GENERAL INFORMATION:  
APPLICANT: Detetic, Vojo  
APPLICANT: Martin, Daniel W.  
TITLE OF INVENTION: DETECTION OF CONVERSION TO MUCOIDY IN  
TITLE OF INVENTION: PSEUDOMONAS AERUGINOSA INFECTING CYSTIC FIBROSIS PATIENTS  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P. O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/017,114  
FILING DATE: 19930212  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Hodgins, Daniel S.  
REGISTRATION NUMBER: 31,026  
REFERENCE/DOCKET NUMBER: UTSK:205/HOD

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512/320-7200  
TELEFAX: 512/474-7577  
TELEX: N/A  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 194 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-017-114-15

Query Match 54.5%; Score 36; DB 1; Length 194;  
Best Local Similarity 71.4%; Pred. No. 91;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPMELVG 7  
|||:|  
DB 81 GPMRWVG 87

Search completed: December 4, 2005, 04:09:43  
Job time : 23.6042 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: December 4, 2005, 04:31:36 ; Search time 100.375 Seconds  
(without alignments)  
77.318 Million cell updates/sec

Title: US-10-632-706-128  
Perfect score: 66  
Sequence: 1 GPMELVGYFDS 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : uniprot\_05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	68.2	279	2	087858_STRCO
2	45	68.2	290	2	082M58_STRAM
3	45	68.2	748	2	Q5NQ32_ZYMMO
4	44	66.7	367	1	MECA_SALTY
5	44	66.7	367	1	MECA_SALTY
6	44	66.7	367	2	Q5PK1_SALPA
7	44	66.7	449	2	Q63M53_BURPS
8	43	65.2	231	2	Q4K719_PSEFS
9	43	65.2	1201	2	Q7UVR6_RHOBA
10	43	65.2	1633	1	YP74_CAEEL
11	43	65.2	7548	2	Q5WRU1_CAEEL
12	42	63.6	272	2	Q748S8_GBOSL
13	42	63.6	381	2	Q6K1T5_ORYSA
14	42	63.6	454	2	Q8TU9V_METAC
15	42	63.6	578	2	Q8D959_VIBVY
16	42	63.6	578	2	Q7MLB3_VIBVY
17	42	63.6	1275	2	Q8O061_METMA
18	41	62.1	211	2	Q8KAK7_PSEAE
19	41	62.1	241	2	Q82347_ARATH
20	41	62.1	273	2	Q7UND8_RHOBA
21	41	62.1	318	2	Q4KEF0_PSEFS
22	41	62.1	491	1	GLNA_ARCFU
23	41	62.1	518	2	Q5LH40_BACRN
24	41	62.1	518	2	Q64XZ7_BACRN
25	41	62.1	613	2	Q6BTL3_DEBHA
26	41	62.1	619	1	GCCR_XENLA
27	41	62.1	619	2	Q5SKA5_THERR
28	41	62.1	619	2	Q6PAK3_XENLA
29	41	62.1	697	1	Y2326_MYCTU
30	41	62.1	697	1	Y2353_MYCBO
31	41	62.1	1350	2	Q9V5J7_DROME

32	41	62.1	1370	2	Q7K0X6_DROME	Q7K0X6_drosophila
33	41	62.1	2581	2	Q7T7T5_9YIRU	Q7T7T5_heterosigma
34	40	60.6	122	2	Q8B357_SHEON	Q8B357_sheanella
35	40	60.6	146	2	Q8UY74_9ADEN	Q8UY74_simian aden
36	40	60.6	206	2	Q6CP97_9ADEN	Q6CP97_simian aden
37	40	60.6	207	2	Q6CPD3_9ADEN	Q6CPD3_simian aden
38	40	60.6	208	2	Q6CPG9_9ADEN	Q6CPG9_simian aden
39	40	60.6	210	2	Q6H1B6_9ADEN	Q6H1B6_human aden
40	40	60.6	210	2	Q8BE16_ADE04	Q8BE16_human aden
41	40	60.6	282	2	Q7N9W4_PROL	Q7N9W4_photobacter
42	40	60.6	304	2	Q87XQ4_PSESM	Q87XQ4_pseudomonas
43	40	60.6	319	2	Q4ZPN4_PSESY	Q4ZPN4_pseudomonas
44	40	60.6	323	2	Q4INB2_GIBZE	Q4INB2_glibbrella
45	40	60.6	392	2	Q8LR17_PETHY	Q8LR17_pecunia hyb

## ALIGNMENTS

```

RESULT 1
ID 087858_STRCO PRELIMINARY; PRT; 279 AA.
AC 087858;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Putative transmembrane sugar transport protein.
GN OrderedLocNames=SC06603; ORFNames=SC8A6.24;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
OC Streptomycetaceae; Streptomycetaceae; Streptomyces.
OK NCBI_TaxId=1902;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleier H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kleier T., Jarke L., Jarke L., Murphy K., O'Neill S.,
RA Rabinowitch E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RL coelicolor A3(2).";
CC Complete genome sequence of the model actinomycete Streptomyces
CC Nature 417:141-147(2002).
CC -I- FUNCTION: Part of a binding-protein-dependent transport system.
CC -I- Probably responsible for the translocation of the substrate across
CC the membrane (By similarity).
CC -I- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -I- SIMILARITY: Belongs to the binding-protein-dependent transport
CC system permease family.
CC EMBL AL939128; CA19796.1; -; Genomic_DNA.
DR PIR: T35791; T35791.
DR GO: GO:0016021; C:Integral to membrane; IEA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005351; F:sugar porter activity; IEA.
DR GO: GO:0005215; F:transporter activity; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR000515; BPD_transp.
DR Pfam: PF00528; BPD_transp_1; 1.
DR PROSITE: PS50928; ABC_TM1; 1.
KW Complete proteome; Sugar transport; Transmembrane; Transport.
SQ
SEQUENCE 279 AA; 30335 MW; 88606338588F8BFA CRC64;
Query Match 68.2%; Score 45; DB 2; Length 279;
Best Local Similarity 77.8%; Pred. No. 25;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

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Db          160 WMLIGYFDS 168

RESULT 2
ID 082M58_STRAW PRELIMINARY; PRT; 290 AA.
AC 082M58;
DT 01-JUN-2003 (TREMblrel. 24, Created)
DT 01-JUN-2003 (TREMblrel. 24, Last sequence update)
DE 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE Putative sugar ABC transporter permease protein.
GN OrderedLocuNames=SAV1802;
OC Streptomyces avermectilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;

RM NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.21143198;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shirose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermectilis: deducing the ability of producing secondary
RT metabolites."
RT Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=22608306; PubMed=12692562; DOI=10.1038/nbt820;
RA Ikeda H., Ishikawa J., Hanamoto A., Shirose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermectilis."
RT Nat. Biotechnol. 21:526-531(2003).
CC -1- FUNCTION: Part of a binding-protein-dependent transport system.
CC Probably responsible for the translocation of the substrate across
CC the membrane (by similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
CC -1- SIMILARITY: Belongs to the binding-protein-dependent transport
CC system permease family.
DR EMBL; BA000030; BAC69513.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005351; F:sugar porter activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000515; BPT transp.
DR Pfam; PF00528; BPT transp. 1; 1.
DR PROSITE; PS50928; ABC TM1.1.
DR Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 290 AA; 3133 MW; 92650429419A5B9 CRC64;

Query Match 68.2%; Score 45; DB 2; Length 290;
Best Local Similarity 77.8%; Pred. No. 26;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy          3 WELVGYFDS 11
Db          171 WMLIGYFDS 179

RESULT 3
ID 05N032_ZYMO PRELIMINARY; PRT; 748 AA.
AC 05N032;
DT 01-FEB-2005 (TREMblrel. 29, Created)
DT 01-FEB-2005 (TREMblrel. 29, Last sequence update)
DE 01-FEB-2005 (TREMblrel. 29, Last annotation update)
DE Polyribonucleotide nucleotidyltransferase (EC 2.7.7.8).
GN Name=pnp; OrderedLocuNames=ZMO0549;
OS Zymomonas mobilis.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC Sphingomonadaceae; Zymomonas.
OX NCBI_TaxID=542;

RM NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 31821 / ZM4 / CP4;
RX PubMed=15592456; DOI=10.1038/nbt1045;
RA Seo J.-S., Chong H., Park H.S., Yoon K.-O., Jung C., Kim J.J.,
RA Hong J.H., Kim H., Kim J.-H., Kil J.-I., Park C.J., Oh H.-M.,
RA Lee J.-S., Jin S.-U., Um H.-W., Lee H.-O., Oh S.-O., Kim J.Y.,
RA Kang H.L., Lee S.Y., Lee K.J., Kang H.S.;
RT "The genome sequence of the ethanologenic bacterium Zymomonas mobilis
RT ZM4."
RT Nat. Biotechnol. 23:63-68(2005).
DR EMBL; AB008692; FAY92173.1; -; Genomic DNA.
DR GO; GO:0000175; F:3'-5'-exoribonuclease activity; IEA.
DR GO; GO:0004654; F:polyribonucleotide nucleotidyltransferase a. .; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006396; P:RNA processing; IEA.
DR InterPro; IPR001247; 3-Exonase.
DR InterPro; IPR004087; KH.
DR InterPro; IPR004088; KH type_1.
DR InterPro; IPR012162; PNPase.
DR InterPro; IPR003029; S1.
DR Pfam; PF00013; KH 1; 1.
DR Pfam; PF03726; PNPase; 1.
DR Pfam; PF01138; RNase PH; 2.
DR Pfam; PF03725; RNase PH_C; 2.
DR Pfam; PF00575; S1; 1.
DR PIRSF; PIRSF005499; PNPase; 1.
DR SMART; SM00322; KH; 1.
DR SMART; SM00316; S1; 1.
DR PROSITE; PS50084; KH type_1; 1.
DR PROSITE; PS50126; S1; 1.
DR Complete proteome; Nucleotidyltransferase; Transferase.
SQ SEQUENCE 748 AA; 81949 MW; EB8C43821F85F6DB CRC64;

Query Match 68.2%; Score 45; DB 2; Length 748;
Best Local Similarity 80.0%; Pred. No. 67;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy          2 PWEVGYFDS 11
Db          230 PWEVGYFDS 239

RESULT 4
ID WECA_SALTI STANDARD; PRT; 367 AA.
AC 082386;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE Undecaprenyl-phosphate alpha-N-acetylglucosaminyl 1-phosphate
DE transferase (EC 2.7.8.-) (UDP-GlcNAc:undecaprenyl-phosphate GlcNAc-1-
DE phosphate transferase).
GN Name=weca; Synonyms=rtf; OrderedLocuNames=STY3637, t3379;
OS Salmomella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmomella.
OX NCBI_TaxID=601;

RM NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sabathia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jagsle K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,

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RA Whitehead S., Barrell B.G.;  
 RT "Complete genome sequence of a multiple drug resistant *Salmonella*  
 RT enterica serovar Typhimurium CT18.";  
 RL Nature 413:848-852(2001).  
 RN [2]  
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=Ty2 / ATCC 700931.  
 RX MEDLINE=25311367; PubMed=12644504;  
 RX DOI=10.1128/JB.185.7.2330-2337.2003;  
 RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,  
 RA Burdland V., Kodoyianni V., Schwartz D.C., Blatter F.R.;  
 RT "Comparative genomes of *Salmonella enterica* serovar Typhimurium strains Ty2  
 RT and CT18.";  
 RL J. Bacteriol. 185:2330-2337(2003).  
 CC -1- FUNCTION: Catalyzes the synthesis of Und-PP-GlcNAc (lipid I), the  
 CC first lipid-linked intermediate involved in ECA synthesis. This  
 CC lipid is also an acceptor for the addition of subsequent sugars to  
 CC complete the biosynthesis of O-antigen (by similarity).  
 CC -1- CATALYTIC ACTIVITY: UDP-N-acetyl-D-glucosamine + undecaprenyl  
 CC phosphate = UMP + N-acetyl-alpha-D-glucosaminylidiphospho-  
 CC undecaprenol.  
 CC -1- COFACTOR: Magnesium and manganese (By similarity).  
 CC -1- PATHWAY: Synthesis of enterobacterial common antigen (ECA).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane  
 CC (By similarity).  
 CC -1- SIMILARITY: Belongs to the glycosyltransferase 4 family. Weca  
 CC subfamily.  
 CC -----  
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 CC removed.  
 CC -----  
 DR EMBL, AF627279; CAD09398.1; -; Genomic DNA.  
 DR EMBL, AE016845; AAC07030.1; -; Genomic DNA.  
 DR InterPro: IPR012750; ECA\_Weca\_rel.  
 DR Pfam: PF00953; Glycos\_transf\_4; 1.  
 DR TIGRfam: TIGR02380; ECA\_weca; 1.  
 KM Complete proteome; Glycosyltransferase; Inner membrane;  
 KM Lipopolysaccharide biosynthesis; Magnesium; Manganese; Membrane;  
 KM TRANSFERASE; Transmembrane.  
 KW TRANSFERASE 3  
 FT TRANSFERASE 23 Potential.  
 FT TRANSFERASE 45 65 Potential.  
 FT TRANSFERASE 69 89 Potential.  
 FT TRANSFERASE 106 126 Potential.  
 FT TRANSFERASE 129 149 Potential.  
 FT TRANSFERASE 158 178 Potential.  
 FT TRANSFERASE 187 207 Potential.  
 FT TRANSFERASE 213 233 Potential.  
 FT TRANSFERASE 242 262 Potential.  
 FT TRANSFERASE 294 314 Potential.  
 FT TRANSFERASE 318 338 Potential.  
 SQ SEQUENCE 367 AA; 41086 MW; 28DA31CB1AE2D930 CRC64;  
 Query Match 66.7%; Score 44; DB 1; Length 367;  
 Best Local Similarity 69.2%; Pred. No. 49;  
 Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;  
 QY 1 GPMELV---GYF 9  
 Db 127 GPMELVGPFGYF 139  
 RESULT 5  
 WECA\_SALTY STANDARD; PRT; 367 AA.  
 ID WECA\_SALTY STANDARD; PRT; 367 AA.  
 AC G9L6R7; O33788;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Undecaprenyl-phosphate alpha-N-acetylglucosaminyl 1-phosphate  
 DE transferase (EC 2.7.8.-) (UDP-GlcNAc:undecaprenyl-phosphate GlcNAc-1-  
 DE phosphate transferase)  
 GN Name=weca; Synonyms=rfe; OrderedLocustNames=STM3918; ORFNames=STMD1.72;  
 OS *Salmonella typhimurium*.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; *Salmonella*.  
 OC NCBI\_TaxID=602;  
 RN [1]  
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RP STRAIN=LT2 / SGSC1412 / ATCC 700720;  
 RC MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;  
 RX McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,  
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,  
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,  
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,  
 RA Waterston R., Wilson R.K.;  
 RT "Complete genome sequence of *Salmonella enterica* serovar Typhimurium  
 RT LT2.";  
 RL Nature 413:852-856(2001).  
 RN [2]  
 RN NUCLEOTIDE SEQUENCE OF 111-367.  
 RP STRAIN=LT2;  
 RC MEDLINE=98409259; PubMed=9738879; DOI=10.1007/s004380050787;  
 RX Mouslim C., Cano D.A., Casadesu J.;  
 RA "The stx, rfe and mecN genes of *Salmonella typhimurium* and their  
 RT involvement in the His(c) pleiotropic response.";  
 RL Mol. Genet. 259:46-53(1998).  
 CC -1- FUNCTION: Catalyzes the synthesis of Und-PP-GlcNAc (lipid I), the  
 CC first lipid-linked intermediate involved in ECA synthesis. This  
 CC lipid is also an acceptor for the addition of subsequent sugars to  
 CC complete the biosynthesis of O-antigen (By similarity).  
 CC -1- CATALYTIC ACTIVITY: UDP-N-acetyl-D-glucosamine + undecaprenyl  
 CC phosphate = UMP + N-acetyl-alpha-D-glucosaminylidiphospho-  
 CC undecaprenol.  
 CC -1- COFACTOR: Magnesium and manganese (By similarity).  
 CC -1- ENZYME REGULATION: Inhibited by tunicamycin.  
 CC -1- PATHWAY: Synthesis of enterobacterial common antigen (ECA).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane  
 CC (By similarity).  
 CC -1- SIMILARITY: Belongs to the glycosyltransferase 4 family. Weca  
 CC subfamily.  
 CC -----  
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 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 DR EMBL, AF233324; AAF33469.1; -; Genomic DNA.  
 DR EMBL, AE008883; AL22767.1; -; Genomic DNA.  
 DR EMBL, AJ002275; CAA05287.1; -; Genomic DNA.  
 DR StyGene; SG77777; rfe.  
 DR InterPro: IPR012750; ECA\_Weca\_rel.  
 DR InterPro: IPR000715; Glyco\_transf\_4.  
 DR Pfam: PF00953; Glycos\_transf\_4; 1.  
 DR TIGRfam: TIGR02380; ECA\_weca; 1.  
 KM Complete proteome; Glycosyltransferase; Inner membrane;  
 KM Lipopolysaccharide biosynthesis; Magnesium; Manganese; Membrane;  
 KM TRANSFERASE; Transmembrane.  
 KW TRANSFERASE 3  
 FT TRANSFERASE 45 65 Potential.  
 FT TRANSFERASE 69 89 Potential.  
 FT TRANSFERASE 106 126 Potential.  
 FT TRANSFERASE 129 149 Potential.  
 FT TRANSFERASE 158 178 Potential.  
 FT TRANSFERASE 187 207 Potential.  
 FT TRANSFERASE 213 233 Potential.  
 FT TRANSFERASE 242 262 Potential.  
 FT TRANSFERASE 294 314 Potential.  
 FT TRANSFERASE 318 338 Potential.  
 FT CONFLICT 118 120 HIG -> ALS (in Ref. 2).

FT CONFLICT 128 138 PHELVIGPGY -> ALGVSNAPLMH (1n Ref. 2).  
 FT CONFLICT 146 148 MAA -> LMG (1n Ref. 2).  
 FT CONFLICT 220 220 S -> C (1n Ref. 2).  
 SQ SEQUENCE 367 AA; 41087 MW; 1ED31C81AE2D938 CRC64;

Query Match 66.7%; Score 44; DB 1; Length 367;  
 Best Local Similarity 69.2%; Pred. No. 49;  
 Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 GPELVY----GYF 9  
 |||||  
 DB 127 GPELVIGPGYF 139

## RESULT 6

OSPK1\_SALPA PRELIMINARY; PRT; 367 AA.

AC OSPK1;  
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)  
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)  
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
 DE Putative undecaprenyl-phosphate alpha-N-acetylglucosaminyltransferase.  
 GN Name: rfe; OrderedLocNames=SPA3756;  
 OS Salmonella paratyphi-a.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Salmonella.  
 OX NCBI\_TaxID=54388;  
 RN [1]

## NUCLEOTIDE SEQUENCE.

RP STRAIN=ATCC 9150;  
 RC PubMed=15531882; DOI=10.1038/ng1470;  
 RA McClelland M., Sanderson K.R., Clifton S.W., Latreille P., Porwollik S., Sabo A., Meyer R., Bieri T., Ozerky P., McCellan M., Hartline C.R., Wang C., Nguyen C., Berghoff A., Elliott G., Kohlberg S., Strong C., Du F., Carter J., Kremizki C., Layman D., Leonard S., Sun H., Fulton L., Nash W., Miner T., Mink P., Delehaunty K., Fronick C., Magrini V., Nhan M., Warren W., Flores L., Speleth J., Wilson R.K.;  
 RT "Comparison of genome degradation in Paratyphi A and Typhi, human-restricted serovars of Salmonella enterica that cause typhoid.";  
 RL Nat. Genet. 36:1268-1274(2004).  
 DR EMBL; CP000026; AAV79540.1; -; Genomic DNA.  
 DR GO; GO:0018666; C:inner membrane; IEA.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.  
 DR GO; GO:0006629; P:lipid metabolism; IEA.  
 DR GO; GO:0009103; P:lipopolysaccharide biosynthesis; IEA.  
 DR InterPro; IPR00715; Glyco\_trans\_4.  
 DR InterPro; IPR001865; Ribosomal\_S2.  
 DR Pfam; PF00953; Glycos\_transf\_4; 1.  
 DR PROSITE; PS00962; RIBOSOMAL\_S2\_1; UNKNOWN 1.  
 KM Complete proteome; Glycosyltransferase; Transferase.  
 SQ SEQUENCE 367 AA; 41086 MW; 1ED31C81AE2D938 CRC64;

## Query Match 66.7%; Score 44; DB 2; Length 367;

Best Local Similarity 69.2%; Pred. No. 49;  
 Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 GPELVY----GYF 9  
 |||||  
 DB 127 GPELVIGPGYF 139

RESULT 7  
 OS3N53\_BURPS PRELIMINARY; PRT; 449 AA.

AC OS3N53;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Hypothetical protein.  
 GN OrderedLocNames=BPS0443;

OS Burkholderia pseudomallei (Pseudomonas pseudomallei).  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Burkholderiaceae; Burkholderia; pseudomallei group.  
 OX NCBI\_TaxID=28450;

## NUCLEOTIDE SEQUENCE.

RP STRAIN=K96243;  
 RC PubMed=15377794; DOI=10.1073/pnas.040302101;  
 RA Holden M.T.G., Titchall R.W., Peacock S.D., Cerdano-Tarraga A.-M., Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.L., Bentley S.D., Sebatina M., Thomson N.R., Bacon N., Beacham I.R., Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I., Chillingworth T., Cronin A., Crosslet B., Davis P., Deshaizer D., RA Felwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagsels K., Ketch K.B., Maddison M., Moulé S., Price C., Quail M.A., RA Rabinowitch E., Rutherford K., Sanders M., Simmonds M., RA Songvilai S., Stevens K., Tamara S., Vesaratchaveest M., RA Whitehead S., Yeats C., Barrett B.G., Oyston P.C.F., Parkhill J.;  
 RT "Genomic plasticity of the causative agent of melioidosis."  
 RL Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).  
 DR EMBL; BX571966; CAH37899.1; -; Genomic DNA.  
 KM Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 449 AA; 49531 MW; F1618B746D15240 CRC64;

Query Match 66.7%; Score 44; DB 2; Length 449;  
 Best Local Similarity 75.0%; Pred. No. 60;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPELVIGY 8  
 |||||  
 DB 183 GPMRLIGY 190

RESULT 8  
 ID Q4K719\_PSEFS PRELIMINARY; PRT; 231 AA.

AC Q4K719;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Phosphoserine phosphatase, putative.  
 GN ORFNames=PFL\_4883;  
 OS Pseudomonas fluorescens (strain Pf-5).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID=220664;  
 RN [1]

## NUCLEOTIDE SEQUENCE.

RP STRAIN=PF-5;  
 RC PubMed=15980861; DOI=10.1038/nbt1110;  
 RA Paulsen I.T., Press C., Ravel J., Kobayashi D., Myers G.S., Mavrodin D., DeBoy R.T., Seshadri R., Ren Q., Madupu R., Dodson R.J., RA Wurtold S., Brinkac L.M., Daugherty S.C., Sullivan S.A., Rodovitz M., RA Gwinn M.L., Zhou L., Nelson W.C., Weidman J., Watkins K., Tran K., RA Khouri H.M., Pierson B., Pierson L., III, Thomasow L., Loper J.;  
 RT "Complete genome sequence of the plant commensal Pseudomonas fluorescens Pf-5.";  
 RL Nat. Biotechnol. 23:873-878(2005).  
 DR EMBL; CP000076; AAY94113.1; -; Genomic DNA.  
 SQ SEQUENCE 231 AA; 25717 MW; A4DEA84C59107CF2 CRC64;

## Query Match 65.2%; Score 43; DB 2; Length 231;

Best Local Similarity 80.0%; Pred. No. 46;  
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PHELVGYFDS 11  
 |||||  
 DB 61 PAELVGYFDS 70

RESULT 9  
 OTUYR6\_RHOBA

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ID 07YUR6_RHOBA PRELIMINARY; PRT; 1201 AA.
AC 07YUR6;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=RB426;
OS Rhodospirillum rubrum.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxId=117;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heilmann K., Rabus R.,
RA Schlesner H., Amann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
RT strain 1."
RT Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
DR EMBL; BX294133; CAD71575.1; -; Genomic_DNA.
DR GO; GO:0020037; F:home binding; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR012282; Cytochrome_c_R.
DR InterPro; IPR011444; DUF1549.
DR InterPro; IPR011429; PSC3.
DR Pfam; PF07635; PSCYtl.1.
DR Pfam; PF07583; PSCYtl2.1.
DR Pfam; PF07587; PSD1.1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 1201 AA; 134482 MW; 728682735130D01 CRC64;

Query Match 65.2%; Score 43; DB 2; Length 1201;
Best Local Similarity 72.7%; Pred. No. 2.4e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GPMELVGYFDS 11
DB 1029 GLWEAVGYTDS 1039

RESULT 10
ID YP74_CAEEL STANDARD; PRT; 1633 AA.
AC 009251; 010908;
DT 01-NOV-1995 (Rel. 32, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Hypothetical protein B0228.4 in chromosome II.
GN ORFNames=B0228.4/B0228.2;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxId=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE REVISION.
RG Wormbase consortium;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL; U23168; AAC38806.2; -; Genomic_DNA.
DR Ensembl; B0228.4; Caenorhabditis elegans.
DR Wormbase; WBGene00015061; B0228.4.
DR WormPep; B0228.4; CB31282.
DR InterPro; IPR010734; Copine.
DR Pfam; PF07002; Copine.1.
DR PRINTS; PR00453; VWRPDOMAIN.
KW Complete proteome; Hypothetical protein.
FT COMBIAS 155 165
FT COMBIAS 316 338 Cys-rich.
FT COMBIAS 892 1019 Lys-rich.
SQ SEQUENCE 1633 AA; 183328 MW; 3B4B46800B7A44D CRC64;

Query Match 65.2%; Score 43; DB 1; Length 1633;
Best Local Similarity 60.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPMELVGYFDS 10
DB 1567 GPMNMGRPD 1576

RESULT 11
ID Q5WRU1_CAEEL PRELIMINARY; PRT; 7548 AA.
AC Q5WRU1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein B0228.4.
GN ORFNames=B0228.4;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxId=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL; U23168; AAU87832.1; -; Genomic_DNA.
DR Ensembl; B0228.4; Caenorhabditis elegans.
DR Wormbase; WBGene00015061; B0228.4.
DR WormPep; B0228.4; CB37470.
DR InterPro; IPR010734; Copine.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF07002; Copine.1.
DR SMART; SM00327; VWA.1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 7548 AA; 840584 MW; 8BEC3CC03D12C1C8 CRC64;

Query Match 65.2%; Score 43; DB 2; Length 7548;
Best Local Similarity 60.0%; Pred. No. 1.5e+03;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPMELVGYFDS 10
DB 7482 GPMNMGRPD 7491

RESULT 12
ID Q748S8_GROSL PRELIMINARY; PRT; 272 AA.
AC Q748S8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Glutamate racemase (EC 5.1.1.13).
GN Name=mult; OrderedLocustNames=GSU2923;

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OS Geobacter sulfurreducens.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
OC Geobacteraceae; Geobacter.
OX NCBI_TaxID=35554;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PCA / ATCC 51573;
RX PubMed=14671304; DOI=10.1126/science.1088727;
RA Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
RA Heidelberg J.F., Wu D., Wu M., Ward N.L., Bennan M.J., Dodson R.J.,
RA Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
RA Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
RA Davidson T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
RA Velman J.E., Khouri H.M., Feldblyum T.V., Ueberback T.R.,
RA Van Aken S.E., Lovley D.R., Fraser C.M.;
RT "Genome of Geobacter sulfurreducens: metal reduction in subsurface
RT environments."
RL Science 302:1967-1969(2003).
DR EMBL, AE017180; AAR36315.1; -; Genomic_DNA.
DR HSSP, P56868; 1B74.
DR TIGR, GSU2923; -.
DR GO; GO:0008881; F:glutamate racemase activity; IEA.
DR GO; GO:0016853; F:isomerase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR GO; GO:0009252; P:peptidoglycan biosynthesis; IEA.
DR InterPro; IPR001920; Asp/Glu race.
DR InterPro; IPR004391; Glu race.
DR Pfam; PF01177; Asp_Glu_race; 1.
DR TIGRfam; TIGR00067; gltC_race; 1.
DR PROSITE; PS00923; ASP_GLU_RACEMASE_1; 1.
DR PROSITE; PS00924; ASP_GLU_RACEMASE_2; 1.
DR Complete proteome; Isomerase.
SQ SEQUENCE 272 AA; 29521 MW; 674BA01437EC4163 CRC64;

Query Match 63.6%; Score 42; DB 2; Length 272;
Best Local Similarity 60.0%; Pred. No. 80;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 PWEIYGVFDS 11
DB 2 PWEIYGVFDS 11

RESULT 13
O6K1T5 ORYSA PRELIMINARY; PRT; 381 AA.
AC O6K1T5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein OSUNBA0038P01.38.
GN Name=OSUNBA0038P01.38;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriocaridaceae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Saeki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nipponbare (GAS) genomic DNA, chromosome 2, BAC
RT clone:OSUNBA0038P01.1."
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL, AP06457; BAD22515.1; -; Genomic_DNA.
DR Gramene; O6K1T5; -.
DR GO; GO:0006512; P:ubiquitin cycle; IEA.
DR InterPro; IPR001810; F-box.
DR Pfam; PF00646; F-box; 1.
KW Hypothetical protein.
SQ SEQUENCE 381 AA; 42714 MW; A50564C2F7224FC4 CRC64;

Query Match 63.6%; Score 42; DB 2; Length 381;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;

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Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPWEIYGVY 8
DB 176 GPWEIYGVY 183

RESULT 14
O8TV9 METAC PRELIMINARY; PRT; 454 AA.
ID O8TV9;
AC O8TV9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein MA3668.
GN OrderedLocustNames=MA3668;
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Methanocicrobia; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=11932238; DOI=10.1101/gr.223902;
RA Galagan J.E., Nisbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA Fitzhugh W., Calvo S., Engels R., Smirnov S., Altner D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., Dearellano K., Johnson R.,
RA Linton L., McSwan P., McKernan K., Talmas J., Tittell K., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Gramme D.A., Guse A.M.,
RA Hedderich R., Ingram-Smith C., Kuetner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Unayam L.A., White O., White R.H., de Macario E.C.,
RA Perry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.T.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Biren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT and physiological diversity."
RL Genome Res. 12:532-542(2002).
DR EMBL, AE011076; AAM07023.1; -; Genomic_DNA.
DR InterPro; IPR010180; Cas_CXXC_CXXC.
DR TIGRfam; TIGR01908; cas_CXXC_CXXC; 1.
DR Complete proteome.
SQ SEQUENCE 454 AA; 52893 MW; 2BBD6A6E629B0A0 CRC64;

Query Match 63.6%; Score 42; DB 2; Length 454;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPWEIYGVY 9
DB 319 GDMWEIYGVY 327

RESULT 15
O8D959 VIBVU PRELIMINARY; PRT; 578 AA.
ID O8D959 VIBVU PRELIMINARY; PRT; 578 AA.
AC O8D959;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Methyl-accepting chemotaxis protein.
GN OrderedLocustNames=V12747;
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=672;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CMCP6;
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RA Choy H.E.;
RT "Complete genome sequence of Vibrio vulnificus CMCP6."
RT Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.

```



DR EMBL; AE016806; AA011091.1; -; Genomic\_DNA.  
DR HSSP; P02942; 1QU7.  
DR GO; GO:0019866; C:inner membrane; IEA.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0004871; F:signal transducer activity; IEA.  
DR GO; GO:0006935; P:chemotaxis; IEA.  
DR GO; GO:0007165; P:signal transduction; IEA.  
DR InterPro; IPR004089; Chntaxis\_transd.  
DR InterPro; IPR003660; H1b\_kin\_HAMP.  
DR Pfam; PF00672; HAMP; 1.  
DR Pfam; PF00015; MCPsignal; 1.  
DR SMART; SM00304; HAMP; 1.  
DR SMART; SM00283; NA; 1.  
DR PROSITE; PSS0111; CHEMOTAXIS\_TRANSDUC\_2; 1.  
DR PROSITE; PSS0885; HAMP; 1.  
KW Complete proteome.  
SQ SEQUENCE 578 AA; 63178 MW; 55004ADC7356DA18 CRC64;

Query Match 63 6%; Score 42; DB 2; Length 578;  
Best Local Similarity 75.0%; Pred. No. 1.7e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Qy 3 WELVGYFD 10  
|||:|  
Db 204 WELICYID 211

Search completed: December 4, 2005, 04:52:22  
Job time : 102.375 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:31:45 ; Search time 15.5833 Seconds  
(without alignments)  
67.918 Million cell updates/sec

Title: US-10-632-706-128  
Perfect score: 66  
Sequence: 1 GPMELVGYFDS 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80:1\*  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	68.2	279	2 T35791	probable transmem
2	44	66.7	367	2 AD0922	probable undecapre
3	43	65.2	1788	2 T29043	hypothetical prote
4	41	62.1	491	2 E69368	glutamine syntheta
5	41	62.1	550	2 B84900	hypothetical prote
6	41	62.1	619	1 S48729	glucokinase regula
7	41	62.1	697	2 G70704	hypothetical prote
8	40	60.6	724	2 B87015	ABC transporter ML
9	40	60.6	726	2 T44905	ABC-type transport
10	40	60.6	888	2 D84824	probable DNA-direc
11	40	60.6	931	2 F84637	probable plasma me
12	39	59.1	239	2 D71051	hypothetical prote
13	39	59.1	320	2 T33303	hypothetical prote
14	39	59.1	459	2 S17907	glutamate dehydrog
15	39	59.1	471	2 S28476	ribL-protein VC024
16	39	59.1	578	2 B82204	methyL-accepting c
17	39	59.1	949	1 PXM0P1	H+-exporting Arpas
18	38	57.6	173	1 S44003	NADH2 dehydrogenas
19	38	57.6	274	2 C75335	glycerol uptake fa
20	38	57.6	409	2 S63614	male protein homol
21	38	57.6	432	2 T17829	ankyrin repeat pro
22	38	57.6	465	2 T26146	hypothetical prote
23	38	57.6	496	2 G16933	apolipoprotein n-a
24	38	57.6	499	2 G97761	apolipoprotein N-a
25	38	57.6	532	2 AF3498	apolipoprotein N-a
26	38	57.6	1091	2 T34247	hypothetical prote
27	38	57.6	1107	2 T34246	hypothetical prote
28	38	57.6	2100	2 T03223	probable polypeptid
29	37	56.1	213	2 C64041	hypothetical prote

30	37	56.1	217	2 A82491	fine protein VCA01
31	37	56.1	226	2 A87664	hypothetical prote
32	37	56.1	235	2 T44679	spu protein homol
33	37	56.1	241	2 T39330	probable 60S acid
34	37	56.1	276	2 A95309	probable ABC trans
35	37	56.1	277	2 AF3216	ABC transporter, m
36	37	56.1	349	2 T31855	hypothetical prote
37	37	56.1	365	2 S61636	hypothetical prote
38	37	56.1	400	2 AF0291	probable drug res
39	37	56.1	413	2 G95965	conserved hypothet
40	37	56.1	426	2 T08550	choline monooxygen
41	37	56.1	462	2 T58179	5HT3 receptor subu
42	37	56.1	468	2 T48615	hypothetical prote
43	37	56.1	502	2 S50519	hypothetical prote
44	37	56.1	601	1 A64222	heat shock protein
45	37	56.1	642	2 G69371	acetyl-CoA synthe

## ALIGNMENTS

RESULT 1  
T35791  
probable transmembrane sugar transport protein - Streptomyces coelicolor  
C/Species: Streptomyces coelicolor  
C/Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 09-Jul-2004  
C/Accession: T35791  
R/Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, July 1998  
A/Reference number: Z21570  
A/Accession: T35791  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-279 <SEB>  
A/Cross-references: UNIPROT:087858; UNIPARC:UP100000DACA7; EMBL:AL031013; PIDN:CAA19796  
A/Experimental source: strain A3(2)  
C/Genetics:  
A/Gene: SC0EDB:SC8A6.24  
C/Superfamily: maltose transport protein malG

Query Match 68.2% Score 45; DB 2; Length 279;  
Best Local Similarity 77.8% Pred. No. 2.8;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 3 WELVGYFDS 11  
DB 160 WMLIGYFDS 168

RESULT 2  
AD0922  
probable undecaprenyl-phosphate alpha-N-acetylglucosaminyltransferase STY3637 [imported]  
C/Species: Salmonella enterica subsp. enterica serovar Typhi  
A/Note: this species has also been called Salmonella typhi  
C/Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 03-Feb-2003  
C/Accession: AD0922  
R/Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Cronin, P.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Garra, P.  
Nature 413, 848-852, 2001  
A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Stevenson, K.,  
A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov  
A/Reference number: AB0502; WUID:21534947; PMID:11677608  
A/Accession: AD0922  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-367 <PAR>  
A/Cross-references: UNIPARC:UP1000005A58F; GB:AL513382; PIDN:CAD09398.1; PID:G16504516;  
C/Genetics:  
A/Gene: STY3637

Query Match 66.7% Score 44; DB 2; Length 367;  
Best Local Similarity 69.2% Pred. No. 5.6;

Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;  
Qy 1 GPMELV---GYF 9  
Db 127 GPMELVLGPGYGF 139

RESULT 3  
729043  
hypothetical protein B0228.2 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T29043  
R:Leimbach, D.  
submitted to the EMBL Data Library, March 1995  
A:Description: The sequence of C. elegans cosmid B0228.  
A:Reference number: Z18324  
A:Accession: T29043  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1788 <LEI>  
A:Cross-references: UNIPROT:Q81G61, UNIPARC:UPI00000851C9, EMBL:U23168, PIDN:AA038806.1,  
A:Experimental source: strain Bristol N2  
A:Gene: CESP:B0228.2  
A:Introns: 1456/2; 1482/3; 1516/2; 1551/3; 1595/3; 1646/1; 1671/1; 1716/2; 1749/3

Query Match 65.2%; Score 43; DB 2; Length 1788;  
Best Local Similarity 60.0%; Pred. No. 44;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GPMELVGYFD 10  
Db 1722 GPMNMGRPD 1731

RESULT 4  
B69368  
glutamine synthetase (glnA) homolog - *Archaeoglobus fulgidus*  
C:Species: *Archaeoglobus fulgidus*  
C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C:Accession: B69368  
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson  
; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirschner, E.F.  
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
Nature 390, 364-370, 1997  
A:Authors: Usterbach, T.; Cotton, M.D.; Spriggs, T.; Artach, P.; Kaine, B.P.; Sykes, S.  
Smith, H.O.; Woese, C.R.; Venter, J.C.  
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaea  
A:Reference number: A69250; MUID:98049343; PMID:9389475  
A:Accession: B69368  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-491 <KLE>  
A:Cross-references: UNIPROT:Q29313; UNIPARC:UPI0000056F0D; GB:AE001039; GB:AE000782; NID  
C:Superfamily: glutamate-ammmonia ligase

Query Match 62.1%; Score 41; DB 2; Length 491;  
Best Local Similarity 66.7%; Pred. No. 25;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PMELVGYFD 10  
Db 482 PMELMKYFD 490

RESULT 5  
B84900  
hypothetical protein At2g46220 [imported] - *Arabidopsis thaliana*  
C:Species: *Arabidopsis thaliana* (mouse-ear cress)  
C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C:Accession: B84900  
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanden, S.E.; Umeyama, L.; Tallon, L.;  
Euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.  
A:Reference number: A64420; MUID:20083487; PMID:10617197  
A:Accession: B84900  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-550 <STO>  
A:Cross-references: UNIPROT:O82347, UNIPARC:UPI000017A71B, GB:AE002093; NID:G3702327, PIDN  
C:Gene: At2g46220  
A:Map position: 2

Query Match 62.1%; Score 41; DB 2; Length 550;  
Best Local Similarity 70.0%; Pred. No. 28;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GPMELVGYFD 10  
Db 176 GPMELRGKFD 185

RESULT 6  
S48729  
glucokinase regulator - African clawed frog  
C:Species: *Xenopus laevis* (African clawed frog)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: S48729; S49339  
R:Veiga-da-cunha, M.; Decheux, M.; Matelet, N.; van Schaftingen, E.  
Eur. J. Biochem. 225, 43-51, 1994  
A:Title: Cloning and expression of a *Xenopus* liver cDNA encoding a fructose-phosphate-kin  
A:Reference number: S48729; MUID:95010134; PMID:7925465  
A:Accession: S48729  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-619 <VEI>  
A:Cross-references: UNIPROT:Q91754; UNIPARC:UPI000012B2E2; EMBL:X80901; NID:G556677; PIDN  
C:Superfamily: glucokinase regulator

Query Match 62.1%; Score 41; DB 1; Length 619;  
Best Local Similarity 63.6%; Pred. No. 32;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GPMELVGYFDS 11  
Db 17 GPMELAGYEESS 27

RESULT 7  
G70704  
hypothetical protein RV2326c - *Mycobacterium tuberculosis* (strain H37RV)  
C:Species: *Mycobacterium tuberculosis*  
C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004  
C:Accession: G70704  
R:Coile, S.T.; Broese, R.; Parbhilli, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.  
; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.  
; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrett, B.G.  
A:Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome  
A:Reference number: A70500; MUID:98295987; PMID:9634230  
A:Accession: G70704  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-697 <COL>  
A:Cross-references: UNIPROT:P71886; UNIPARC:UPI000013BA74; GB:Z79702; GB:AL123456; NID:G3702327, PIDN  
C:Experimental source: strain H37RV  
A:Gene: RV2326c

Query Match 62.1%; Score 41; DB 2; Length 697;  
Best Local Similarity 66.7%; Pred. No. 36;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PWEVLGYFD 10  
 |||:|||||  
 DB 196 PWWLLGYFN 204

## RESULT 8

ABC transporter ML0848 [imported] - Mycobacterium leprae

C:Species: Mycobacterium leprae

C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004

C:Accession: B87015

R:Coile, S.T.; Elzmeier, K.; Parhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho

R.; Davis, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,

eam, M.A.; Rutherford, K.M.

Nature 409, 1007-1011, 2001

A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq

A:Title: Massive gene decay in the leprosy bacillus.

A:Reference number: A86909; MUID:21128732; PMID:11234002

A:Accession: B87015

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-724 <STO>

A:Cross-references: UNIPROT:O9CCF9; UNIPARC:UPI00000C6D27; GB:AL450380; NID:G13092926; F

C:Genetics:

A:Gene: ML0848

Query Match 60.6%; Score 40; DB 2; Length 724;  
 Best Local Similarity 75.0%; Pred. No. 57;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PWEVLGYF 9  
 |||:|||||  
 DB 224 PWWLLGYF 231

## RESULT 9

ABC-type transporter homolog [imported] - Mycobacterium leprae

C:Species: Mycobacterium leprae

C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 09-Jul-2004

C:Accession: T44905

R:Parhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, August 1997

A:Reference number: Z22864

A:Accession: T44905

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-726 <PAR>

A:Cross-references: UNIPROT:O32971; UNIPARC:UPI0000BBD0E; EMBL:Z98741; PIDN:CAB11403.1

C:Genetics:

A:Experimental source: cosmid B22

A:Note: MLCB22.38c

Query Match 60.6%; Score 40; DB 2; Length 726;  
 Best Local Similarity 75.0%; Pred. No. 57;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PWEVLGYF 9  
 |||:|||||  
 DB 226 PWWLLGYF 233

## RESULT 10

probable DNA-directed RNA polymerase II subunit [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004

C:Accession: D84824

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.

eues, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: D84824

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-888 <STO>

A:Cross-references: UNIPROT:O04206; UNIPARC:UPI00000A517F; GB:AE002093; NID:G2088656; PI

C:Genetics:

A:Gene: At2g40030

A:Map position: 2

Query Match 60.6%; Score 40; DB 2; Length 888;  
 Best Local Similarity 63.6%; Pred. No. 70;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPEVLGYFDS 11  
 |||:|||||  
 DB 544 GPKETLGFDS 554

## RESULT 11

probable plasma membrane proton ATPase [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 31-Dec-2004

C:Accession: F84637

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.

eues, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: F84637

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-931 <STO>

A:Cross-references: UNIPARC:UPI000016237B; GB:AE002093; NID:G4572678; PIDN:AAD23893.1; G

C:Genetics:

A:Gene: At2g24520

A:Map position: 2

C:Superfamily: Na(+)/K(+)-transporting ATPase alpha chain; ATPase nucleotide-binding dom

Query Match 60.6%; Score 40; DB 2; Length 931;  
 Best Local Similarity 85.7%; Pred. No. 74;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPEVLVG 7  
 |||:|||||  
 DB 457 GPEVLVG 463

## RESULT 12

hypothetical protein PH1107 - Pyrococcus horikoshii

C:Species: Pyrococcus horikoshii

C:Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 31-Dec-2004

C:Accession: D71051

R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Hatakeyama, Y.; Hino, Y.; Yamamoto, S.; Sekin

M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushiida, N.; Oguchi

DNA Res. 5, 55-76, 1998

A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a

A:Reference number: A71000; MUID:98344137; PMID:9679194

A:Accession: D71051

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-239 <KAN>

A:Cross-references: UNIPROT:O58834; UNIPARC:UPI0000062FB7; GB:AP000005; NID:G3236132; PI

A:Experimental source: strain 073

A:Note: this accession replaces an interim accession for a sequence replaced by GenBank

C:Genetics:

A:Gene: PH1107

C:Superfamily: glycosidase, PH1107 type

Query Match 59.1%; Score 39; DB 2; Length 299;  
 Best Local Similarity 60.0%; Pred. No. 33;  
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 PWEVGYFDS 11  
 |||||  
 DB 247 PWEVGHVDN 256

## RESULT 13

T33303  
 Hypothetical protein R01B10.4 - *Caenorhabditis elegans*  
 C.Species: *Caenorhabditis elegans*  
 C.Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
 C.Accession: T33303

R.Langanon, Y.; Beck, C.  
 Submitted to the EMBL Data Library, May 1998  
 A.Description: The sequence of C. elegans cosmid R01B10.  
 A.Reference number: 221318  
 A.Accession: T33303

A.Status: preliminary; translated from GB/EMBL/DBJ  
 A.Molecule type: DNA  
 A.Residues: 1-320 <LAN>

A.Cross-references: UNIPROT:O61975; UNIPARC:UPI0000080228; EMBL:AF068718; PIDN:AC17768.  
 A.Experimental source: strain Bristol N2; clone R01B10  
 C.Genetics:

A.Gene: CESP:R01B10.4

A.Map position: 5  
 A.Introns: 25/2; 73/2; 211/3; 241/2

Query Match 59.1%; Score 39; DB 2; Length 320;  
 Best Local Similarity 55.6%; Pred. No. 36;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 WELVGYFDS 11  
 |||||  
 DB 65 WDTIGHFDS 73

## RESULT 14

S17907  
 Glutamate dehydrogenase (NADP) (EC 1.4.1.4) - yeast (*Schwanniomycetes occidentalis* var. oc

C.Species: *Schwanniomycetes occidentalis* var. *occidentalis*  
 C.Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 05-Oct-2004  
 C.Accession: S17907

R.de Zoysa, P.A.; Connerton, I.F.; Watson, D.C.; Johnston, J.R.  
 Curr. Genet. 20, 219-224, 1991  
 A.Title: Cloning, sequencing and expression of the *Schwanniomycetes occidentalis* NADP-depe

A.Reference number: S17907; MUID:92035089; PMID:1934128  
 A.Accession: S17907  
 A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-459 <DEZ>

A.Cross-references: UNIPROT:P29507; UNIPARC:UPI00001292P9

C.Superfamily: glutamate dehydrogenase

C.Keywords: NADP; oxidoreductase

Query Match 59.1%; Score 39; DB 2; Length 459;  
 Best Local Similarity 66.7%; Pred. No. 52;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PWEVGYFDS 10  
 |||||  
 DB 308 PMAVGHFD 316

## RESULT 15

S28476

rfBL protein VCO249 [similarity] - *Vibrio cholerae* (strain N16961 serogroup O1)  
 C.Species: *Vibrio cholerae*  
 C.Date: 12-Mar-1993 #sequence\_revision 12-Mar-1993 #text\_change 09-Jul-2004  
 C.Accession: S28476; H82346

R.Manning, P.A.  
 Submitted to the EMBL Data Library, May 1991  
 A.Reference number: S28467  
 A.Accession: S28476

A.Molecule type: DNA  
 A.Residues: 1-471 <MAN>

A.Cross-references: UNIPROT:O06959; UNIPARC:UPI00000D470B; EMBL:X59554; NID:G48381; PIDN:

A.Experimental source: strain 017  
 R.Heideberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;

Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, P  
 1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
 Nature 406, 477-483, 2000

A.Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.  
 A.Reference number: A82035; MUID:20406833; PMID:10952301

A.Accession: H82346

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-471 <HEI>

A.Cross-references: UNIPARC:UPI00000D470B; GB:AE004113; GB:AE003852; NID:G9654648; PIDN:

A.Experimental source: serogroup O1; strain N16961; biotype El Tor

C.Genetics:

A.Gene: rfbL; VCO249

A.Map position: 1

C.Superfamily: 4-coumarate-CoA ligase homology <ACI>  
 F/47-468/Domain: acetate-CoA ligase homology

Query Match 59.1%; Score 39; DB 2; Length 471;  
 Best Local Similarity 60.0%; Pred. No. 54;  
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 PWEVGYFDS 11  
 |||||  
 DB 329 PMMDGYFEN 338

Search completed: December 4, 2005, 04:53:34  
 Job time: 17.5833 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

# OM protein - protein search, using sw model

Run on: December 4, 2005, 04:09:54 ; Search time 95.5625 Seconds  
(without alignments).  
50.576 Million cell updates/sec

Title: US-10-632-706-128  
Perfect score: 66  
Sequence: 1 GPMELVGFDS 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues  
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

A\_Geneseq\_21:\*

- 1: geneeqp1980s:\*
- 2: geneeqp1990s:\*
- 3: geneeqp2000s:\*
- 4: geneeqp2001s:\*
- 5: geneeqp2002s:\*
- 6: geneeqp2003as:\*
- 7: geneeqp2003bs:\*
- 8: geneeqp2004s:\*
- 9: geneeqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	66	100.0	11	8	ADR38726
2	44	66.7	306	6	Abu45531 Protein e
3	44	66.7	367	6	ABU47042
4	44	66.7	367	6	ABU47877 Protein e
5	43	65.2	207	8	ADH12894
6	42	63.6	415	7	ABM89126
7	41	62.1	114	4	AAO08773
8	41	62.1	121	4	AAAR8504
9	41	62.1	475	6	ABU20453
10	41	62.1	792	7	ADCO7986
11	41	62.1	1352	4	ABM67542
12	40	60.6	146	6	ABP56656
13	40	60.6	283	6	ABM70292
14	40	60.6	477	8	ADY22314
15	40	60.6	885	3	AAAG32050
16	40	60.6	931	3	AAAG32049
17	40	60.6	956	3	AAAG32048
18	39.5	59.8	511	8	ADK89844
19	39	59.1	79	3	AAAG13553
20	39	59.1	103	3	AAAG13552
21	39	59.1	112	4	AAAG13551
22	39	59.1	166	3	AAAM06860
23	39	59.1	211	8	ADMS7065
24	39	59.1	233	3	AAAG05440

25	39	59.1	233	3	AAAG38801
26	39	59.1	242	5	ABG69053
27	39	59.1	254	3	AAAG30761
28	39	59.1	257	3	AAAG38800
29	39	59.1	257	3	AAAG05439
30	39	59.1	266	3	AAAG05438
31	39	59.1	266	3	AAAG38799
32	39	59.1	266	5	ABB92172
33	39	59.1	274	9	ABM95054
34	39	59.1	278	3	AAAG30760
35	39	59.1	287	3	AAAG30759
36	39	59.1	537	8	ADT60469
37	39	59.1	670	6	ABU18890
38	39	59.1	696	4	ABG20404
39	39	59.1	775	4	AAU48754
40	39	59.1	775	6	ABM65954
41	39	59.1	775	6	ABM45273
42	39	59.1	877	3	AAAG36913
43	39	59.1	885	3	AAAG36912
44	39	59.1	949	3	AAAG36911
45	38	57.6	48	4	AAAG95055

## ALIGNMENTS

RESULT 1  
ID ADR38726 standard; peptide, 11 AA.  
AC ADR38726;  
DT 02-DEC-2004 (first entry)  
DE Mouse heavy chain variable region CDR3 seqid 128.  
KM antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;  
KM BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
KM toxin neutralisation; botulinum neurotoxin poisoning; mouse;  
KM heavy chain variable region; complementarily determining region; CDR3.  
OS Mus sp.  
XX US2004175385-A1.  
XX 09-SEP-2004.  
XX 01-AUG-2003; 2003US-00632706.  
XX PF 31-AUG-1998; 98US-00144886.  
XX PR 01-AUG-2002; 2002US-0400721P.  
XX (REGC ) UNIV CALIFORNIA.  
XX Marks JD, Amerdortfer P;  
XX WPI; 2004-652009/63.  
XX  
XX New isolated antibody that neutralizes botulinum neurotoxin type A,  
XX useful for diagnosing botulism or for treating pathologies associated  
XX with botulinum neurotoxin poisoning.  
XX  
XX Example 3; SEQ ID NO 128; 110pp; English.  
XX  
XX The invention describes an isolated antibody (I) that specifically binds  
XX to an epitope specifically bound by an antibody expressed by a specific  
XX clone where (I) binds to and neutralises botulinum neurotoxin type A  
XX (BoNT/A). An isolated antibody (II) that specifically binds to an epitope  
XX specifically bound by an antibody expressed by a clone chosen from clone  
XX S25, C39, I06, 3D12, B4, 1F3, huC25, Ar1, Ar2, WRI (V), WRI (V), 3-1,  
XX 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum  
XX neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)  
XX comprising BoNT/A neutralising epitope having an epitope that is

CC specifically bound by an antibody expressed by clones as mentioned in (I)  
CC producing (1); and a composition (II) comprising several anti-  
CC botulinum neurotoxin antibodies, where each antibody is specific for a  
CC different epitope of a botulinum neurotoxin and the combination of  
CC antibodies shows greater toxin neutralisation than the single antibodies  
CC in surplus. The following are disclosed: a pharmaceutical composition  
CC comprising (I); and a kit comprising (I). (I) is useful for neutralising  
CC BONT/A antibody and for neutralising a botulinum neurotoxin which  
CC involves contacting neurotoxin with (I) in surplus, where each of (I) is  
CC specific for a different epitope of the botulinum neurotoxin and the  
CC combination of antibodies shows greater toxin neutralisation than the  
CC single antibodies in surplus. (I) is useful for diagnosing the botulinum  
CC or for treating pathologies associated with botulinum neurotoxin  
CC poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)  
CC enables rapid detection or diagnosis of botulism. This is the amino acid  
CC sequence of mouse heavy chain variable region complementarity determining  
CC region 3 (CDR3) from anti-botulinum neurotoxin antibodies.  
XX  
SQ Sequence 11 AA;  
Query Match 100.0%; Score 66; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.00019;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GPMELVGYFDS 11  
Db 1 GPMELVGYFDS 11  
RESULT 2  
ABU45531  
ID ABU45531 standard; protein; 306 AA.  
XX  
AC ABU45531;  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by Prokaryotic essential gene #31058.  
XX  
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
OS Salmomella paratyphi.  
XX  
PN WO200277183-A2.  
XX  
PD 03-OCT-2002.  
XX  
PF 21-MAR-2002; 2002WO-US009107.  
XX  
PR 21-MAR-2001; 2001US-00815242.  
XX  
PR 06-SEP-2001; 2001US-00948993.  
XX  
PR 25-OCT-2001; 2001US-0342923P.  
XX  
PR 08-FEB-2002; 2002US-00072851.  
XX  
PR 06-MAR-2002; 2002US-0362699P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX  
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW,  
XX  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX  
DR WPI; 2003-029926/02.  
XX  
DR N-PSDB; ACA49401.  
XX  
PT New antisense nucleic acids, useful for identifying proteins or screening  
XX  
PT for homologous nucleic acids required for cellular proliferation to  
XX  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
PS Claim 25; SEQ ID NO 73455; 1766bp; English.  
XX  
CC The invention relates to an isolated nucleic acid comprising any one of  
XX  
CC the 623 antisense sequences given in the specification where expression  
XX  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
XX  
CC (1) a vector comprising a promoter operably linked to the nucleic acid

CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 306 AA;  
Query Match 66.7%; Score 44; DB 6; Length 306;  
Best Local Similarity 69.2%; Pred. No. 40;  
Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;  
QY 1 GPMELV----GYF 9  
Db 66 GPMELVAGPFGYF 78  
RESULT 3  
ABU47042  
ID ABU47042 standard; protein; 367 AA.  
XX  
AC ABU47042;  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by Prokaryotic essential gene #32569.  
XX  
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
OS Salmomella typhimurium.  
XX  
PN WO200277183-A2.  
XX  
PD 03-OCT-2002.  
XX  
PF 21-MAR-2002; 2002WO-US009107.  
XX  
PR 21-MAR-2001; 2001US-00815242.  
XX  
PR 06-SEP-2001; 2001US-00948993.  
XX  
PR 25-OCT-2001; 2001US-0342923P.  
XX  
PR 08-FEB-2002; 2002US-00072851.  
XX  
PR 06-MAR-2002; 2002US-0362699P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX  
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW,  
XX  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX  
DR WPI; 2003-029926/02.  
XX  
DR N-PSDB; ACA50912.



PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids, required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
XX  
PS Claim 25; SEQ ID NO 74966; 1766pp; English.  
CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 367 AA;  
XX  
Query Match 66.7%; Score 44; DB 6; Length 367;  
Best Local Similarity 69.2%; Pred. No. 48;  
Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;  
QY 1 GPMELV----GYF 9  
Db 127 GPMELVLGPRGYF 139  
RESULT 4  
ABU47877  
ID ABU47877 standard; protein; 367 AA.  
XX  
XX ABU47877;  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by Prokaryotic essential gene #33404.  
XX  
XX Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
OS *Salmonella typh.*  
XX  
PN MO20027183-A2.  
XX  
XX  
PD 03-OCT-2002.  
XX  
XX 21-MAR-2002; 2002MO-US009107.  
XX  
XX 21-MAR-2001; 2001US-00815242.  
XX  
XX 06-SEP-2001; 2001US-00948993.  
XX  
XX 25-OCT-2001; 2001US-0342923P.  
XX  
XX 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.  
XX  
XX (EliT-) ELITRA PHARM INC.  
XX  
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX  
XX WPI, 2003-029926/02.  
XX  
XX N-PSDB; ACh51747.  
XX  
XX  
PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
XX Claim 25; SEQ ID NO 75801; 1766pp; English.  
XX  
XX The invention relates to an isolated nucleic acid comprising any one of  
XX the 6213 antisense sequences given in the specification where expression  
XX of the nucleic acid inhibits proliferation of a cell. Also included are:  
XX (1) a vector comprising a promoter operably linked to the nucleic acid  
XX encoding a polypeptide whose expression is inhibited by the antisense  
XX nucleic acid; (2) a host cell containing the vector; (3) an isolated  
XX polypeptide or its fragment whose expression is inhibited by the  
XX antisense nucleic acid; (4) an antibody capable of specifically binding  
XX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
XX proliferation or the activity of a gene in an operon required for  
XX proliferation; (7) identifying a compound that influences the activity of  
XX the gene product or that has an activity against a biological pathway  
XX required for proliferation, or that inhibits cellular proliferation; (8)  
XX identifying a gene required for cellular proliferation or the biological  
XX pathway in which a proliferation-required gene or its gene product lies  
XX or a gene on which the test compound that inhibits proliferation of an  
XX organism acts; (9) manufacturing an antibiotic; (10) profiling a  
XX compound's activity; (11) a culture comprising strains in which the gene  
XX product is overexpressed or underexpressed; (12) determining the extent  
XX to which each of the strains is present in a culture or collection of  
XX strains; or (13) identifying the target of a compound that inhibits the  
XX proliferation of an organism. The antisense nucleic acids are useful for  
XX identifying proteins or screening for homologous nucleic acids required  
XX for cellular proliferation to isolate candidate molecules for rational  
XX drug discovery programs, or for screening homologous nucleic acids  
XX required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
XX *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
XX the target prokaryotic essential genes. Note: The sequence data for this  
XX patent did not form part of the printed specification, but was obtained  
XX in electronic format directly from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 367 AA;  
XX  
Query Match 66.7%; Score 44; DB 6; Length 367;  
Best Local Similarity 69.2%; Pred. No. 48;  
Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;  
QY 1 GPMELV----GYF 9  
Db 127 GPMELVLGPRGYF 139  
RESULT 5  
ADH12894  
ID ADH12894 standard; protein; 207 AA.  
XX  
XX ADH12894;  
XX  
XX 25-MAR-2004 (first entry)  
XX  
XX *Francisella tularensis* immunogenic protein 75, SEQ ID NO:75.  
XX  
XX Immunogenic protein; protective immune response; vaccine;  
XX genetic vaccine; antibacterial.  
XX  
XX *Francisella tularensis*.

```

XX FN WO2004003009-A2.
XX PD 08-JAN-2004.
XX PF 26-JUN-2003; 2003WO-GB002718.
XX PR 28-JUN-2002; 2002GB-00014942.
XX PA (MINA ) UK SEC FOR DEFENCE.
XX PI Titball RW, Mayers CN, Duffield ML, Miller J, Rowe SC;
XX DR N-PSDB; ADH12994.
XX
XX New protein, useful as a vaccine for producing a protective immune
XX PT response in a mammal against infection by Francisella tularensis, or
XX PR preventing or treating Francisella tularensis infection in a mammal.
XX PS Claim 1; SEQ ID NO 75; 217pp; English.
XX
XX The invention relates to 100 potentially immunogenic proteins from
XX CC Francisella tularensis (ADH12820-ADH12919) and nucleic acids encoding
XX CC them (ADH12920-ADH13019) which may be used in vaccines. The nucleic acids
XX CC may be contained within a vaccine, bacterial or plasmid vector. The
XX CC invention also relates to a pharmaceutical composition comprising the
XX CC protein or the nucleic acid in combination with a pharmaceutical carrier
XX CC or excipient. The proteins and nucleic acids are useful in vaccine
XX CC compositions for producing a protective immune response against
XX CC Francisella tularensis infection in a mammal, or for preventing or
XX CC treating Francisella tularensis infection in a mammal. The present
XX CC sequence represents a Francisella tularensis protein of the invention.
XX SQ Sequence 207 AA;
XX
XX Query Match 65.2%; Score 43; DB 8; Length 207;
XX Best Local Similarity 100.0%; Pred. NO. 39;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GPMELVG 7
XX |||||
XX 120 GPMELVG 126
XX
XX RESULT 6
XX ID ABM89126 standard; protein; 415 AA.
XX AC ABM89126;
XX DT 02-JUN-2005 (first entry)
XX DE Rice abiotic stress responsive polypeptide SEQ ID NO:7372.
XX KM abiotic stress tolerance; transgenic plant; cereal; agriculture.
XX OS Oryza sativa.
XX PN MO2003008540-A2.
XX PD 30-JAN-2003.
XX PF 21-JUN-2002; 2002WO-US019668.
XX PR 22-JUN-2001; 2001US-0300113P.
XX PR 24-AUG-2001; 2001US-0314662P.
XX PR 26-SEP-2001; 2001US-0325277P.
XX PR 21-NOV-2001; 2001US-03321332P.
XX PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
XX Kreps J, Briggs SP, Cooper B, Glaesbrook J, Goff SA, Katagiri F;

```

PI	Moughamer T, Provart N, Ricke D, Zhu T;
XX	
DR	WPI; 2003-248011/24.
XX	
XX	New stress-responsive nucleic acid, useful for altering the
PT	responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
PT	stress, salt stress or osmotic stress.
PT	
PS	Claim 1; SEQ ID NO 7372; 89pp, English.
XX	
XX	The invention relates to novel abiotic stress responsive polynucleotides
CC	and polypeptides. Also disclosed are vectors, expression cassettes, host
CC	cells, and plants containing such polynucleotides. Also disclosed are
CC	methods for using the polynucleotides and polypeptides to alter the
CC	responsiveness of a plant to abiotic stress. The invention is useful in
CC	agriculture. The nucleic acid is useful for determining whether a test
CC	plant has been exposed to an abiotic stress condition. It is also useful
CC	for selecting an agent that alters abiotic stress regulated
CC	polynucleotide expression in a plant cell, and to identify a homolog or
CC	ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
CC	responsible and the polypeptide encoded by it are useful in altering the
CC	responsiveness of a plant to an abiotic stress, such as cold stress, salt
CC	stress, osmotic stress or any of their combinations. The present sequence
CC	is used in the exemplification of the invention
XX	
XX	Sequence 415 AA;
Query Match	63.6%; Score 42; DB 7; Length 415;
Best Local Similarity	75.0%; Pred. No. 1.2e+02;
Matches	6; Conservative 1; Mismatches 1; Indels 0; Gaps 0
OY	1 GPMELVGY 8       
Db	176 GPMELVGF 183
RESULT 7	
AA008773	
ID	AA008773 standard; protein; 114 AA.
XX	
AC	AA008773;
XX	
DT	06-NOV-2001 (first entry)
XX	
DE	Human polypeptide SEQ ID NO 22665.
XX	
KW	Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW	vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW	tissue growth factor; immunomodulatory; cancer; leukaemia;
XX	nervous system disorders; arthritis; inflammation.
XX	
OS	Homo sapiens.
XX	
PN	WO200164835-A2.
XX	
PD	07-SEP-2001.
XX	
PF	26-FEB-2001; 2001WO-US004927.
XX	
PR	28-FEB-2000; 2000US--00515126.
XX	
PR	18-MAY-2000; 2000US--00577409.
XX	
PA	(HYSE-) HYSEQ INC.
XX	
PI	Tang YT, Liu C, Drmanac RT;
XX	
DR	WPI; 2001-514838/56.
XX	
DR	N-PSDB; AA188704.
XX	
PT	Isolated nucleic acids and polypeptides, useful for preventing diagnosing
PT	and treating e.g. leukemia, inflammation and immune disorders.
XX	
PS	Claim 20; SEQ ID NO 22665; 1399pp + Sequence Listing; English.

XX The invention relates to human polynucleotides (AA179941-AA193841) and  
CC the encoded proteins (AA000010-AA013910) that exhibit activity elating to  
CC cytokine, cell proliferation or cell differentiation or which may induce  
CC production of other cytokines in other cell populations. The  
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
CC peptide therapy. The polypeptides have various cytokine-like activities,  
CC e.g. stem cell growth factor activity, haematopoietic regulating  
CC activity, tissue growth factor activity, immunomodulatory activity and  
CC activating/inhibiting activity and may be useful in the diagnosis and/or  
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
CC inflammation. Note: the sequence data for this patent did not form part  
CC of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX

SQ Sequence 114 AA;

Query Match 62.1%; Score 41; DB 4; Length 114;  
Best Local Similarity 55.6%; Pred. No. 46;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPMELVGYF 9  
DB 76 GPMKFLGFF 84

RESULT 8

AA088504 standard; protein; 121 AA.

AA088504;

31-JUL-1996 (first entry)

VHmu for antibody BT34/A5.

Antibody; variable heavy chain; VHmu; human; monoclonal; Mab; BT34/A5;

BT32/A6; cell cycle independent; tumour specific; glioma; therapy;

detection; complementarity determining region; CDR.

Homo sapiens.

Location/Qualifiers

31..35  
/note="complementarity determining region (specifically  
claimed)"

50..66  
/note="complementarity determining region (specifically  
claimed)"

99..110  
/note="complementarity determining region (specifically  
claimed)"

Region

MO9535374-A1.

28-DEC-1995.

16-JUN-1995; 95MO-CA000361.

21-JUN-1994; 94US-00264093.

(DANM/) DAN M D.

Dan MD;

WPI, 1996-058411/06.

N-PSDB; AA110938.

Novel monoclonal antibodies, BT34/A5 and BT32/A6 - used to characterise  
glioma specific cell surface antigens, and in the treatment of glioma.

Claim 8, Page 33; 53pp; English.

CC AA088504-R88510 represent regions of the human monoclonal antibodies  
CC (Mab's) BT34/A5 and BT32/A6. This sequence represents the variable region  
CC of the heavy chain, subgroup mu, (VHmu) of BT34/A5. The complementarity  
CC determining regions (CDR's) of this sequence are specifically claimed.  
CC This sequence preferably has an N-terminal extension comprising the  
CC signal sequence represented in AA088505. The BT34/A5 and BT32/A6 Mab's  
CC recognise a cell cycle independent tumour specific antigen. They also  
CC bind equally well to tumour cells in vitro regardless of their culture  
CC viability, growth characteristics, or culture density. The antibodies  
CC effectively label the tumour cells by binding to the antigen present on  
CC the cell surface. The Mab's are useful in the detection and the treatment  
CC of glioma. These Mab's are specific for glioma and show none of the cross  
CC reactivity seen with previous antibodies  
XX

SQ Sequence 121 AA;

Query Match 62.1%; Score 41; DB 2; Length 121;  
Best Local Similarity 60.0%; Pred. No. 49;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPMELVGYFD 10  
DB 100 GVMIDLNYFD 109

RESULT 9

ABU20453 standard; protein; 475 AA.

ABU20453;

19-JUN-2003 (first entry)

Protein encoded by prokaryotic essential gene #5980.

Antisense; prokaryotic essential gene; cell proliferation; drug design.

Bacteroides fragilis.

MO20027183-A2.

03-OCT-2002.

21-MAR-2002; 2002MO-US009107.

21-MAR-2001; 2001US-00815242.

06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342823P.

08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.

(ELITR-) ELITRA PHARM INC.

Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KU, Zyckind JW,

Wall D, Trawick JD, Carr GT, Yamamoto R, Forsyth RA, Xu HH;

WPI; 2003-029926/02.

N-PSDB; ACA24323.

New antisense nucleic acids, useful for identifying proteins or screening

for homologous nucleic acids required for cellular proliferation to

isolate candidate molecules for rational drug discovery programs.

Claim 25; SEQ ID NO 48377; 1766pp; English.

The invention relates to an isolated nucleic acid comprising any one of  
the 6213 antisense sequences given in the specification where expression  
of the nucleic acid inhibits proliferation of a cell. Also included are:  
(1) a vector comprising a promoter operably linked to the nucleic acid  
encoding a polypeptide whose expression is inhibited by the antisense  
nucleic acid; (2) a host cell containing the vector; (3) an isolated  
polypeptide or its fragment whose expression is inhibited by the  
antisense nucleic acid; (4) an antibody capable of specifically binding

CC the polypeptide;(5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
CC  
SQ Sequence 475 AA;

Query Match 62.1% Score 41; DB 6; Length 475;  
Best Local Similarity 54.5%; Pred. No. 2.1e+02;  
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 GPWELVGYFDS 11  
| | | | | | | | | |  
Db 404 GPMKLIYYVDS 414

RESULT 10  
ADCO7986  
ID ADCO7986 standard; protein; 792 AA.  
AC ADCO7986;  
DT 18-DEC-2003 (first entry)  
DE Rice protein sequence Seq ID252 related to grain filling.  
XX  
XX plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;  
XX carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;  
XX tomato; banana; canola; cotton; peanut; tobacco; sugarcane;  
XX wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;  
XX gene; ds; plant.  
XX  
XX Oryza sativa.  
XX  
XX WO2003000905-A2.  
XX  
XX 03-JAN-2003.  
XX  
XX 21-JUN-2002; 2002WO-1B002450.  
XX  
XX 22-JUN-2001; 2001US-0300112P.  
XX 26-SEP-2001; 2001US-0325277P.  
XX 20-DEC-2001; 2001US-0342327P.  
XX  
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.  
XX  
XX Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T,  
XX Glazebrook J, Katagiri F, Krens J, Provart N, Riecke D;  
XX MPI: 2003-229341/22.  
XX N-PSDB; ADCO7985.  
XX  
XX New plant genes encoding polypeptides having an activity involved in or  
XX associated with the synthesis, metabolism or degradation of carbohydrates

PT in the plant grain useful in generating plants having improved  
PT nutritional properties.  
XX  
XX  
PS Claim 23; SEQ ID NO 252; 130pp; English.

XX This invention, in the area of plant biotechnology, relates to novel  
XX polynucleotides comprising a nucleotide sequence encoding a protein which  
XX is involved in or associated with the synthesis, metabolism or  
XX degradation of carbohydrates in the plant grain and the expression of  
XX which is up-regulated during grain filling. The plant is selected from  
XX corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,  
XX sugarcane, wheat, and rice. The invention may be useful for the  
XX improvement of protein, oil, starch, fibre and moisture content of the  
XX cereal grains. In addition, carbohydrate levels may be modified to a more  
XX desirable level using the present invention. The present sequence is the  
XX amino acid sequence of a rice protein of the invention. Note: The  
XX sequence data for this patent did not form part of the printed  
XX specification, but was obtained in electronic format directly from WIPO  
XX at ftp.wipo.int/pub/publishedpct\_sequences.

Query Match 62.1% Score 41; DB 7; Length 792;  
Best Local Similarity 66.7%; Pred. No. 3.6e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 PWEVLGYFDP 10  
| | | | | | | | | |  
Db 245 PWOGLGYD 253

RESULT 11  
ABB67542  
ID ABB67542 standard; protein; 1352 AA.  
XX  
XX ABB67542;  
XX  
XX 26-MAR-2002 (first entry)  
XX  
XX Drosophila melanogaster polypeptide SEQ ID NO 29418.  
XX  
XX Drosophila; developmental biology; cell signalling; insecticide;  
XX pharmaceutical.  
XX  
XX Drosophila melanogaster.  
XX  
XX WO200171042-A2.  
XX  
XX 27-SEP-2001.  
XX  
XX 23-MAR-2001; 2001WO-US009231.  
XX  
XX 23-MAR-2000; 2000US-0191637P.  
XX 11-JUL-2000; 2000US-00614150.  
XX  
XX (PEKE ) PE CORP NY.  
XX  
XX Venter JC, Adams M, Li PWD, Myers EW,  
XX MPI: 2001-656860/75.  
XX N-PSDB; ABB11645.  
XX  
XX New isolated nucleic acid detection reagent for detecting 1000 or more  
XX genes from Drosophila and for elucidating cell signalling and cell-cell  
XX interactions.  
XX  
XX Discloure; SEQ ID NO 29418; 21pp + sequence listing; English.  
XX  
XX The invention relates to an isolated nucleic acid detection reagent  
XX capable of detecting 1000 or more genes from Drosophila. The invention is  
XX useful in developmental biology and in elucidating cell signalling and  
XX cell-cell interactions in higher eukaryotes for the development of  
XX insecticides, therapeutics and pharmaceutical drugs. The invention



CC therapeutically (to treat microbial infection by bacteria or fungi that  
CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as  
CC biopesticides. Other uses of the genes and the proteins are as virulence  
CC factors and for identifying targets of human diseases for which P.  
CC luminescens is a model (particularly plague and whooping cough). This  
CC sequence represents one of the isolated P. luminescens proteins  
XX

SQ Sequence 283 AA;

Query Match 60.6%; Score 40; DB 6; Length 283;  
Best Local Similarity 66.7%; Pred. No. 1.8e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 MELVGFDS 11  
DB 238 MELVGFDA 246

RESULT 14  
ID ADY22314 standard; protein; 477 AA.  
AC ADY22314;  
DT 21-APR-2005 (first entry)  
XX  
XX Plant full length insert polypeptide seqid 70098.  
XX  
XX plant protectant; plant growth regulant; gene therapy; plant;  
XX recombinant DNA construct; physical array; plant breeding marker;  
XX cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
XX extreme osmotic condition; pathogen tolerance; pest tolerance;  
XX growth rate; cell cycle pathway; disease resistance;  
XX galactomannan production; lignin production; plant growth regulator;  
XX yield; plant growth; plant development; seed oil; protein yield;  
XX protein content.  
XX  
XX Unidentified.  
XX OS  
XX US2004034888-A1.  
XX PN  
XX 19-FEB-2004.  
XX PD  
XX 28-APR-2003; 2003US-00425114.  
XX PF  
XX 06-MAY-1999; 99US-00304517.  
XX PR 05-NOV-2001; 2001US-00985678.  
XX  
XX (LIUJ/) LIU J.  
XX (ZHOU/) ZHOU Y.  
XX (KOVA/) KOVALIC D K.  
XX (SCRE/) SCREEN S E.  
XX (TABAS/) TABASKA J E.  
XX (CAOY/) CAO Y.  
XX  
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
XX MPI, 2004-180133/17.  
XX  
XX New recombinant DNA construct, useful for improving plant tolerance to  
XX cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
XX pests, for conferring increased resistance to plant disease, or for  
XX improving yield.  
XX  
XX Claim 1; SEQ ID NO 70098; 15pp; English.  
XX  
XX The invention describes a recombinant DNA construct comprising a  
XX polynucleotide consisting of a sequence encoding an amino acid sequence  
XX available in electronic form from the US patent office at  
XX ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide  
XX of the invention are also useful in physical arrays of molecules and as  
XX plant breeding markers. The recombinant DNA construct is useful for  
XX improving plant tolerance to cold, heat, drought, herbicides, extreme

CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
CC plant cells by modification of the cell cycle pathway, for conferring  
CC increased resistance to plant disease, for producing galactomannan,  
CC lignin or plant growth regulators, for increasing the rate of homologous  
CC recombination in plants, for improving yield by modification of  
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
CC or by providing improved plant growth and development under at least one  
CC stress condition or for modifying seed oil or protein yield and/or  
CC content. This is the amino acid sequence of a plant full length insert  
CC polypeptide that can be used in the recombinant DNA construct of the  
CC invention.  
XX

SQ Sequence 477 AA;

Query Match 60.6%; Score 40; DB 8; Length 477;  
Best Local Similarity 60.0%; Pred. No. 3.1e+02;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 GPMELVGYFD 10  
DB 307 GPMELVGYFD 316

RESULT 15  
ID AAG32050 standard; protein; 885 AA.  
AC AAG32050;  
DT 17-OCT-2000 (first entry)  
XX  
XX Arabidopsis thaliana protein fragment SEQ ID NO: 38593.  
XX  
XX Protein identification; signal transduction pathway; metabolic pathway;  
XX hybridisation assay; genetic mapping; gene expression control; promoter;  
XX termination sequence.  
XX  
XX Arabidopsis thaliana.  
XX OS  
XX EP1033405-A2.  
XX PN  
XX 06-SEP-2000.  
XX PD  
XX 25-FEB-2000; 2000EP-00301439.  
XX PF  
XX 25-FEB-1999; 99US-0121825P.  
XX PR 05-MAR-1999; 99US-0123180P.  
XX PR 09-MAR-1999; 99US-0123548P.  
XX PR 23-MAR-1999; 99US-0125788P.  
XX PR 25-MAR-1999; 99US-0126264P.  
XX PR 29-MAR-1999; 99US-0126785P.  
XX PR 01-APR-1999; 99US-0127462P.  
XX PR 06-APR-1999; 99US-0128234P.  
XX PR 08-APR-1999; 99US-0128714P.  
XX PR 16-APR-1999; 99US-0129845P.  
XX PR 19-APR-1999; 99US-0130077P.  
XX PR 21-APR-1999; 99US-0130449P.  
XX PR 23-APR-1999; 99US-0130510P.  
XX PR 28-APR-1999; 99US-0130891P.  
XX PR 30-APR-1999; 99US-0131449P.  
XX PR 30-APR-1999; 99US-0132048P.  
XX PR 04-MAY-1999; 99US-0132407P.  
XX PR 04-MAY-1999; 99US-0132464P.  
XX PR 05-MAY-1999; 99US-0132485P.  
XX PR 06-MAY-1999; 99US-0132486P.  
XX PR 07-MAY-1999; 99US-0132487P.  
XX PR 11-MAY-1999; 99US-0132863P.  
XX PR 14-MAY-1999; 99US-0134218P.  
XX PR 14-MAY-1999; 99US-0134221P.  
XX PR 14-MAY-1999; 99US-0134221P.  
XX PR 18-MAY-1999; 99US-0134370P.  
XX PR 18-MAY-1999; 99US-0134768P.

PR 19-MAY-1999; 99US-0134841P.  
 PR 20-MAY-1999; 99US-0135124P.  
 PR 21-MAY-1999; 99US-0135353P.  
 PR 24-MAY-1999; 99US-0135629P.  
 PR 25-MAY-1999; 99US-0136021P.  
 PR 27-MAY-1999; 99US-0136392P.  
 PR 28-MAY-1999; 99US-0136782P.  
 PR 01-JUN-1999; 99US-0137222P.  
 PR 03-JUN-1999; 99US-0137528P.  
 PR 04-JUN-1999; 99US-0137502P.  
 PR 07-JUN-1999; 99US-0137724P.  
 PR 08-JUN-1999; 99US-0138094P.  
 PR 10-JUN-1999; 99US-0138540P.  
 PR 10-JUN-1999; 99US-0138847P.  
 PR 14-JUN-1999; 99US-0139119P.  
 PR 16-JUN-1999; 99US-0139452P.  
 PR 16-JUN-1999; 99US-0139453P.  
 PR 17-JUN-1999; 99US-0139492P.  
 PR 18-JUN-1999; 99US-0139454P.  
 PR 18-JUN-1999; 99US-0139455P.  
 PR 18-JUN-1999; 99US-0139456P.  
 PR 18-JUN-1999; 99US-0139457P.  
 PR 18-JUN-1999; 99US-0139458P.  
 PR 18-JUN-1999; 99US-0139459P.  
 PR 18-JUN-1999; 99US-0139460P.  
 PR 18-JUN-1999; 99US-0139461P.  
 PR 18-JUN-1999; 99US-0139462P.  
 PR 18-JUN-1999; 99US-0139463P.  
 PR 18-JUN-1999; 99US-0139750P.  
 PR 18-JUN-1999; 99US-0139763P.  
 PR 21-JUN-1999; 99US-0139817P.  
 PR 22-JUN-1999; 99US-0139899P.  
 PR 23-JUN-1999; 99US-0140353P.  
 PR 24-JUN-1999; 99US-0140659P.  
 PR 28-JUN-1999; 99US-0140823P.  
 PR 29-JUN-1999; 99US-0140891P.  
 PR 30-JUN-1999; 99US-0141287P.  
 PR 01-JUL-1999; 99US-0141842P.  
 PR 01-JUL-1999; 99US-0142154P.  
 PR 02-JUL-1999; 99US-0142055P.  
 PR 06-JUL-1999; 99US-0142390P.  
 PR 08-JUL-1999; 99US-0142803P.  
 PR 09-JUL-1999; 99US-0142920P.  
 PR 12-JUL-1999; 99US-0142977P.  
 PR 13-JUL-1999; 99US-0143542P.  
 PR 14-JUL-1999; 99US-0143624P.  
 PR 15-JUL-1999; 99US-0144005P.  
 PR 16-JUL-1999; 99US-0144085P.  
 PR 16-JUL-1999; 99US-0144086P.  
 PR 19-JUL-1999; 99US-0144325P.  
 PR 19-JUL-1999; 99US-0144331P.  
 PR 19-JUL-1999; 99US-0144332P.  
 PR 19-JUL-1999; 99US-0144333P.  
 PR 19-JUL-1999; 99US-0144334P.  
 PR 19-JUL-1999; 99US-0144335P.  
 PR 20-JUL-1999; 99US-0144352P.  
 PR 20-JUL-1999; 99US-0144632P.  
 PR 20-JUL-1999; 99US-0144884P.  
 PR 21-JUL-1999; 99US-0144884P.  
 PR 21-JUL-1999; 99US-0145086P.  
 PR 21-JUL-1999; 99US-0145088P.  
 PR 22-JUL-1999; 99US-0145085P.  
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 PR 04-AUG-1999; 99US-0147302P.  
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 PR 18-AUG-1999; 99US-0149426P.  
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 PR 23-AUG-1999; 99US-0149902P.  
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Query Match 60.6%; Score 40; DB 3; Length 885;  
 Best Local Similarity 85.7%; Pred. No. 6e+02; 0; Indels 0; Gaps 0;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GPMQLVG 7  
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 |||:  
 |||:  
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 Db 411 GPMQLVG 417

Search completed: December 4, 2005, 04:44:57  
 Job time : 98.5625 secs



GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: December 4, 2005, 04:08:08 ; Search time 3.20833 Seconds  
(without alignments)  
16.417 Million cell updates/sec

Title: US-10-632-706-128

Perfect score: 66

Sequence: 1 GPWELVGYFDS 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA\_New.\*  
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3: /cgn2\_6/ptodata/1/pubppaa/US07\_NEW\_PUB.pep.\*  
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8: /cgn2\_6/ptodata/1/pubppaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	54.5	792	6	US-10-467-657-6026
2	36	54.5	792	6	US-10-467-657-7528
3	35	53.0	356	6	US-10-467-657-1210
4	34	51.5	322	7	US-11-074-176-36
5	34	51.5	723	6	US-10-467-657-1916
6	34	51.5	926	6	US-10-841-129-2
7	33.5	50.8	478	7	US-11-037-829A-4
8	33	50.0	198	7	US-11-082-389-302
9	33	50.0	281	7	US-11-082-389-304
10	33	50.0	431	7	US-11-055-822-76
11	33	50.0	724	6	US-10-131-826A-60
12	33	50.0	1510	6	US-11-055-822-72
13	33	50.0	2725	7	US-11-113-424-52
14	32	48.5	465	6	US-10-467-657-4150
15	32	48.5	533	7	US-11-147-047-33
16	32	48.5	771	7	US-11-147-047-34
17	31.5	47.7	532	7	US-11-184-380-6
18	31.5	47.7	544	6	US-10-719-311-18
19	31.5	47.7	588	7	US-11-184-380-5
20	31.5	47.7	598	6	US-10-719-311-16
21	31.5	47.7	724	7	US-11-184-380-4
22	31.5	47.7	734	6	US-10-719-311-4
23	31.5	47.7	735	7	US-11-184-380-24
24	31	47.0	142	6	US-10-821-234-1030
25	31	47.0	229	6	US-10-510-386-228

26	31	47.0	290	6	US-10-793-626-214	Sequence 214, App
27	31	47.0	393	6	US-10-821-234-1292	Sequence 1292, App
28	31	47.0	490	6	US-10-131-826A-310	Sequence 310, App
29	31	47.0	626	6	US-10-467-657-6426	Sequence 6426, App
30	31	47.0	626	6	US-10-467-657-7618	Sequence 7618, App
31	31	47.0	745	7	US-11-109-156-14	Sequence 14, App
32	31	47.0	766	6	US-10-522-789-2	Sequence 2, App
33	30	45.5	31	6	US-10-467-657-2188	Sequence 2188, App
34	30	45.5	180	6	US-10-665-455-11	Sequence 11, App
35	30	45.5	221	7	US-11-055-822-82	Sequence 82, App
36	30	45.5	389	6	US-10-979-821-2	Sequence 2, App
37	30	45.5	400	6	US-10-793-626-3116	Sequence 3116, App
38	30	45.5	450	6	US-10-467-657-2126	Sequence 2126, App
39	30	45.5	457	7	US-11-055-822-80	Sequence 80, App
40	30	45.5	479	6	US-10-821-234-871	Sequence 871, App
41	30	45.5	934	6	US-10-858-730-8	Sequence 8, App
42	30	45.5	1857	7	US-11-102-217-2	Sequence 2, App
43	29.5	44.7	17	6	US-10-939-890-116	Sequence 116, App
44	29.5	44.7	178	6	US-10-508-263-32	Sequence 32, App
45	29.5	44.7	178	6	US-10-508-263-46	Sequence 46, App

## ALIGNMENTS

RESULT 1  
US-10-467-657-6026  
Sequence 6026, Application US/10467657  
Publication No. US20050260581A1  
GENERAL INFORMATION:  
APPLICANT: CHIRON SPA  
APPLICANT: FONTANA Maria Rita  
APPLICANT: PIZZA Mariagrazia  
APPLICANT: MASIGNANI Vega  
APPLICANT: MONACI Elisabetta  
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/10/467,657  
CURRENT FILING DATE: 2003-08-11  
PRIOR APPLICATION NUMBER: GB-0103424.8  
NUMBER OF SEQ ID NOS: 9218  
SOFTWARE: SeqMan99, version 1.04  
SEQ ID NO 6026  
LENGTH: 792  
TYPE: PRT  
ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-6026

Query Match 54.5% ; Score 36 ; DB 6 ; Length 792 ;  
Best Local Similarity 75.0% ; Pred. No. 27 ;  
Matches 6 ; Conservative 2 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;

QY 4 ELVGYFDS 11  
DB 390 ELVGYFDN 397

RESULT 2  
US-10-467-657-7528  
Sequence 7528, Application US/10467657  
Publication No. US20050260581A1  
GENERAL INFORMATION:  
APPLICANT: CHIRON SPA  
APPLICANT: FONTANA Maria Rita  
APPLICANT: PIZZA Mariagrazia  
APPLICANT: MASIGNANI Vega  
APPLICANT: MONACI Elisabetta  
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/10/467,657  
CURRENT FILING DATE: 2003-08-11  
PRIOR APPLICATION NUMBER: GB-0103424.8

/ PRIOR FILING DATE: 2001-02-12  
/ NUMBER OF SEQ ID NOS: 9218  
/ SOFTWARE: SeqMin99, version 1.04  
/ SEQ ID NO: 7528  
/ LENGTH: 792  
/ TYPE: PRT  
/ ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-7528

Query Match 54.5%; Score 36; DB 6; Length 792;  
Best Local Similarity 75.0%; Pred. No. 27;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 ELVGYFDS 11  
DB 390 ELVGYFDN 397

RESULT 3  
US-10-467-657-1210  
/ Sequence 1210, Application US/10467657  
/ Publication No. US20050260581A1  
/ GENERAL INFORMATION:  
/ APPLICANT: CHIRON SPA  
/ APPLICANT: FONTANA Maria Rita  
/ APPLICANT: PIZZA Mariagrazia  
/ APPLICANT: MASIGNANI Vega  
/ APPLICANT: MONACI Elisabetta  
/ TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
/ FILE REFERENCE:  
/ CURRENT APPLICATION NUMBER: US/10/467,657  
/ CURRENT FILING DATE: 2003-08-11  
/ PRIOR APPLICATION NUMBER: GB-0103424.8  
/ PRIOR FILING DATE: 2001-02-12  
/ NUMBER OF SEQ ID NOS: 9218  
/ SOFTWARE: SeqMin99, version 1.04  
/ SEQ ID NO: 1210  
/ LENGTH: 356  
/ TYPE: PRT  
/ ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-1210

Query Match 53.0%; Score 35; DB 6; Length 356;  
Best Local Similarity 62.5%; Pred. No. 19;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPMELVGY 8  
DB 45 GPMELVGY 52

RESULT 4  
US-11-074-176-36  
/ Sequence 36, Application US/11074176  
/ Publication No. US20050250135A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Kleenhammer, Todd R.  
/ APPLICANT: Russell, William M.  
/ APPLICANT: Altermann, Eric  
/ APPLICANT: McAniff, Olivia  
/ APPLICANT: Perill, Andrea Azcarate  
/ TITLE OF INVENTION: Nucleic Acid Sequences Encoding  
/ FILE REFERENCE: 5051-694  
/ CURRENT APPLICATION NUMBER: US/11/074,176  
/ CURRENT FILING DATE: 2003-03-07  
/ PRIOR APPLICATION NUMBER: 60/551,161  
/ PRIOR FILING DATE: 2004-03-08  
/ NUMBER OF SEQ ID NOS: 381  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO: 36  
/ LENGTH: 322  
/ TYPE: PRT

/ ORGANISM: Lactobacillus acidophilus  
US-11-074-176-36

Query Match 51.5%; Score 34; DB 7; Length 322;  
Best Local Similarity 85.7%; Pred. No. 25;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 ELVGYFD 10  
DB 43 ELVGYFD 49

RESULT 5  
US-10-467-657-1916  
/ Sequence 1916, Application US/10467657  
/ Publication No. US20050260581A1  
/ GENERAL INFORMATION:  
/ APPLICANT: CHIRON SPA  
/ APPLICANT: FONTANA Maria Rita  
/ APPLICANT: PIZZA Mariagrazia  
/ APPLICANT: MASIGNANI Vega  
/ APPLICANT: MONACI Elisabetta  
/ TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
/ FILE REFERENCE:  
/ CURRENT APPLICATION NUMBER: US/10/467,657  
/ CURRENT FILING DATE: 2003-08-11  
/ PRIOR APPLICATION NUMBER: GB-0103424.8  
/ PRIOR FILING DATE: 2001-02-12  
/ NUMBER OF SEQ ID NOS: 9218  
/ SOFTWARE: SeqMin99, version 1.04  
/ SEQ ID NO: 1916  
/ LENGTH: 723  
/ TYPE: PRT  
/ ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-1916

Query Match 51.5%; Score 34; DB 6; Length 723;  
Best Local Similarity 53.3%; Pred. No. 55;  
Matches 8; Conservative 0; Mismatches 1; Indels 6; Gaps 1;

QY 1 GPMELV-----GYF 9  
DB 260 GPMELVNSKAPGYF 274

RESULT 6  
US-10-841-129-2  
/ Sequence 2, Application US/10841129  
/ Publication No. US20050250113A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Zuker, Charles S.  
/ APPLICANT: Erlenbach, Isolda  
/ APPLICANT: Hoon, Mark A.  
/ APPLICANT: Ryda, Nicholas J. P.  
/ APPLICANT: Zhang, Yifeng  
/ APPLICANT: The Regents of the University of California  
/ APPLICANT: The Government of the United States of America  
/ APPLICANT: as represented by the Secretary of the  
/ Department of Health and Human Services  
/ TITLE OF INVENTION: A Mammalian Magnesium/Manganese Sensing G Protein  
/ FILE REFERENCE: 023078-145400US  
/ CURRENT APPLICATION NUMBER: US/10/841,129  
/ CURRENT FILING DATE: 2004-05-07  
/ NUMBER OF SEQ ID NOS: 7  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO: 2  
/ LENGTH: 926  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
/ FEATURES:  
/ OTHER INFORMATION: human magnesium/manganese sensing G protein  
/ OTHER INFORMATION: coupled receptor (GPCR) R5.24, Mg receptor, Mn

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; OTHER INFORMATION: receptor
US-10-841-129-2
Query Match          51.5%; Score 34; DB 6; Length 926;
Best Local Similarity 83.3%; Pred. No. 70;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 PWELVG 7
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Db      443 PWELVG 448

RESULT 7
US-11-037-829A-4
; Sequence 4, Application US/11037829A
; Publication No. US2005025551A1
; GENERAL INFORMATION:
; APPLICANT: Targacept, Inc
; APPLICANT: Catholic Healthcare West
; APPLICANT: Bencherif, Merouane
; APPLICANT: Lukas, Ronald J.
; TITLE OF INVENTION: Methods and Compositions Relating to Chimeric
; TITLE OF INVENTION: Nicotinic Receptor Subunits
; FILE REFERENCE: T103 1520.PCT
; CURRENT APPLICATION NUMBER: US/11/037,829A
; PRIOR FILING DATE: 2005-01-18
; PRIOR APPLICATION NUMBER: US 60/397,380
; PRIOR FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Homo sapien
US-11-037-829A-4

Query Match          50.8%; Score 33.5; DB 7; Length 478;
Best Local Similarity 58.3%; Pred. No. 45;
Matches 7; Conservative 1; Mismatches 1; Indels 3; Gaps 1;

QY      1 GPWELVG---YF 9
      |||||:|
Db      207 GPWELVG-LVLPF 218

RESULT 8
US-11-082-389-302
; Sequence 302, Application US/11082389
; Publication No. US2005024935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Krogger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberbauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; FILE REFERENCE: BGI-131CPCN
; CURRENT APPLICATION NUMBER: US/11/082,389
; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
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; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 302
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 4
; OTHER INFORMATION: Xaa = Phe, Ser, Tyr, or Cys
US-11-082-389-302

Query Match          50.0%; Score 33; DB 7; Length 198;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      3 WELVGY 8
      |||||
Db      99 WQLTGY 104

RESULT 9
US-11-082-389-304
; Sequence 304, Application US/11082389
; Publication No. US2005024935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Krogger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberbauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; FILE REFERENCE: BGI-131CPCN
; CURRENT APPLICATION NUMBER: US/11/082,389
; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 304
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-304
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Query Match 50.0%; Score 33; DB 7; Length 281;  
Best Local Similarity 66.7%; Pred. No. 33;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 WELVGY 8  
|:|:|  
DB 153 WQIIGY 158

## RESULT 10

US-11-055-822-76  
; Sequence 76, Application US/11055822  
; Publication No. US20050260707A1  
; GENERAL INFORMATION:  
; APPLICANT: Pompeius, Markus  
; APPLICANT: Kroger, Burkhard  
; APPLICANT: Schroder, Hartwig  
; APPLICANT: Zelder, Oskar  
; APPLICANT: Haberbauer, Gregor  
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING  
; FILE REFERENCE: BGI-121CPCN  
; CURRENT APPLICATION NUMBER: US/11/055,822  
; CURRENT FILING DATE: 2005-02-11  
; PRIOR APPLICATION NUMBER: 09/606,740  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: 60/141,031  
; PRIOR FILING DATE: 1999-06-25  
; PRIOR APPLICATION NUMBER: 60/142,101  
; PRIOR FILING DATE: 1999-07-02  
; PRIOR APPLICATION NUMBER: 60/148,613  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 60/187,970  
; PRIOR FILING DATE: 2000-03-09  
; PRIOR APPLICATION NUMBER: DE 19930476.9  
; PRIOR FILING DATE: 1999-07-01  
; PRIOR APPLICATION NUMBER: DE 19931415.2  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19931418.7  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19931419.5  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19931420.9  
; PRIOR FILING DATE: 1999-07-08  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 1158  
; SEQ ID NO 76  
; LENGTH: 431  
; TYPE: PRT  
; ORGANISM: Corynebacterium glutamicum  
US-11-055-822-76

Query Match 50.0%; Score 33; DB 7; Length 431;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPMEL 5  
|:|:|  
DB 284 GPMEL 288

## RESULT 11

US-10-131-826A-60  
; Sequence 60, Application US/10131826A  
; Publication No. US20050245730A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3330R1C128  
; CURRENT APPLICATION NUMBER: US/10/131,826A  
; CURRENT FILING DATE: 2002-04-24

; PRIOR APPLICATION NUMBER: 60/049911  
; PRIOR FILING DATE: 1997-06-18  
; PRIOR APPLICATION NUMBER: 60/056974  
; PRIOR FILING DATE: 1997-08-26  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059115  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059117  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059122  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059184  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059352  
; PRIOR FILING DATE: 1997-09-19  
; PRIOR APPLICATION NUMBER: 60/059588  
; PRIOR FILING DATE: 1997-09-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 60  
; LENGTH: 724  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-131-826A-60

Query Match 50.0%; Score 33; DB 6; Length 724;  
Best Local Similarity 50.0%; Pred. No. 82;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 WELVGYFD 10  
|:|:|  
DB 83 WDMYDFD 90

## RESULT 12

US-11-055-822-72  
; Sequence 72, Application US/11055822  
; Publication No. US20050260707A1  
; GENERAL INFORMATION:  
; APPLICANT: Pompeius, Markus  
; APPLICANT: Kroger, Burkhard  
; APPLICANT: Schroder, Hartwig  
; APPLICANT: Zelder, Oskar  
; APPLICANT: Haberbauer, Gregor  
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING  
; FILE REFERENCE: BGI-121CPCN  
; CURRENT APPLICATION NUMBER: US/11/055,822  
; CURRENT FILING DATE: 2005-02-11  
; PRIOR APPLICATION NUMBER: 09/606,740  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: 60/141,031  
; PRIOR FILING DATE: 1999-06-25  
; PRIOR APPLICATION NUMBER: 60/142,101  
; PRIOR FILING DATE: 1999-07-02

```

; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 72
; LENGTH: 1510
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-72
```

```
Query Match          50.0%; Score 33; DB 7; Length 1510;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GPMEL 5
      |||||
Db      1063 GPMEL 1067
```

```

RESULT 13
US-11-113-424-52
; Sequence 52, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangoli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/332,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 2725
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-113-424-52
```

```
Query Match          50.0%; Score 33; DB 7; Length 2725;
Best Local Similarity 60.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      1 GPMELVGYFD 10
      |||||
```

```
Db      503 GPMWLAIFYND 512
```

```

RESULT 14
US-10-467-657-4150
; Sequence 4150, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 4150
; LENGTH: 456
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4150
```

```
Query Match          48.5%; Score 32; DB 6; Length 456;
Best Local Similarity 57.1%; Pred. No. 78;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 PWEIVGY 8
      |||||
Db      154 PWEIVASY 160
```

```

RESULT 15
US-11-147-047-33
; Sequence 33, Application US/11147047
; Publication No. US2005026068A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdock, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoying
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GPS0016
; CURRENT APPLICATION NUMBER: US/11/147,047
; CURRENT FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US/10/221,097
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: PCT/US01/07143
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/187,107
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/236,874
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/188,916
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/237,846
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 533
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-147-047-33
```

```
Query Match          48.5%; Score 32; DB 7; Length 533;
Best Local Similarity 83.3%; Pred. No. 90;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

Oy	2	PWELVG	7
Db	178	PWEAVG	183

Search completed: December 4, 2005, 04:37:49  
Job time : 4.20833 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:09:54 / Search time 130.312 Seconds  
(without alignments)  
50.576 Million cell updates/sec

Title: US-10-632-706-197  
Sequence: 1 EPDMLMGDRGALDV 15

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 2443163 seqs, 439378781 residues  
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21.\*  
1: geneseq19808.\*  
2: geneseq19908.\*  
3: geneseq20008.\*  
4: geneseq20018.\*  
5: geneseq20028.\*  
6: geneseq20038.\*  
7: geneseq20038.\*  
8: geneseq20048.\*  
9: geneseq20058.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	89	100.0	15	8	ADR38727	Ad38727 Mouse hea
2	89	100.0	15	8	ADR38728	Ad38728 Mouse hea
3	89	100.0	15	8	ADR38792	Ad38792 Mouse hea
4	89	100.0	15	8	ADR38795	Ad38795 Mouse hea
5	89	100.0	15	8	ADR38798	Ad38798 Mouse hea
6	89	100.0	15	8	ADR38729	Ad38729 Mouse hea
7	75	84.3	15	8	ADR38801	Ad38801 Mouse hea
8	51	57.3	201	8	ADJ98189	Adj98189 Prochlo
9	48	53.9	229	8	ABO66015	Ab066015 Klebsiell
10	48	53.9	775	3	AB13560	Ab13560 Streptomy
11	48	53.9	775	3	AB13560	Ab13560 Streptomy
12	47	52.8	59	2	AAV48365	AAV48365 Human pro
13	47	52.8	455	4	ABG22524	Abg22524 Novel hum
14	47	52.8	904	8	ADS23387	AdS23387 Bacterial
15	46	51.7	186	4	AAW24399	AAW24399 Human EST
16	45	50.6	54	5	ABP03542	Abp03542 Human ORF
17	45	50.6	372	6	ABU04008	Abu04008 Protein e
18	45	50.6	450	8	ADN47961	Adn47961 Thermococ
19	45	50.6	614	7	ADF06781	Adf06781 Bacterial
20	44	49.4	70	3	AAG15847	AAg15847 Arabidops
21	44	49.4	137	6	ADA21119	Ada21119 Human sec
22	44	49.4	342	3	AAB51737	Aab51737 Human sec
23	44	49.4	409	4	AAB96393	Aab96393 Putative
24	44	49.4	472	7	ADC86881	Adc86881 Human GPC

25	44	49.4	687	8	ADS42446	AdS42446 Bacterial
26	43	48.3	100	8	ADO65091	Ado65091 Novel hum
27	43	48.3	345	2	AAV38595	AAV38595 Neisseria
28	43	48.3	345	2	ABE49036	ABe49036 N. gonorr
29	43	48.3	383	2	AAV38596	AAV38596 Neisseria
30	43	48.3	383	6	ABP79536	ABp79536 N. gonorr
31	43	48.3	383	9	ABE49038	ABe49038 N. gonorr
32	43	48.3	546	2	AAW26164	AAW26164 KF-1 prot
33	43	48.3	582	2	AAU30396	AAU30396 Novel hum
34	43	48.3	616	8	ADS20416	AdS20416 Crab-eat1
35	43	48.3	683	3	AAW26163	AAW26163 Mouse KF-
36	43	48.3	683	9	ADZ04210	AdZ04210 Novel apo
37	43	48.3	685	2	AAW26165	AAW26165 Human KF-
38	43	48.3	685	9	ADX07646	AdX07646 Cyclin-de
39	43	48.3	685	9	ADZ04207	AdZ04207 Novel apo
40	43	48.3	732	9	ABM94428	ABm94428 M. xanthu
41	43	48.3	2519	7	ABM8218	ABm8218 Rice abio
42	42.5	47.8	315	4	ABE09181	ABe09181 Pseudomon
43	42.5	47.8	315	6	ABU15664	Abu15664 Protein e
44	42.5	47.8	320	7	ABO69555	ABo69555 Pseudomon
45	42	47.2	53	4	AAU65794	AAu65794 Protoninb

## ALIGNMENTS

RESULT 1  
ID ADR38727 standard; peptide; 15 AA.  
AC ADR38727;  
DT 02-DEC-2004 (first entry)  
DE Mouse heavy chain variable region CDR3 seqid 129.  
KW antibacterial; antibody; botulinum neurotoxin type A; BONT/A;  
KW BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
KW toxin neutralisation; botulinum neurotoxin poisoning; mouse;  
KW heavy chain variable region; complementarity determining region; CDR3.  
OS Mus sp.  
PN US2004175385-A1.  
XX 09-SEP-2004.  
PF 01-AUG-2003; 2003US-00632706.  
PR 31-AUG-1998; 98US-00144886.  
PR 01-AUG-2002; 2002US-0400721P.  
PA (REGC ) UNIV CALIFORNIA.  
PI Marks JD, Amersdorfer P;  
DR WPI; 2004-652009/63.  
XX New isolated antibody that neutralizes botulinum neurotoxin type A,  
PT useful for diagnosing botulism or for treating pathologies associated  
PT with botulinum neurotoxin poisoning.  
PS Example 3; SEQ ID NO 129; 110P; English.  
XX The invention describes an isolated antibody (I) that specifically binds  
CC to an epitope specifically bound by an antibody expressed by a specific  
CC clone where (I) binds to and neutralizes botulinum neurotoxin type A  
CC (BONT/A). An isolated antibody (I) that specifically binds to an epitope  
CC specifically bound by an antibody expressed by a clone chosen from clone  
CC S25, C29, C39, 1C6, 3D12, B4, 1F3, hUC25, Ar1, Ar2, WR1(V), WR1(T), 3-1,  
CC 3-8, 3-10 and INGI, where (I) binds to and neutralizes botulinum  
CC neurotoxin type A (BONT/A). Also described are: a polypeptide (II)  
CC comprising BONT/A neutralising epitope having an epitope that is

CC specifically bound by an antibody expressed by clones as mentioned in (I)  
 CC ; producing (I); and a composition (III) comprising several anti-  
 CC botulinum neurotoxin antibodies, where each antibody is specific for a  
 CC different epitope of a botulinum neurotoxin and the combination of  
 CC antibodies shows greater toxin neutralisation than the single antibodies  
 CC in surplus. The following are disclosed: a pharmaceutical composition  
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising  
 CC BoNT/A antibody and for neutralising a botulinum neurotoxin which  
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is  
 CC specific for a different epitope of the botulinum neurotoxin and the  
 CC combination of antibodies shows greater toxin neutralisation than the  
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism  
 CC or for treating pathologies associated with botulinum neurotoxin  
 CC poisoning. (II) exhibits specificity and affinity towards BoNT/A. (I)  
 CC enables rapid detection or diagnosis of botulism. This is the amino acid  
 CC sequence of mouse heavy chain variable region complementarity determining  
 CC region 3 (CDR3) from anti-botulinum neurotoxin antibodies.

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 89; DB 8; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPDWLTMGDRGALDV 15  
 |||||  
 Db 1 EPDWLTMGDRGALDV 15

RESULT 2  
 ADR38728  
 ID ADR38728 standard; peptide; 15 AA.

XX AC ADR38728;

XX DT 02-DEC-2004 (first entry)

XX DE Mouse heavy chain variable region CDR3 seqid 130.

XX antibody; anti-botulinum neurotoxin type A; BoNT/A;  
 XX BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
 XX toxin neutralisation; botulinum neurotoxin poisoning; mouse;  
 XX heavy chain variable region; complementarity determining region; CDR3.

XX OS Mus sp.

XX PN US2004175385-A1.

XX PD 09-SEP-2004.

XX PF 01-AUG-2003; 2003US-00632706.

XX PR 31-AUG-1998; 98US-00144886.

XX PR 01-AUG-2002; 2002US-0400721P.

XX PA (REGC ) UNIV CALIFORNIA.

XX PI Marks JD, Amerdorfer P;

XX DR WPI; 2004-652009/63.

XX PT New isolated antibody that neutralizes botulinum neurotoxin type A,  
 XX useful for diagnosing botulism or for treating pathologies associated  
 XX with botulinum neurotoxin poisoning.

XX PS Example 3; SEQ ID NO 130; 110pp; English.

XX CC The invention describes an isolated antibody (I) that specifically binds  
 XX to an epitope specifically bound by an antibody expressed by a specific  
 XX clone where (I) binds to and neutralises botulinum neurotoxin type A  
 XX (BoNT/A). An isolated antibody (I) that specifically binds to an epitope  
 XX specifically bound by an antibody expressed by a clone chosen from clone  
 XX S25, C25, C39, 1C6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1,

CC 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum  
 CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)  
 CC comprising BoNT/A neutralising epitope having an epitope that is  
 CC specifically bound by an antibody expressed by clones as mentioned in (I)  
 CC ; producing (I); and a composition (III) comprising several anti-  
 CC botulinum neurotoxin antibodies, where each antibody is specific for a  
 CC different epitope of a botulinum neurotoxin and the combination of  
 CC antibodies shows greater toxin neutralisation than the single antibodies  
 CC in surplus. The following are disclosed: a pharmaceutical composition  
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising  
 CC BoNT/A antibody and for neutralising a botulinum neurotoxin which  
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is  
 CC specific for a different epitope of the botulinum neurotoxin and the  
 CC combination of antibodies shows greater toxin neutralisation than the  
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism  
 CC or for treating pathologies associated with botulinum neurotoxin  
 CC poisoning. (II) exhibits specificity and affinity towards BoNT/A. (I)  
 CC enables rapid detection or diagnosis of botulism. This is the amino acid  
 CC sequence of mouse heavy chain variable region complementarity determining  
 CC region 3 (CDR3) from anti-botulinum neurotoxin antibodies.

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 89; DB 8; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPDWLTMGDRGALDV 15  
 |||||  
 Db 1 EPDWLTMGDRGALDV 15

RESULT 3  
 ADR38792  
 ID ADR38792 standard; peptide; 15 AA.

XX AC ADR38792;

XX DT 02-DEC-2004 (first entry)

XX DE Mouse heavy chain anti-BoNT-antibody CDR3 seqid 194.

XX antibody; anti-BoNT-antibody; botulinum neurotoxin type A; BoNT/A;  
 XX BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
 XX toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;  
 XX CDR3; complementarity determining region 1.

XX OS Mus sp.

XX PN US2004175385-A1.

XX PD 09-SEP-2004.

XX PF 01-AUG-2003; 2003US-00632706.

XX PR 31-AUG-1998; 98US-00144886.

XX PR 01-AUG-2002; 2002US-0400721P.

XX PA (REGC ) UNIV CALIFORNIA.

XX PI Marks JD, Amerdorfer P;

XX DR WPI; 2004-652009/63.

XX PT New isolated antibody that neutralizes botulinum neurotoxin type A,  
 XX useful for diagnosing botulism or for treating pathologies associated  
 XX with botulinum neurotoxin poisoning.

XX PS Example 4; SEQ ID NO 194; 110pp; English.

XX CC The invention describes an isolated antibody (I) that specifically binds  
 XX to an epitope specifically bound by an antibody expressed by a specific  
 XX clone where (I) binds to and neutralises botulinum neurotoxin type A



(BONT/A). An isolated antibody (I) that specifically binds to an epitope specifically bound by an antibody expressed by a clone chosen from clone CC 325, C25, C39, 3D12, B4, 1F3, huC25, Ar1, Ar2, WR1(V), WR1(T), 3-1, CC 3-8, 3-10 and INGI, where (I) binds to and neutralizes botulinum neurotoxin type A (BONT/A). Also described are: a polypeptide (II) comprising BONT/A neutralising epitope having an epitope that is specifically bound by an antibody expressed by clones as mentioned in (I) ; producing (I) ; and a composition (III) comprising several anti-botulinum neurotoxin antibodies, where each antibody is specific for a different epitope of a botulinum neurotoxin and the combination of antibodies shows greater toxin neutralisation than the single antibodies in surplus. The following are disclosed: a pharmaceutical composition comprising (I) ; and a kit comprising a botulinum neurotoxin which BONT/A antibody and for neutralising a botulinum neurotoxin which CC involves contacting neurotoxin with (I) in surplus, where each of (I) is specific for a different epitope of the botulinum neurotoxin and the CC combination of antibodies shows greater toxin neutralisation than the CC single antibodies in surplus. (I) is useful for diagnosing the botulinum CC or for creating pathologies associated with botulinum neurotoxin CC poisoning. (I) exhibits specificity and affinity towards BONT/A. (I) CC enables rapid detection or diagnosis of botulinum. This is the amino acid CC sequence of mouse heavy chain anti-BONT-antibody CDR3.

XX SEQ Sequence 15 AA;

Query Match 100.0%; Score 89; DB 8; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPDMLMGDRGALDV 15  
| | | | | | | | | | | | | | | |  
Db 1 EPDMLMGDRGALDV 15

RESULT 4  
ADR38795  
ID ADR38795 standard; peptide; 15 AA.

XX AC ADR38795;

XX DT 02-DEC-2004 (first entry)

DE Mouse heavy chain anti-BONT-antibody CD3 seqid 197.

XX antibacterial; antibody; botulinum neurotoxin type A; BONT/A;

KM BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;

KM toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;

XX CDR3; complementarity determining region 1.

OS Mus sp.

XX US2004175385-A1.

XX PD 09-SEP-2004.

XX PF 01-AUG-2003; 2003US-00632706.

XX PR 31-AUG-1998; 98US-00144886.

XX PR 01-AUG-2002; 2002US-0400721P.

XX PA (REGC ) UNIV CALIFORNIA.

XX PI Marke JD, Amersdorfer P;

XX DR WPI; 2004-652009/63.

XX New isolated antibody that neutralizes botulinum neurotoxin type A,

XX useful for diagnosing botulinum or for treating pathologies associated

XX with botulinum neurotoxin poisoning.

XX Example 4; SEQ ID NO 197; 110pp; English.

XX The invention describes an isolated antibody (I) that specifically binds

to an epitope specifically bound by an antibody expressed by a specific CC clone where (I) binds to and neutralizes botulinum neurotoxin type A CC (BONT/A). An isolated antibody (I) that specifically binds to an epitope CC specifically bound by an antibody expressed by a clone chosen from clone CC 325, C25, C39, 3D12, B4, 1F3, huC25, Ar1, Ar2, WR1(V), WR1(T), 3-1, CC 3-8, 3-10 and INGI, where (I) binds to and neutralizes botulinum neurotoxin type A (BONT/A). Also described are: a polypeptide (II) CC comprising BONT/A neutralising epitope having an epitope that is specifically bound by an antibody expressed by clones as mentioned in (I) CC ; producing (I) ; and a composition (III) comprising several anti-botulinum neurotoxin antibodies, where each antibody is specific for a different epitope of a botulinum neurotoxin and the combination of antibodies shows greater toxin neutralisation than the single antibodies in surplus. The following are disclosed: a pharmaceutical composition comprising (I) ; and a kit comprising a botulinum neurotoxin which CC BONT/A antibody and for neutralising a botulinum neurotoxin which CC involves contacting neurotoxin with (I) in surplus, where each of (I) is specific for a different epitope of the botulinum neurotoxin and the CC combination of antibodies shows greater toxin neutralisation than the CC single antibodies in surplus. (I) is useful for diagnosing the botulinum CC or for creating pathologies associated with botulinum neurotoxin CC poisoning. (I) exhibits specificity and affinity towards BONT/A. (I) CC enables rapid detection or diagnosis of botulinum. This is the amino acid CC sequence of mouse heavy chain anti-BONT-antibody CDR3.

XX SEQ Sequence 15 AA;

Query Match 100.0%; Score 89; DB 8; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPDMLMGDRGALDV 15  
| | | | | | | | | | | | | | | |  
Db 1 EPDMLMGDRGALDV 15

RESULT 5  
ADR38798  
ID ADR38798 standard; peptide; 15 AA.

XX AC ADR38798;

XX DT 02-DEC-2004 (first entry)

DE Mouse heavy chain anti-BONT-antibody CD3 seqid 200.

XX antibacterial; antibody; botulinum neurotoxin type A; BONT/A;

KM BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;

KM toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;

XX CDR3; complementarity determining region 1.

OS Mus sp.

XX US2004175385-A1.

XX PD 09-SEP-2004.

XX PF 01-AUG-2003; 2003US-00632706.

XX PR 31-AUG-1998; 98US-00144886.

XX PR 01-AUG-2002; 2002US-0400721P.

XX PA (REGC ) UNIV CALIFORNIA.

XX PI Marke JD, Amersdorfer P;

XX DR WPI; 2004-652009/63.

XX New isolated antibody that neutralizes botulinum neurotoxin type A,

XX useful for diagnosing botulinum or for treating pathologies associated

XX with botulinum neurotoxin poisoning.

XX Example 4; SEQ ID NO 200; 110pp; English.

XX The invention describes an isolated antibody (I) that specifically binds  
 CC to an epitope specifically bound by an antibody expressed by a specific  
 CC clone where (I) binds to and neutralizes botulinum neurotoxin type A  
 CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope  
 CC specifically bound by an antibody expressed by a clone chosen from clone  
 CC S25, C39, C39, 1C6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1,  
 CC 3-8, 3-10 and INGI, where (I) binds to and neutralizes botulinum  
 CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)  
 CC comprising BoNT/A neutralising epitope having an epitope that is  
 CC specifically bound by an antibody expressed by clones as mentioned in (I)  
 CC ; producing (I); and a composition (III) comprising several anti-  
 CC botulinum neurotoxin antibodies, where each antibody is specific for a  
 CC different epitope of a botulinum neurotoxin and the combination of  
 CC antibodies shows greater toxin neutralisation than the single antibodies  
 CC in surplus. The following are disclosed: a pharmaceutical composition  
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising  
 CC BoNT/A antibody and for neutralising a botulinum neurotoxin which  
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is  
 CC specific for a different epitope of the botulinum neurotoxin and the  
 CC combination of antibodies shows greater toxin neutralisation than the  
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism  
 CC or for treating pathologies associated with botulinum neurotoxin  
 CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)  
 CC enables rapid detection or diagnosis of botulism. This is the amino acid  
 CC sequence of mouse heavy chain anti-BoNT-antibody CDR3.

XX Sequence 15 AA;

Query Match 100.0%; Score 89; DB 8; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.8e-06; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPPWLMGDRGALDV 15  
 |||||  
 Db 1 EPPWLMGDRGALDV 15

RESULT 6

ADR38729 ADR38729 standard; peptide; 15 AA.

AC ADR38729;

DT 02-DEC-2004 (first entry)

DE Mouse heavy chain variable region CDR3 seqid 131.

XX antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;  
 XX BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
 XX toxin neutralisation; botulinum neurotoxin poisoning; mouse;  
 XX heavy chain variable region; complementarity determining region; CDR3.

OS Mus sp.

PN US2004175385-A1.

PD 09-SEP-2004.

PF 01-AUG-2003; 2003US-00632706.

PR 31-AUG-1998; 98US-00144886.

XX 01-AUG-2002; 2002US-0400721P.

PA (REGC ) UNIV CALIFORNIA.

PI Marks JD, Amerdorfer P;

DR MPI; 2004-652009/63.

XX New isolated antibody that neutralizes botulinum neurotoxin type A,  
 PT useful for diagnosing botulism or for treating pathologies associated  
 PT with botulinum neurotoxin poisoning.

XX Example 3; SEQ ID NO 131; 110pp; English.

PS The invention describes an isolated antibody (I) that specifically binds  
 CC to an epitope specifically bound by an antibody expressed by a specific  
 CC clone where (I) binds to and neutralizes botulinum neurotoxin type A  
 CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope  
 CC specifically bound by an antibody expressed by a clone chosen from clone  
 CC S25, C39, C39, 1C6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1,  
 CC 3-8, 3-10 and INGI, where (I) binds to and neutralizes botulinum  
 CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)  
 CC comprising BoNT/A neutralising epitope having an epitope that is  
 CC specifically bound by an antibody expressed by clones as mentioned in (I)  
 CC ; producing (I); and a composition (III) comprising several anti-  
 CC botulinum neurotoxin antibodies, where each antibody is specific for a  
 CC different epitope of a botulinum neurotoxin and the combination of  
 CC antibodies shows greater toxin neutralisation than the single antibodies  
 CC in surplus. The following are disclosed: a pharmaceutical composition  
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising  
 CC BoNT/A antibody and for neutralising a botulinum neurotoxin which  
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is  
 CC specific for a different epitope of the botulinum neurotoxin and the  
 CC combination of antibodies shows greater toxin neutralisation than the  
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism  
 CC or for treating pathologies associated with botulinum neurotoxin  
 CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)  
 CC enables rapid detection or diagnosis of botulism. This is the amino acid  
 CC sequence of mouse heavy chain variable region complementarity determining  
 CC region 3 (CDR3) from anti-botulinum neurotoxin antibodies.

XX Sequence 15 AA;

Query Match 100.0%; Score 89; DB 8; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.8e-06; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPPWLMGDRGALDV 15  
 |||||  
 Db 1 EPPWLMGDRGALDV 15

RESULT 7

ADR38801 ADR38801 standard; peptide; 15 AA.

AC ADR38801;

DT 02-DEC-2004 (first entry)

DE Mouse heavy chain anti-BoNT-antibody CDR3 seqid 203.

XX antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;  
 XX BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
 XX toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;  
 XX CDR3; complementarity determining region 1.

OS Mus sp.

PN US2004175385-A1.

PD 09-SEP-2004.

PF 01-AUG-2003; 2003US-00632706.

PR 31-AUG-1998; 98US-00144886.

XX 01-AUG-2002; 2002US-0400721P.

PA (REGC ) UNIV CALIFORNIA.

PI Marks JD, Amerdorfer P;

DR MPI; 2004-652009/63.

PT New isolated antibody that neutralizes botulinum neurotoxin type A.  
PT Useful for diagnosing botulism or for treating pathologies associated  
PT with botulinum neurotoxin poisoning.  
PS Example 4; SEQ ID NO 203; 110pp; English.  
XX  
CC The invention describes an isolated antibody (I) that specifically binds  
CC to an epitope specifically bound by an antibody expressed by a specific  
CC clone where (I) binds to and neutralises botulinum neurotoxin type A  
CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope  
CC specifically bound by an antibody expressed by a clone chosen from clone  
CC S25, C39, 1G6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1,  
CC 3-8, 3-10 and INGI, where (I) binds to and neutralizes botulinum  
CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)  
CC comprising BoNT/A neutralising epitope having an epitope that is  
CC specifically bound by an antibody expressed by clones as mentioned in (I)  
CC ; producing (I); and a composition (III) comprising several anti-  
CC botulinum neurotoxin antibodies, where each antibody is specific for a  
CC different epitope of a botulinum neurotoxin and the combination of  
CC antibodies shows greater toxin neutralisation than the single antibodies  
CC in surplus. The following are disclosed: a pharmaceutical composition  
CC comprising (I); and a kit comprising (I). (I) is useful for neutralising  
CC BoNT/A antibody and for neutralising a botulinum neurotoxin which  
CC involves contacting neurotoxin with (I) in surplus, where each of (I) is  
CC specific for a different epitope of the botulinum neurotoxin and the  
CC combination of antibodies shows greater toxin neutralisation than the  
CC single antibodies in surplus. (I) is useful for diagnosing the botulism  
CC or for treating pathologies associated with botulinum neurotoxin  
CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)  
CC enables rapid detection or diagnosis of botulism. This is the amino acid  
CC sequence of mouse heavy chain anti-BoNT-antibody CDR3.  
XX  
SQ Sequence 15 AA;  
XX  
Query Match 84.3%; Score 75; DB 8; Length 15;  
Best Local Similarity 93.3%; Pred. No. 0.00023;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 EPPDMLMGDRGALDV 15  
1 EPPDRLMGDRGALDV 15  
DB  
RESULT 8  
ABG20331  
ID ABG20331 standard; protein; 334 AA.  
XX  
AC ABG20331;  
XX  
DT 13-FEB-2002 (first entry)  
XX  
DE Novel human diagnostic protein #20322.  
XX  
KW Human; chromosome mapping; gene mapping; forensic;  
KW Food supplement; medical imaging; diagnostic; genetic disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO200175067-A2.  
XX  
PD 11-OCT-2001.  
XX  
PF 30-MAR-2001; 2001WO-US008631.  
XX  
PR 31-MAR-2000; 2000US-00540217.  
PR 23-AUG-2000; 2000US-00649167.  
XX  
PA (HYSB-) HYSBQ INC.  
XX  
PI Drmanac RT, Liu C, Tang YT;  
XX  
DR WPI; 2001-639362/73.  
DR N-PSDB; AAS84518.  
DR

XX  
PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.  
PS Claim 20; SEQ ID NO 50690; 103pp; English.  
XX  
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
CC sequences. (I) is useful as hybridisation probes, polymerase chain  
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
CC and in recombinant production of (II). The polynucleotides are also used  
CC in diagnostics as expressed sequence tags for identifying expressed  
CC genes. (I) is useful in gene therapy techniques to restore normal  
CC activity of (II) or to treat disease states involving (II). (II) is  
CC useful for generating antibodies against it, detecting or quantitating a  
CC polypeptide in tissue, as molecular weight markers and as a food  
CC supplement. (II) and its binding partners are useful in medical imaging  
CC of sites expressing (II). (I) and (II) are useful for treating disorders  
CC involving aberrant protein expression or biological activity. The  
CC polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic  
CC amino acid sequences of the invention. Note: The sequence data for this  
CC patent did not appear in the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 334 AA;  
XX  
Query Match 57.3%; Score 51; DB 4; Length 334;  
Best Local Similarity 53.3%; Pred. No. 23;  
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
QY 1 EPPDMLMGDRGALDV 15  
263 KPDMSWGPSPGMDIV 277  
DB  
RESULT 9  
ADJ98189  
ID ADJ98189 standard; protein; 201 AA.  
XX  
AC ADJ98189;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Prochlorococcus marinus str MIT 9313 phycol kinase protein.  
XX  
KW phycol kinase; tocopherol biosynthesis; plant; drought resistance;  
KW enzyme.  
XX  
OS Prochlorococcus marinus str. MIT 9313.  
XX  
PN WO2004013312-A2.  
XX  
PD 12-FEB-2004.  
XX  
PF 05-AUG-2003; 2003WO-US025276.  
XX  
PR 05-AUG-2002; 2002US-0400689P.  
PR 05-AUG-2003; 2003US-00634548.  
XX  
PA (MONS ) MONSANTO TECHNOLOGY LLC.  
XX  
PI Norris SR, Lincoln K, Abad MS, Eilers R, Hartuysen KK,  
PI Hirschberg J, Karunanandaa B, Moshiri F, Stein JC, Valentin HB;  
PI Venkatesh TV;  
XX  
DR WPI; 2004-157125/15.  
XX

PT New phycol kinase polynucleotides, useful in mediating tocopherol  
PT biosynthesis and in producing plants with increased drought resistance.  
XX  
PS Claim 1; SEQ ID NO 27; 189pp; English.

CC The invention relates to a novel substantially purified nucleic acid  
CC molecule encoding a phycol kinase. The nucleic acid molecules and  
CC polypeptides of the invention may be useful in mediating tocopherol  
CC biosynthesis and in producing plants with increased drought resistance.  
CC The current sequence is that of a phycol kinase protein of the invention.  
XX

SO Sequence 201 AA;

Query Match 53.9%; Score 48; DB 8; Length 201;  
Best Local Similarity 50.0%; Pred. No. 39;  
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 PDMILMGDRGAL 13  
DB 123 PNMILWGQRKSI 134

RESULT 10

AB06015 standard; protein; 229 AA.

AC AB06015;

DT 29-JUL-2004 (first entry)

XX Klebsiella pneumoniae polypeptide seqid 12532.

XX Klebsiella pneumoniae polypeptide seqid 12532.

KM Recombinant expression vector; transcription regulatory element;  
KM Klebsiella pneumoniae protein; antibacterial; Vaccine.

OS Klebsiella pneumoniae.

PN US610836-B1.

PD 26-AUG-2003.

PF 27-JAN-2000; 2000US-00489039.

PR 29-JAN-1999; 99US-0117747P.

PA (GENO-) GENOME THERAPEUTICS CORP.

PI Breton GL, Osborne M;

DR WPI; 2003-895346/82.

DR N-PSDB; ACH99566.

PT New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for  
PT preparing a vaccine composition against Klebsiella pneumoniae.

PS Disclosure; SEQ ID NO 12532; 932pp; English.

CC The invention describes a new isolated nucleic acid encoding a Klebsiella  
CC pneumoniae polypeptide. Also described are: a recombinant expression  
CC vector comprising the nucleic acid, operably linked to a transcription  
CC regulatory element; and a cell comprising the recombinant expression  
CC vector. The nucleic acid is useful for preparing a vaccine composition  
CC against Klebsiella pneumoniae. This is the amino acid sequence of a  
CC Klebsiella pneumoniae polypeptide of the invention  
XX

SO Sequence 229 AA;

Query Match 53.9%; Score 48; DB 7; Length 229;  
Best Local Similarity 57.1%; Pred. No. 44;  
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 EPDWILMGDRGALD 14

DB 32 ERSWCKWGDRPAID 45

RESULT 11

AB13560 standard; protein; 775 AA.

AC AB13560;

DT 06-MAR-2001 (first entry)

XX Streptomyces globisporus C-1027 gene cluster ORF -1.

XX Eneidyne C-1027 biosynthesis gene cluster; apoprotein; chromophore;  
XX open reading frame -1; cancer.

OS Streptomyces globisporus.

PN WO200040596-A1.

PD 13-JUL-2000.

PF 06-JAN-2000; 2000WO-US000446.

PR 06-JAN-1999; 99US-0115434P.

PR 05-JAN-2000; 2000US-00477962.

PA (REGC ) UNIV CALIFORNIA.

PI Shen B, Liu W, Christenson SD, Standage S;

DR WPI; 2000-465947/40.

DR N-PSDB; AAA63348, AAA63349.

PT Isolated nucleic acid comprising a nucleic acid encoding any of C-1027  
PT open reading frames (ORFs) -7 to 42, excluding ORF 9 (cgaA), useful for  
PT the production of enediyne C-1027 antitumor antibiotics.

PS Claim 15; Page 87-91; 160pp; English.

CC The present sequence is the protein which is encoded by open reading  
CC frame -1 of the Streptomyces globisporus enediyne C-1027 gene cluster.  
CC Eneidyne C-1027 is an antibiotic, consisting of an apoprotein and a non-  
CC peptidic chromophore, which acts by damaging DNA. The sequences within  
CC the gene cluster, and the proteins they encode, can be used in the  
CC treatment of cancer, along with antagonists of the protein. This protein  
CC is an ABC transport/UvrA-like protein  
XX

SO Sequence 775 AA;

Query Match 53.9%; Score 48; DB 3; Length 775;  
Best Local Similarity 53.8%; Pred. No. 1.6e+02;  
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 PDMILMGDRGALD 14  
DB 195 PDMQIMAKSGRLD 207

RESULT 12

AAV48365 standard; protein; 59 AA.

AC AAV48365;

DT 08-DEC-1999 (first entry)

XX Human prostate cancer-associated protein 62.

XX Expressed sequence tag; EST; prostate; tumor; treatment; gene therapy;  
XX cancer; tissue specificity; human.

OS Homo sapiens.

XX	DR	WPI: 2001-639362/73.	
XX	DR	N-PSDB: AAS86711.	
PT	XX	New isolated polynucleotide and encoded polypeptides, useful in	
PT	XX	diagnostics, forensics, gene mapping, identification of mutations	
PT	XX	responsible for genetic disorders or other traits and to assess	
PT	XX	biodiversity.	
PS	XX	Claim 20: SEQ ID NO 52883; 103bp; English.	
XX	XX	The invention relates to isolated polynucleotide (I) and polypeptide (II)	
CC	XX	sequences. (I) is useful as hybridisation probes, polymerase chain	
CC	XX	reaction (PCR) primers, oligomers, and for chromosome and gene mapping.	
CC	XX	and in recombinant production of (II). The polynucleotides are also used	
CC	XX	in diagnostics as expressed sequence tags for identifying expressed	
CC	XX	genes. (I) is useful in gene therapy techniques to restore normal	
CC	XX	activity of (II) or to treat disease states involving (II). (II) is	
CC	XX	useful for generating antibodies against it, detecting or quantitating a	
CC	XX	polypeptide in tissue, as molecular weight markers and as a food	
CC	XX	supplement. (II) and its binding partners are useful in medical imaging	
CC	XX	of sites expressing (II). (I) and (II) are useful for treating disorders	
CC	XX	involving aberrant protein expression or biological activity. The	
CC	XX	polypeptide and polynucleotide sequences have applications in	
CC	XX	diagnostics, forensics, gene mapping, identification of mutations	
CC	XX	responsible for genetic disorders or other traits to assess biodiversity	
CC	XX	and to produce other types of data and products dependent on DNA and	
CC	XX	amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic	
CC	XX	amino acid sequences of the invention. Note: The sequence data for this	
CC	XX	patent did not appear in the printed specification, but was obtained in	
CC	XX	electronic format directly from WIPO at	
CC	XX	ftp.wipo.int/pub/published_pct_sequences	
CC	XX	Sequence 455 AA;	
Query Match	52.8%	Score 47; DB 4; Length 455;	

Matches	7;	Conservative	3;	Mismatches	3;	Indels	0;	Gaps	0;
QY	1	EPDMLWGRGAL	13						
		I I I I I							

Db 93 EQNWLWCERGVM 105

ID	AD523387	standard; protein; 904 AA.
XX		
AC	AD523387;	
XX		
DT	02-DEC-2004	(first entry)
XX		
DE	Bacterial polypeptide #12420.	
XX		
KW	Recombinant DNA construct; transformed plant; improved plant property;	
KW	cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;	
KW	pathogen tolerance; pest tolerance; plant disease resistance;	
KW	cell cycle pathway modification; plant growth regulator;	
KW	homologous recombination; seed oil yield; protein yield; carbohydrate;	
KW	nitrogen; phosphorus; photosynthesis; lignin; galactomannan;	
KW	bacterial polypeptide.	
XX		
OS	Bacteria.	
XX		
PN	US2003233675-A1.	
XX		
PD	18-DEC-2003.	
XX		
PF	20-FEB-2003; 2003US-00369493.	
XX		
PR	21-FEB-2002; 2002US-0360039P.	
XX		

PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
XX  
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS,  
XX WPI, 2004-061375/06.  
XX  
XX New recombinant DNA construct comprising a promoter positioned to provide  
PT expression of a polynucleotide encoding a polypeptide from a  
PT microbial source, useful for producing plants with improved properties.  
PS Claim 1, SEQ ID NO 12420; 122pp; English.  
XX  
XX The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transformed plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved plant growth and development under at least one stress  
CC condition, improved lignin production or improved galactomannan  
CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).  
CC  
SQ Sequence 904 AA;  
Query Match 52.8%; Score 47; DB 8; Length 904;  
Best Local Similarity 70.0%; Pred. No. 2.6e+02;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 4 WLMGDRGAL 13  
DB 460 WLMGDKXTSL 469  
RESULT 15  
AAM24399  
ID AAM24399 standard; protein, 186 AA.  
XX  
AC AAM24399;  
XX  
DT 12-OCT-2001 (first entry)  
XX  
DE Human EST encoded protein SEQ ID NO: 1924.  
XX  
XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;  
XX tomato; monkey; dog; sea urchin; expressed sequence tag; EST;  
XX diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;  
XX gene therapy; nutrition.  
OS Homo sapiens.  
XX  
XX MO200154477-A2.  
XX  
XX 02-AUG-2001.  
XX  
XX

PF 25-JAN-2001; 2001WO-US002687.  
XX  
XX 25-JAN-2000; 2000US-00491404.  
XX 17-JUL-2000; 2000US-00617746.  
PR 03-AUG-2000; 2000US-00631451.  
PR 15-SEP-2000; 2000US-0063870.  
XX  
XX (HYSE-) HYSEQ INC.  
XX  
XX Tang YF, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Aundl V,  
PI Cao Y, Dermanac RA, Zhang J, Werhman T;  
XX WPI; 2001-476164/51.  
XX  
DR N-PSDB; AAH99058.  
XX  
XX  
PT Isolated polypeptide for treatment of diseases, diagnostics, raising  
PT antibodies and research use.  
XX  
XX Claim 20; Page 1235; 1275pp; English.  
XX  
XX The present invention provides the protein and coding sequences of novel  
CC proteins from a variety of organisms, including human, dog, cat, horse,  
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea  
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)  
CC from the organism of interest. They can be used in diagnostics,  
CC forensics, gene mapping, identification of mutations, to assess  
CC biodiversity and for nutritional purposes. The present sequence is a  
CC protein of the invention  
XX  
SQ Sequence 186 AA;  
Query Match 51.7%; Score 46; DB 4; Length 186;  
Best Local Similarity 53.3%; Pred. No. 71;  
Matches 8; Conservative 3; Mismatches 2; Indels 2; Gaps 1;  
QY 2 PDWLMG--DRGALD 14  
DB 168 PGWLMGKXKRGKLN 182

Search completed: December 4, 2005, 04:44:59  
Job time : 132.312 secs

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: December 4, 2005, 04:31:45 ; Search time 21.25 Seconds  
(without alignments)  
67.918 Million cell updates/sec

Title: US-10-632-706-197

Perfect score: 89  
Sequence: 1 EPDMLMGDRGALDV 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	51.7	373	2 D71142	hypothetical prote
2	45.5	51.1	298	2 AB3234	transcriptional re
3	45	50.6	203	2 G70595	probable entd prot
4	45	50.6	601	2 AG0066	probable AMP-bind
5	44.5	50.0	1076	2 T30842	serine-repeat anti
6	44	49.4	237	2 G82768	virulence protein
7	44	49.4	409	2 B75010	hypothetical prote
8	44	49.4	491	2 T10930	3C3.21 protein - S
9	44	49.4	601	2 E95296	probable ABC-type
10	43	48.3	321	2 S77614	phosphotibosylform
11	43	48.3	462	2 T50422	homolog to yeast o
12	43	48.3	683	2 JC5393	zinc finger protei
13	43	48.3	685	2 JC5392	zinc finger protei
14	43	48.3	698	2 A82593	hypothetical prote
15	42.5	47.8	315	2 H83276	probable lipase PA
16	42	47.2	71	2 G98356	hypothetical prote
17	42	47.2	139	2 AG2925	hypothetical prote
18	42	47.2	397	2 E53240	allergen Amb a II
19	42	47.2	408	1 A69819	chiamin phosphoe
20	42	47.2	482	1 A10554	chiamin biosynthes
21	42	47.2	482	2 E90688	probable oxidoredu
22	42	47.2	482	2 T46944	chiamin biosynthes
23	42	47.2	482	2 A85539	probable oxidoredu
24	42	47.2	482	2 G64771	yaJX protein - Bsc
25	42	47.2	486	2 T51431	glucosyltransferas
26	42	47.2	486	2 H87311	hypothetical prote
27	42	47.2	492	2 T38156	citrate lyase - fl
28	42	47.2	566	2 H84037	long-chain fatty-a
29	42	47.2	604	2 T49577	hypothetical prote

30	42	47.2	608	2 T34994	probable long-chain
31	42	47.2	804	2 AG0565	probable membrane
32	42	47.2	804	2 G64780	probable membrane
33	42	47.2	804	2 A85549	probable oxidoredu
34	42	47.2	804	2 G90698	probable oxidoredu
35	42	47.2	993	2 B97219	conserved membrane
36	41	46.1	36	2 B84416	hypothetical prote
37	41	46.1	248	2 T36093	probable DNA methy
38	41	46.1	262	2 F75093	hypothetical prote
39	41	46.1	288	2 AG0888	probable Arac-fam
40	41	46.1	359	2 C70735	probable idsa prot
41	41	46.1	403	2 T10847	y4M protein - Rhi
42	41	46.1	408	2 AG0305	probable L-iditol
43	41	46.1	438	2 T37786	probable RNA-bind
44	41	46.1	442	2 D84600	probable xylose
45	41	46.1	459	2 T27657	hypothetical prote

#### ALIGNMENTS

RESULT 1  
D71142  
hypothetical protein PH0351 - *Pyrococcus horikoshii*  
C/Species: *Pyrococcus horikoshii*  
C/Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 09-Jul-2004  
C/Accession: D71142  
R/Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Halkawa, Y.; Hino, Y.; Yamamoto, S.; Sekin  
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kuchida, N.; Oguchi  
DNA Res. 5, 55-76, 1998  
A/Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a  
A/Reference number: AT1000; MUID:98344137; PMID:9679194  
A/Accession: D71142  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-373 <KAW>  
A/Cross-references: UNIPROT:O58089; UNIPARC:UPI0000062DB7; GB:AF000002; NID:g3236129; PI  
A/Experimental source: strain OT3  
A/Note: This accession replaces an interim accession for a sequence replaced by GenBank  
C/Genetics:  
A/Gene: PH0351

Query Match 51.7% Score 46; DB 2; Length 373;  
Best Local Similarity 43.5%; Pred. No. 19;  
Matches 10; Conservative 1; Mismatches 2; Indels 10; Gaps 1;

QY 2 PDMLM-----GDRGALD 14  
Db 318 PGMILMGLILMGRIGNPGALD 340

RESULT 2  
AB3234  
transcriptional regulator, lyxR family gcvA [imported] - *Agrobacterium tumefaciens* (stra  
C/Species: *Agrobacterium tumefaciens*  
C/Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004  
C/Accession: AB3234  
R/Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L  
erage, G.; Gillitt, W.; Grant, C.; Guenther, D.; Kuyavain, T.; Levy, R.; Li, M.; McClell  
; Karp, P.; Romero, P.; Zhang, S.  
Science 294, 2317-2323, 2001  
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
ster, E.W.  
A/Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.  
A/Reference number: AB2577; MUID:21608550; PMID:11743193  
A/Accession: AB3234  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-298 <KUR>  
A/Cross-references: UNIPROT:O8U680; UNIPARC:UPI00000D2764; GB:AE008690; PIDN:AAL46291.1;  
A/Experimental source: strain C58 (Dupont)  
C/Genetics:  
A/Gene: gcvA



A:Genome: plasmid  
C:Superfamily: regulatory protein ampr

Query Match 51.1%; Score 45.5; DB 2; Length 298;  
Best Local Similarity 56.2%; Pred. No. 10;  
Matches 9; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1 EPDMLM-GDRGALDV 15  
|||  
DB 199 EPDMLMCAQAGVADV 214

## RESULT 3

G70595

probable end protein - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C>Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004

C:Accession: G70595

R:Coile, S.T.; Broesch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentile, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998

A:Authors: Squares, R.; Suleston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A>Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: G70595

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-203 <CON>

A:Cross-references: UNIPROT:Q05852; UNIPARC:UPI000016534B; GB:Z95120; GB:AL123456; NID:9

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: end

C:Superfamily: cofactor-dependent phosphoglycerate mutase; phosphoglycerate mutase homol

Query Match 50.6%; Score 45; DB 2; Length 203;  
Best Local Similarity 85.7%; Pred. No. 15;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPDMLM 7  
|||  
DB 103 EPDMLM 109

## RESULT 4

AG0066

probable AMP-binding enzyme-family protein YPO0537 [imported] - Yersinia pestis (strain

C:Species: Yersinia pestis

C>Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004

C:Accession: AG0066

R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tlball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarrage, A.M.; Killamworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; H. M.; Rutherford, K.; Stimpson, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, N.

Nature 413, 523-527, 2001

A>Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: AG0066

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-601 <KUN>

A:Cross-references: UNIPROT:Q82IG5; UNIPARC:UPI00000DCD42; GB:AL590842; PIDN:CAC89394.1;

C:Genetics:

A:Gene: YPO0537

C:Superfamily: Synchocystis long-chain-fatty-acid-CoA ligase; acetate-CoA ligase homol

Query Match 50.6%; Score 45; DB 2; Length 601;  
Best Local Similarity 64.3%; Pred. No. 42;  
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EPDMLMGDRGALD 14  
|||  
DB 440 EDGWLKGTGAGALD 453

## RESULT 5

T30842

serine-repeat antigen 3 - Plasmidium vivax

C:Species: Plasmidium vivax

C>Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 09-Jul-2004

C:Accession: T30842

R:Kiefer, M.C.; Crawford, K.A.; Boley, L.J.; Landsberg, K.E.; Gibson, H.L.; Kaslow, D.C.

Mol. Biochem. Parasitol. 78, 55-65, 1996

A>Title: Identification and cloning of a locus of serine repeat antigen (serra)-related g-

A:Reference number: Z20898; MUID:96408670; PMID:8813677

A:Accession: T30842

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1076 <KTE>

A:Cross-references: UNIPROT:Q26154; UNIPARC:UPI00000809B3; EMBL:U51723; NID:g1381087; PIR

C:Genetics:

A:Insertions: 12/1; 253/1; 302/1

A:Note: V-SERA 3

C:Superfamily: Plasmidium vivax serine-repeat antigen

Query Match 50.0%; Score 44.5; DB 2; Length 1076;  
Best Local Similarity 40.9%; Pred. No. 87;  
Matches 9; Conservative 2; Mismatches 4; Indels 7; Gaps 1;

QY 1 EPDML-----MGDRGALDV 15  
|||  
DB 743 KPYWLLQNSKMGKMGDKGTFRV 764

## RESULT 6

G82768

virulence protein XFO754 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004

C:Accession: G82768

R:anonymous. The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc

Nature 406, 151-157, 2000

A>Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717; PMID:10910347

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: G82768

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-237 <SIM>

A:Cross-references: UNIPROT:Q9PFC4; UNIPARC:UPI00000C24F4; GB:AE003916; GB:AE003849; NID:

A:Experimental source: strain 9a5c

R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvares, R.; A

B:Rios, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrez, H.

as-Neto, E.; Docena, C.; El-Dorri, H.; Facinanci, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Frome

J.D.; Unqueira, M.L.; Kemper, E.L.; Kitzling, J.P.; Krieger, J.B.; Kuzmae, E.E.; Laigret

chado, M.A.; Medeira, A.M.B.N.; Medeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;

F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.A.

Rodrigues, V.; Rosa, A.J.; de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Savasak-

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira-

M.; Teuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

A:Gene: XFO754

C:Superfamily: type IV secretory pathway, vir component

Query Match 49.4%; Score 44; DB 2; Length 237;  
Best Local Similarity 58.3%; Pred. No. 24;  
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 WLWMDRGALDV 15  
|||  
DB 151 WLWMDRGHTRDV 162



## RESULT 7

hypothetical protein PAB1063 - *Pyrococcus abyssi* (strain Orsay)  
B75010  
C:Species: *Pyrococcus abyssi*  
C>Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004  
C/Accession: B75010  
R:anonymous, Genoscope  
submitted to the EMBL Data Library, July 1999  
A:Description: *Pyrococcus abyssi* genome sequence: insights into archaeal chromosome stru  
A:Reference number: A75001  
A:Accession: B75010  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-409 <KAM>  
A:Cross-references: UNIPROT:Q9Y92; UNIPARC:UPI0000034560; GB:AJ248288; GB:AL056836; NID  
A:Experimental source: strain Orsay  
C:Genetics:  
A:Gene: PAB1063

## Query Match

49.4%; Score 44; DB 2; Length 409;  
Best Local Similarity 39.1%; Pred. No. 41;  
Matches 9; Conservative 2; Mismatches 2; Indels 10; Gaps 1;

QY 2 PDMLM-----GDRGALD 14

DB 354 PGWILWILILMGRVNGPCALD 376

## RESULT 8

3C3.21 protein - *Streptomyces coelicolor*  
T10930  
C:Species: *Streptomyces coelicolor*  
C>Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
C/Accession: T10930  
R:Faircliff, J.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, August 1998  
A:Reference number: Z17215  
A:Accession: T10930  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-491 <PAR>  
A:Cross-references: UNIPROT:O86654; UNIPARC:UPI00000DAD67; EMBL:AL031231; NID:e1315070;  
A:Experimental source: strain A3 (2)  
C:Genetics:  
A:Gene: 3C3.21

## Query Match

49.4%; Score 44; DB 2; Length 491;  
Best Local Similarity 61.5%; Pred. No. 49;  
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 DMLMGDRGALDV 15

DB 413 EFWLHGDRGALDL 425

## RESULT 9

probable ABC-type iron transport system protein Sma0525 [imported] - *Sinorhizobium meliloti*  
E95296  
C:Species: *Sinorhizobium meliloti*  
C>Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 09-Jul-2004  
C/Accession: E95296  
R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowe  
; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.  
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001  
A:Title: Nucleotide sequence and predicted functions of the entire *Sinorhizobium meliloti*  
A:Reference number: A95262; MUID:21396509; PMID:11481432  
A:Accession: E95296  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-601 <KIR>  
A:Cross-references: UNIPROT:Q930C1; UNIPARC:UPI00000C803E; GB:AE006469; PIDN:AAK64935.1;  
A:Experimental source: strain 1021, megaplasmid pSymA

R.Gallbert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,  
Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;  
L.; Hyman, R.W.; Jones, T.  
Science 293, 668-672, 2001

A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,  
habault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.  
A:Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.  
A:Reference number: A96039; MUID:21368234; PMID:11474104  
A:Contents: annotation  
C:Genetics:  
A:Gene: Sma0525

A:Genome: plasmid

## Query Match

49.4%; Score 44; DB 2; Length 601;  
Best Local Similarity 85.7%; Pred. No. 59;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PDMLMG 8

DB 169 PDMLMAG 175

## RESULT 10

phosphoribosylformylglycinamide synthase (EC 6.3.5.3) component II - *Synechococcus* sp  
S77614  
N:Alternate names: FGA synthetase  
C:Species: *Synechococcus* sp.  
A:Variety: PCC 7942  
C>Date: 29-Jul-1997 #sequence\_revision 24-Oct-1998 #text\_change 31-Dec-2004  
C/Accession: S77614; S77613  
R:Liu, Y.; Tsinoemas, N.F.  
submitted to the EMBL Data Library, August 1995  
A:Description: Unusual gene arrangement for the putative chromosome replication origin a  
A:Reference number: S77614  
A:Accession: S77614  
A:Molecule type: DNA  
A:Residues: 1-112 <LIV>  
A:Cross-references: UNIPROT:O55037; UNIPARC:UPI0000176276; EMBL:U3322; NID:g974613; PID  
A:Experimental source: PCC 7942  
R:Liu, Y.; Tsinoemas, N.F.; Golden, S.S.; Kondo, T.; Johnson, C.H.  
Mol. Microbiol. 20, 1071-1081, 1996  
A:Title: Circadian expression of genes involved in the purine biosynthetic pathway of *cy*  
A:Reference number: S77612; MUID:9640530; PMID:8809759  
A:Accession: S77613  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 113-321 <LIM>

A:Cross-references: UNIPARC:UPI00000BE4A4; EMBL:U33211  
A:Experimental source: PCC 7942  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1995  
C:Genetics:  
A:Gene: purL  
C:Function:  
A:Description: catalyzes the condensation of 5'-phosphoribosylformylglycinamide with ATP  
A:Pathway: purine nucleotide biosynthesis  
A:Note: fourth step in pathway  
C:Keywords: ligase; purine nucleotide biosynthesis

## Query Match

48.3%; Score 43; DB 2; Length 321;  
Best Local Similarity 63.6%; Pred. No. 46;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 PDMLMGDRGA 12

DB 240 PDMLFAEGGA 250

## RESULT 11

homolog to yeast orf yori66c. [imported] - fission yeast (*Schizosaccharomyces pombe*)  
T50422  
C:Species: *Schizosaccharomyces pombe*  
C>Date: 09-Jun-2000 #sequence\_revision 09-Jun-2000 #text\_change 09-Jul-2004  
C/Accession: T50422

R/Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.  
 Submitted to the EMBL Data Library, February 2000  
 A/Reference number: Z25039  
 A/Accession: T50422  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-462 <SBR>  
 A/Cross-references: UNIPROT:O9P7J1; UNIPARC:UPI000006AAB1; EMBL:AL157991, PIDN:CAE76224.  
 A/Experimental source: strain 972h(-); coamid c24B10  
 C/Genetics:  
 A/Gene: SPDB:SPCC24B10.15  
 A/Map position: 3

Query Match 48.3%; Score 43; DB 2; Length 462;  
 Best Local Similarity 55.6%; Pred. No. 65;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 DMLMGDRG 11  
 Db 394 EWMWABRG 402

## RESULT 12

JC5393  
 zinc finger protein Kf-1 precursor - mouse  
 C/Species: Mus musculus (house mouse)  
 C/Date: 04-Jun-1997 #sequence\_revision 18-Jul-1997 #text\_change 09-Jul-2004  
 C/Accession: JC5393  
 R/Yasojima, K.; Tsujimura, A.; Mizuno, T.; Shigeyoshi, Y.; Inazawa, J.; Kikuno, R.; Kuma  
 Biochem. Biophys. Res. Commun. 231, 481-487, 1997  
 A/Title: Cloning of human and mouse cDNAs encoding novel zinc finger proteins expressed  
 A/Reference number: JC5392; MUID:97223484; PMID:9070305  
 A/Accession: JC5393  
 A/Status: nucleic acid sequence not shown  
 A/Molecule type: mRNA  
 A/Residues: 1-683 <YAS>  
 A/Cross-references: UNIPROT:O08883; UNIPARC:UPI000008061; DBJ:D76445; NID:g2058262; PI  
 A/Experimental source: brain  
 C/Comment: This protein is involved in membranous protein-sorting apparatus similarly to

C/Genetics:  
 A/Gene: Kf-1  
 C/Superfamily: zinc finger protein Kf-1 precursor; RING finger homology  
 C/Keywords: glycoprotein; phosphoprotein; zinc  
 F.1-19/Domain: signal sequence #status predicted <SIG>  
 F.326-344/Domain: transmembrane #status predicted <TM1>  
 F.352-380/Domain: transmembrane #status predicted <TM2>  
 F.615-666/Domain: RING finger homology <RING>  
 F.100,155,228,273,301,398,536/Binding site: carbohydrate (Asn) (covalent) #status predic  
 F.664/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 48.3%; Score 43; DB 2; Length 683;  
 Best Local Similarity 85.7%; Pred. No. 95;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EPDWLW 7  
 Db 603 EPDWLW 609

## RESULT 13

JC5392  
 zinc finger protein Kf-1 precursor - human  
 C/Species: Homo sapiens (man)  
 C/Date: 04-Jun-1997 #sequence\_revision 18-Jul-1997 #text\_change 09-Jul-2004  
 C/Accession: JC5392  
 R/Yasojima, K.; Tsujimura, A.; Mizuno, T.; Shigeyoshi, Y.; Inazawa, J.; Kikuno, R.; Kuma

Biochem. Biophys. Res. Commun. 231, 481-487, 1997  
 A/Title: Cloning of human and mouse cDNAs encoding novel zinc finger proteins expressed  
 A/Reference number: JC5392; MUID:97223484; PMID:9070305  
 A/Accession: JC5392  
 A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA  
 A/Residues: 1-685 <YAS>  
 A/Cross-references: UNIPROT:O00237; UNIPARC:UPI0000073P2A; DBJ:D76444; NID:g1945614; PI  
 A/Experimental source: brain  
 C/Comment: This protein is involved in membranous protein-sorting apparatus similarly to  
 C/Genetics:  
 A/Gene: Kf-1  
 C/Superfamily: zinc finger protein Kf-1 precursor; RING finger homology  
 C/Keywords: zinc  
 F.1-19/Domain: signal sequence #status predicted <SIG>  
 F.326-344/Domain: transmembrane #status predicted <TM1>  
 F.352-380/Domain: transmembrane #status predicted <TM2>  
 F.617-668/Domain: RING finger homology <RING>

Query Match 48.3%; Score 43; DB 2; Length 685;  
 Best Local Similarity 85.7%; Pred. No. 95;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EPDWLW 7  
 Db 605 EPDWLW 611

## RESULT 14

A82593  
 hypothetical protein XF2169 [imported] - Xylella fastidiosa (strain 945C)  
 C/Species: Xylella fastidiosa  
 C/Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
 C/Accession: A82593  
 R/Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen  
 Nature 406, 151-157, 2000  
 A/Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
 A/Reference number: A82515; MUID:20365717; PMID:10910347  
 A/Note: for a complete list of authors see reference number A59328 below  
 A/Accession: A82593  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-698 <STM>  
 A/Cross-references: UNIPROT:O9PBH5; UNIPARC:UPI00000C2968; GB:AB004030; GB:AB003849; NID

A/Experimental source: strain 945C  
 R/Simpson, A.J.G.; Reimach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A  
 B/iones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carreir, H  
 as-Neto, E.; Docena, C.; El-Dorri, H.; Facinani, A.P.; Ferreira, A.J.S.  
 submitted to GenBank, June 2000

A/Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Frohm  
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitejima, J.P.; Kitzler, J.E.; Kutzmae, E.E.; Laigr  
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E  
 A/Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;  
 , F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A  
 Rodrigues, V.; Rosa, A.C.R.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Savasak  
 A/Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir  
 M.; Tsunako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z  
 A/Reference number: A59328  
 A/Contents: annotation  
 C/Genetics:

Query Match 48.3%; Score 43; DB 2; Length 698;  
 Best Local Similarity 63.6%; Pred. No. 97;  
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 DMLMGDRGAL 13  
 Db 554 DMLMGDRGSL 564

## RESULT 15

H83276  
 probable lipase PA2949 [imported] - Pseudomonas aeruginosa (strain PAO1)  
 C/Species: Pseudomonas aeruginosa  
 C/Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 12-Jul-2004  
 C/Accession: H83276  
 R/Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lapid, K.; Lim,  
 :; Lory, S.; Olson, M.V.  
 Nature 406, 959-964, 2000  
 A>Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho  
 A;Reference number: A82950; MUID:20437337; PMID:10984043  
 A;Accession: H83276  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-315 <STO>  
 A;Cross-references: UNIPROT:Q9KJG6; UNIPARC:UPI00000C4EC6; GB:AE004721; GB:AE004091; NID  
 A;Experimental source: strain PA01  
 C;Genetics:  
 A;Gene: PA2949  
 C;Superfamily: tropinesterase

Query Match 47.8%; Score 42.5; DB 2; Length 315;  
 Best Local Similarity 66.7%; Pred. No. 54;  
 Matches 10; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
 QY 2 PDLMLGDRG-ALDV 15  
 | ||||| ||  
 Db 249 PTLMLGDRDRVLDV 263

Search completed: December 4, 2005, 04:53:46  
 Job time : 33.25 secs

**This Page Blank (USP: )**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 4, 2005, 04:31:36 ; Search time 136.875 Seconds  
(without alignments)  
77.318 Million cell updates/sec

Title: US-10-632-706-197  
Perfect score: 89  
Sequence: 1 EPDMLMGDGRGALDV 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot 05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	56.2	441	2	Q5LQ90_SILPO
2	49	55.1	208	2	Q5YQ86_NOCFA
3	49	55.1	405	2	Q5N4J9_SYNP6
4	49	55.1	779	2	Q6H084_FREDDI
5	48	53.9	217	2	Q7V3U3_PROWM
6	48	53.9	252	2	Q8BJP9_SHEON
7	48	53.9	426	2	Q5SS50_CRINE
8	48	53.9	448	2	Q9S4Z3_SALEN
9	48	53.9	775	2	Q59SA1_CANAL
10	48	53.9	784	2	Q8GM13_STRCL
11	48	53.9	793	2	Q59S70_CANAL
12	48	53.9	804	2	Q8ZR90_SALTY
13	47.5	53.4	527	2	Q6ZDZ2_ORYSA
14	47	52.8	61	2	Q6UHZ8_HUMAN
15	47	52.8	364	2	Q7UG34_RHOBA
16	47	52.8	369	2	Q5KXN7_CRYNE
17	47	52.8	375	2	Q55ZB2_CRYNE
18	47	52.8	471	2	Q4TPV5_GSPHN
19	47	52.8	1517	2	Q5AIP9_BMENT
20	47	52.8	1547	2	Q9CIA0_ASFPU
21	47	52.8	1547	2	Q4WDD4_ASFPU
22	46	51.7	214	2	Q4JX96_CORJK
23	46	51.7	350	1	COBT_PBSRM
24	46	51.7	356	2	Q6C1B2_YARLI
25	46	51.7	373	2	Q58089_PYRO
26	46	51.7	396	2	Q70GK6_CHLRS
27	46	51.7	1562	2	Q9Y840_MYCGR
28	45.5	51.1	266	2	Q7D2M8_AGRFS
29	45.5	51.1	298	2	Q8U680_AGRFS
30	45	50.6	91	2	Q85AE3_GCARD
31	45	50.6	141	2	Q9NU66_HUMAN

32	45	50.6	203	2	Q6MWZ7_MYCTU	Q6MWZ7 mycobacteri
33	45	50.6	228	2	Q7TWZ8_MYCBO	Q7TWZ8 mycobacteri
34	45	50.6	203	2	Q7DSX2_MYCTU	Q7DSX2 mycobacteri
35	45	50.6	246	2	Q7U9T4_SYNPX	Q7U9T4 synchococc
36	45	50.6	370	2	Q8BJL2_PSEPK	Q8BJL2 pseudomonas
37	45	50.6	381	2	Q5P2Z9_AZOSE	Q5P2Z9 azococcus sp
38	45	50.6	450	2	Q5JDB4_PYRO	Q5JDB4 pseudomonas
39	45	50.6	505	2	Q5JRO6_SILPO	Q5JRO6 silicibacte
40	45	50.6	601	2	Q6EBL9_YERPS	Q6EBL9 yerstinia ps
41	45	50.6	601	2	Q8ZIG5_YERPE	Q8ZIG5 yerstinia pe
42	45	50.6	781	2	Q4HYZ0_GIBZB	Q4HYZ0 gibberella
43	45	50.6	892	2	Q4KIVA_PSEFS	Q4KIVA pseudomonas
44	45	50.6	907	2	Q4ZNE9_PSEFS	Q4ZNE9 pseudomonas
45	45	50.6	1326	2	Q6ATH6_ORYSA	Q6ATH6 oryza sativ

## ALIGNMENTS

```

RESULT 1
Q5LQ90_SILPO
ID Q5LQ90_SILPO PRELIMINARY; PRT; 441 AA.
AC Q5LQ90;
DT 01-FEB-2005 (TREMBLrel. 29, Created)
DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
DE TRAP dicarboxylate transporter, DctW subunit.
GN OrderedLocusNames=SP02605;
OS Silicibacter pomeroyi.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Silicibacter.
OX NCBI_TaxID=89184;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=DS-3 / ATCC 700808 / DSM 15171;
RX PubMed=15602564; DOI=10.1038/nature03170;
RA Moran M.A., Buchan A., Gonzalez J.M., Heidelberg J.F., Whitman W.B.,
RA Kiene R.P., Henriksen J.R., King G.W., Belas R., Fugua C.,
RA Brinkac L.M., Lewis S., Jollet S., Weaver B., Pal G., Bisen J.A.,
RA Rahe B., Sheldon W.M., Ye W., Miller T.R., Carlton J., Raske D.A.,
RA Paulsen I.T., Ren Q., Daugherty S.C., Deboy R.T., Dodson R.J.,
RA Durkin A.S., Madupu R., Nelson W.C., Sullivan S.A., Rosovitz M.J.,
RA Haft D.H., Selengut J., Ward N.;
RT "Genome sequence of Silicibacter pomeroyi reveals adaptations to the
RT marine environment."
RL Nature 432:910-913(2004).
DR EMBL; CP000031; AAV95851.1; -; Genomic_DNA.
DR InterPro; IPR010556; DctW.
DR InterPro; IPR000252; DctA.
DR Pfam; PF06808; DctW; 1.
DR Pfam; PF00597; DctA; 1.
KW Complete proteome.
SQ SEQUENCE 441 AA; 48056 MW; 8E59B0A462757858 CRC64;

Query Match      56.2%; Score 50; DB 2; Length 441;
Best Local Similarity 72.7%; Pred. No. 23;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 LMGDRGALDV 15
DB 38 LMGDRGALDV 48

RESULT 2
Q5YQ86_NOCFA
ID Q5YQ86_NOCFA PRELIMINARY; PRT; 208 AA.
AC Q5YQ86;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=nfa48030;
OS Nocardia farcinica.

```

```

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Nocardia; Nocardia.
OX NCBI_TaxID=37329;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RP STRAIN=IFM 10152;
RX PubMed=15466710; DOI=10.1073/pnas.0406410101;
RA Ishikawa J., Yamashita A., Mikami Y., Hoshino Y., Kurita H., Hotta K.,
RA Shiba T., Hattori M.;
RT "The complete genomic sequence of Nocardia farcinica IFM 10152."
RL Proc. Natl. Acad. Sci. U.S.A. 101:14925-14930(2004).
DR EMBL; AP006618; BAD59655.1; -; Genomic_DNA.
KM Complete proteome; Hypothetical protein.
SQ SEQUENCE 208 AA; 22565 MW; EBE3243D9E52094E CRC64;

Query Match 55.1%; Score 49; DB 2; Length 208;
Best Local Similarity 46.7%; Pred. No. 16;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPPWLMGDRGALDV 15
Db 111 DDDWYVLMNRDEIDV 125

RESULT 3
OSN4J9 SYN6 PRELIMINARY; PRT; 405 AA.
ID OSN4J9 SYN6 PRELIMINARY; PRT; 405 AA.
AC OSN4J9;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Sun protein.
GN Name=sun; OrderedLocustNames=syc0580 d;
OC Synecococcus sp. (strain PCC 6301) (Anacyetis nidulans).
OC Bacteria; Cyanobacteria; Chroococcales; Synecococcus.
OX NCBI_TaxID=269084;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RP STRAIN=PCC6301;
RA Sugita M.;
RT "Complete genome structure of the unicellular cyanobacterium Anacyetis
RT nidulans 6301 (Synecococcus sp. PCC6301).";
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP008231; BAD78770.1; -; Genomic_DNA.
DR GO; GO:0008649; F:RNA methyltransferase activity; IEA.
DR GO; GO:0006364; P:RNA processing; IEA.
DR InterPro; IPR004573; Fmu_mtrase.
DR InterPro; IPR001678; Fmu_NOL1/NOP2p.
DR InterPro; IPR006027; NusB_Ramb_TIM44.
DR InterPro; IPR006174; NusB_mtrase.
DR InterPro; IPR000051; SAM_Bind.
DR Pfam; PF01189; NOL1_NOP2_Fmu; 1.
DR Pfam; PF01029; NusB; 1.
DR ProDom; PD005242; NusB_region; 1.
DR TIGRFAMs; TIGR00563; rmb; 1.
KM Complete proteome.
SQ SEQUENCE 405 AA; 44708 MW; 89F6C51BB6590C4 CRC64;

Query Match 55.1%; Score 49; DB 2; Length 405;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 10; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 2 PDWMLMGDRGALD 14
Db 110 PDWMLVQMSDRGLD 124

RESULT 4
OSH084 FREDI PRELIMINARY; PRT; 779 AA.
ID OSH084 FREDI PRELIMINARY; PRT; 779 AA.
AC OSH084;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

```

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DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein (Fragment).
OS Fremyella diplosiphon (Calothrix PCC 7601).
OC Bacteria; Cyanobacteria; Nostocales; Microchaetaceae; Microchaete.
OX NCBI_TaxID=1197;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RP STRAIN=FDJ3;
RA Stowe-Evans E.L., Ford J., Kehoe D.M.;
RT "Genomic DNA Microarray Analysis: Identification of New Genes
RT Regulated by Light Color in the Cyanobacterium Fremyella
RT diplosiphon.";
RL J. Bacteriol. 186:4338-4349(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FDJ3;
RA Stowe-Evans E., Ford J., Kehoe D.M.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY548438; AAT41885.1; -; Genomic_DNA.
KM Hypothetical protein.
FT NON TER 779
SQ SEQUENCE 779 AA; 85897 MW; 67144DE68472F0AD CRC64;

Query Match 55.1%; Score 49; DB 2; Length 779;
Best Local Similarity 77.8%; Pred. No. 60;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPPWLMGCD 9
Db 422 EPPWLMGCD 430

RESULT 5
QV3J33 PROMM PRELIMINARY; PRT; 217 AA.
ID QV3J33 PROMM PRELIMINARY; PRT; 217 AA.
AC QV3J33;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein precursor.
GN OrderedLocustNames=PMT2247;
OC Prochlorococcus marinus (strain MIT 9313).
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococaceae;
OC Prochlorococcus.
OX NCBI_TaxID=74547;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RP MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;
RA Roca G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P.,
RA Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
RA Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M.,
RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
RA Webb E.A., Zinser E.R., Chisholm S.W.;
RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
RT niche differentiation.";
RL Nature 424:1042-1047(2003).
DR EMBL; BX572101; CA822421.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004605; F:phosphatidate cytidyltransferase activity; IEA.
DR GO; GO:0008654; F:phospholipid biosynthesis; IEA.
DR InterPro; IPR00374; PC_trans.
DR Pfam; PF01148; CTP_transf_1; 1.
KM Complete proteome; Hypothetical protein; Signal.
FT SIGNAL 21
FT SIGNAL 1
SQ SEQUENCE 217 AA; 23832 MW; 522AA449B4033FEC CRC64;

Query Match 53.9%; Score 48; DB 2; Length 217;
Best Local Similarity 50.0%; Pred. No. 24;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 PDWMLMGDRGAL 13
Db 139 PNMWLMGGRKSI 150

```

## RESULT 6

Q8EJF9 SHEON

ID Q8EJF9 SHEON PRELIMINARY; PRT; 262 AA.

AC Q8EJF9

DT 01-MAR-2003 (TREMBLrel. 23, Created)

DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)

DE Hypothetical protein S00508.

GN Ordered locus names=SO0508;

OS Shewanella oneidensis.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;

OC Shewanellaceae; Shewanella.

OX NCBI\_TaxId=70863;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=NR-1;

RX MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;

RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos B.J., Nelson W.C.,

RA Read T.D., Eisen J.A., Seshadri R., Ward N.L., Methe B.A.,

RA Clayton R.A., Meyer T., Tsapin A., Scott J., Beaman M.J.,

RA Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,

RA Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A.,

RA Lee K., Berry K.J., Lee C., Mueller J., Kouri H.W., Gill J.,

RA Venter J.C., Neilson K.H., Fraser C.M.;

RA "Genome sequence of the dissimilatory metal ion-reducing bacterium

RT Shewanella oneidensis."

RL Nat. Biotechnol. 20:1118-1123(2002).

DR EMBL; AF015498; AAN53589.1; -; Genomic\_DNA.

DR TIGR; SO0508; -.

KM Complete proteome.

SQ SEQUENCE 262 AA; 29556 MW; 5E5B6F4D52DC44C CRC64;

Query Match 53.9%; Score 48; DB 2; Length 262;

Best Local Similarity 61.5%; Pred. No. 29;

Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 PDMWLGDRGALD 14  
|||:|||||  
DB 58 PDMWLGDRGALD 70

## RESULT 7

Q5SS50 CRYNE

ID Q5SS50 CRYNE PRELIMINARY; PRT; 426 AA.

AC Q5SS50

DT 13-SEP-2005 (TREMBLrel. 31, Created)

DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)

DE Hypothetical protein.

GN ORFNames=CNBE1140;

OS Cryococcus neoformans var. neoformans B-3501A.

OC Eukaryota; Fungi; Basidiomycota; Hymenycetes; Heterobasidiomycetes;

OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.

OX NCBI\_TaxId=283643;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=B-3501A;

RX Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,

RA Wicks B.L., Fu J., Davis R.W.;

RA "Cryptococcus neoformans serotype D sequencing."

RT Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.

CC -1- CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

CC preliminary data.

CC EMBL; AAEY0100024; EAL20751.1; -; Genomic\_DNA.

KM Hypothetical protein.

SQ SEQUENCE 426 AA; 47024 MW; A0FBD1F268A28310 CRC64;

Query Match 53.9%; Score 48; DB 2; Length 426;

Best Local Similarity 53.3%; Pred. No. 47;

Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 EPDWLMDRGALDV 15  
|||:|||||  
DB 328 KPDVWVGQRGALDV 342

## RESULT 8

Q9S4Z3 SALEN

ID Q9S4Z3 SALEN PRELIMINARY; PRT; 448 AA.

AC Q9S4Z3

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DE Hypothetical protein (Fragment).

DE Salmonella enteritidis.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Salmonella.

OX NCBI\_TaxId=592;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=S1400;

RX MEDLINE=99377131; PubMed=10447888;

RA Pattery T., Hernalsteens J.-P., De Greve H.;

RT "Identification and molecular characterization of a novel Salmonella

RT enteritidis pathogenicity islet encoding an ABC transporter."

RL Mol. Microbiol. 33:791-805(1999).

DR EMBL; AF102556; AAD51877.1; -; Genomic\_DNA.

DR GO; GO:0016020; C:membrane; IEA.

DR InterPro; IPR003838; DUF214.

DR Pfam; PF02687; PfsX; 1.

KM Hypothetical protein.

FT NON TER 1

SQ SEQUENCE 448 AA; 49706 MW; 389077E50235C42A CRC64;

Query Match 53.9%; Score 48; DB 2; Length 448;

Best Local Similarity 87.5%; Pred. No. 49;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EPDWLMD 8  
|||:|||||  
DB 408 EPDWLMD 415

## RESULT 9

Q59SA1 CANAL

ID Q59SA1 CANAL PRELIMINARY; PRT; 775 AA.

AC Q59SA1

DT 10-MAY-2005 (TREMBLrel. 30, Created)

DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)

DE Hypothetical protein.

GN ORFNames=CaO19.10974;

OS Candida albicans SC5314.

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetidae; mltosporic Saccharomycetales; Candida.

OX NCBI\_TaxId=237561;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=SC5314;

RX PubMed=15133810; DOI=10.1073/pnas.0401648101;

RA Jones T., Federspiel N.A., Chidana H., Dungan J., Kalman S.,

RA Magee B.B., Newport G., Thorstensen Y.R., Agabian N., Magee P.T.,

RA Davis R.W., Scherer S.;

RT "The diploid genome sequence of Candida albicans."

RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=SC5314;

RA Dungan J., Kuo A., Newport G., Ian C.-Y., Iijima C., Adegoke O.,

RA Roberts J., Peterson K., Donnelly S., Favoreto S., Tzung K.-W.,

RA Jones T., Scherer S., Agabian N.;

RT "Annotation of the Genome of *Candida albicans*.";  
 RL Submitted (Apr-2004) to the EMBL/Genbank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is  
 preliminary data.  
 CC EMBL; AAC00100154; EAK93359.1; -; Genomic DNA.  
 DR Hypothetical protein.  
 KW Hypothetical protein.  
 SQ SEQUENCE 775 AA; 88474 MW; 685118C6B2C914A8 CRC64;

Query Match 53.9%; Score 48; DB 2; Length 775;  
 Best Local Similarity 54.5%; Pred. No. 86;  
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 PDWLMGDRGA 12  
 DB 718 PEMAVMGSGCA 728

RESULT 10  
 Q8GM13 STRGL PRELIMINARY; PRT; 784 AA.

AC Q8GM13-  
 DT 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)  
 DE UvrA-like drug resistance pump.  
 OS Streptomyces globisporus.  
 CC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomycetaceae; Streptomycetaceae; Streptomycetes;  
 NCBI\_TaxId=1908;  
 RN NUCLEOTIDE SEQUENCE.

RP STRAIN=C-1027;  
 RC MEDLINE=22171413; PubMed=12183628; DOI=10.1126/science.1072110;  
 RA Liu W., Christensen S.D., Standage S., Shen B.,  
 RT "Biosynthesis of the enediyne antitumor antibiotic C-1027."  
 RL Science 297:1170-1173(2002).  
 CC -!- SIMILARITY: Belongs to the ABC transporter family.  
 DR EMBL; AY048670; AAL0654.1; -; Genomic DNA.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0016887; F:ATPase activity; IEA.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR003439; ABC transp\_like.  
 DR Pfam; PF00005; ABC trans\_2.

DR PROSITE; PS00211; ABC\_TRANSPORTER\_1; 1.  
 DR PROSITE; PS50893; ABC\_TRANSPORTER\_2; 2.  
 KW ATP-binding; Membrane; Nucleotide-binding; Transport.  
 SQ SEQUENCE 784 AA; 83960 MW; DABC2D965720A5E7 CRC64;

Query Match 53.9%; Score 48; DB 2; Length 784;  
 Best Local Similarity 53.8%; Pred. No. 87;  
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 PDWLMGDRGALD 14  
 DB 204 PDMQIMAKSGRLD 216

RESULT 11  
 Q59S70 CANAL PRELIMINARY; PRT; 793 AA.  
 AC Q59S70-  
 DT 10-MAY-2005 (TREMBlrel. 30, Created)  
 DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)  
 DE Hypothetical protein.  
 GN ORFNames=Ca019.3470;  
 OS *Candida albicans* SC5314.  
 CC Bacteria; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.  
 NCBI\_TaxId=237561;

RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=SC5314;  
 RX PubMed=15123810; DOI=10.1073/pnas.0401648101;  
 RA Jones T., Federle N.A., Chidana H., Dungan J., Kalman S.,  
 RA Magee B.B., Newport G., Thorstensen Y.R., Agabian N., Magee P.T.,  
 RA Davis R.W., Scherer S.  
 RT "The diploid genome sequence of *Candida albicans*."  
 RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).  
 RN [2]

RP NUCLEOTIDE SEQUENCE.

RC Dungan J., Kuo A., Newport G., Ian C.-Y., Iijima C., Adegoja O.,  
 RA Roberts J., Persson K., Donnelly S., Favoreto S., Tzung K.-W.,  
 RA Jones T., Scherer S., Agabian N.,  
 RT "Annotation of the Genome of *Candida albicans*."  
 RL Submitted (Apr-2004) to the EMBL/Genbank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is  
 preliminary data.  
 CC EMBL; AAC00100155; EAK93328.1; -; Genomic DNA.  
 DR Hypothetical protein.  
 KW SEQUENCE 793 AA; 90808 MW; 870A0A0508ADFB27 CRC64;

Query Match 53.9%; Score 48; DB 2; Length 793;  
 Best Local Similarity 54.5%; Pred. No. 88;  
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 PDWLMGDRGA 12  
 DB 735 PEMAVMGSGCA 745

RESULT 12  
 Q8ZR90 SALTY PRELIMINARY; PRT; 804 AA.

AC Q8ZR90-  
 DT 01-MAR-2002 (TREMBlrel. 20, Created)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Putative inner membrane protein.  
 GN Name=ybbp; OrderedLocustNames=STW0508;  
 OS *Salmonella typhimurium*.  
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; *Salmonella*.  
 NCBI\_TaxId=602;

RN NUCLEOTIDE SEQUENCE.

RP STRAIN=LT2;  
 RC MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;  
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,  
 RA Courtney L., Porrolik S., Ail J., Dante M., Du F., Hou S., Layman D.,  
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,  
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,  
 RA Waterston R., Wilson R.K.;  
 RT "Complete genome sequence of *Salmonella enterica* serovar Typhimurium  
 LT2."  
 RL Nature 413:852-856(2001).  
 DR EMBL; AE008719; AAL19462.1; -; Genomic DNA.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR InterPro; IPR003838; DUF214.  
 DR Pfam; PF02687; Ptex; 2.  
 KW Complete proteome.

SQ SEQUENCE 804 AA; 88772 MW; 72A29069A7021F11 CRC64;

Query Match 53.9%; Score 48; DB 2; Length 804;  
 Best Local Similarity 87.5%; Pred. No. 89;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EPDWLMG 8  
 DB 764 EPDWRLMG 771



RESULT 13  
Q6ZDZ2\_ORYSA PRELIMINARY; PRT; 527 AA.  
AC Q6ZDZ2;  
DT 05-JUL-2004 (TReMBLrel. 27, Created)  
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
DE Hypothetical protein P0507H12.22.  
GN Name=P0507H12.22;  
OS Oryza sativa (japonica cultivar-group). Embryophyta; Tracheophyta;  
OC Eukaryota; Viridiplantae; Streptophyta; Liliopsida; Poales; Poaceae;  
OC Euphorbiaceae; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Euphorbiaceae; Oryzae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Sasaki T., Matsumoto T., Yamamoto K.;  
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, PAC  
clone: P0507H12.22";  
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AP004338; BAC83511.1; -; Genomic\_DNA.  
DR Gramene; Q6ZDZ2; -;  
DR GO; GO:0004519; F:endonuclease activity; IEA.  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
DR GO; GO:0006281; F:DNA repair; IEA.  
DR InterPro; IPR004843; M-Pesterase.  
DR Pfam; PF00149; Metallophos; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 527 AA; 61478 MW; 265FE1451BC92BE6 CRC64;

Query Match 53.4%; Score 47.5; DB 2; Length 527;  
Best Local Similarity 50.0%; Pred. No. 70;  
Matches 9; Conservative 3; Mismatches 3; Indels 3; Gaps 1;  
QY 1 EPDMLL--WSDRGALDV 15  
DB 86 EPNWLDWYMGDKTGTNV 103

RESULT 14  
Q6JH28\_HUMAN PRELIMINARY; PRT; 61 AA.  
AC Q6JH28;  
DT 05-JUL-2004 (TReMBLrel. 27, Created)  
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
DE HCV-E2 binding protein 1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Zhang J., Cheng J., Wang L., Shao Q., Lu Y., Chen T., Hong Y.;  
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY459290; AAR23235.1; -; mRNA.  
SQ SEQUENCE 61 AA; 6607 MW; 4E162AA3444E7A56 CRC64;

Query Match 52.8%; Score 47; DB 2; Length 61;  
Best Local Similarity 87.5%; Pred. No. 9.3;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 WLLMGDRG 11  
DB 46 WLLMGSRG 53

RESULT 15  
Q7UG34\_RHOBA PRELIMINARY; PRT; 364 AA.  
AC Q7UG34;

DT 01-OCT-2003 (TReMBLrel. 25, Created)  
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
GN OrderedLocustNames=R38157;  
OS Rhodospirillum rubrum.  
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;  
OC Planctomycetaceae; Pirellula.  
OX NCBI\_TaxID=117;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=1;  
RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;  
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,  
RA Ludwig W., Gade D., Beck A., Borzym K., Heilmann K., Rabus R.,  
RA Schlesner H., Amann R., Reinhardt R.;  
RT "Complete genome sequence of the marine planctomycete Pirellula sp.  
strain 1.";  
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).  
DR EMBL; BX294147; CAD78495.1; -; Genomic\_DNA.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 364 AA; 40878 MW; 2284324F0722E6AB CRC64;

Query Match 52.8%; Score 47; DB 2; Length 364;  
Best Local Similarity 58.3%; Pred. No. 57;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 3 DWLLMGDRGALD 14  
DB 162 DWLLMGDRGALD 173

Search completed: December 4, 2005, 04:52:25  
Job time : 139.875 secs

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## OM protein - protein search, using sw model

Run on: December 4, 2005, 03:59:51 ; Search time 32.1875 Seconds  
(without alignments)  
38.528 Million cell updates/sec

Title: US-10-632-706-197

Perfect score: 89  
Sequence: 1 EPPDWLMGDRGALDV 15Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Parents AA:\*

- 1: /cgn2\_6/prodata/1/aa/5.COMB.pep:\*
- 2: /cgn2\_6/prodata/1/aa/6.COMB.pep:\*
- 3: /cgn2\_6/prodata/1/aa/H.COMB.pep:\*
- 4: /cgn2\_6/prodata/1/aa/PCTUS.COMB.pep:\*
- 5: /cgn2\_6/prodata/1/aa/RE.COMB.pep:\*
- 6: /cgn2\_6/prodata/1/aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	48	53.9	229	2	US-09-489-039A-12532	Sequence 12532, A
2	45	50.6	614	2	US-09-543-681A-7066	Sequence 7066, Ap
3	44	49.4	80	2	US-09-248-796A-22630	Sequence 22630, A
4	43	48.3	345	2	US-09-303-518D-194	Sequence 194, App
5	43	48.3	383	2	US-09-303-518D-196	Sequence 196, App
6	43	48.3	638	2	US-09-949-016-9984	Sequence 9984, Ap
7	43	48.3	732	2	US-09-902-540-13627	Sequence 13627, A
8	42.5	47.8	320	2	US-09-252-991A-18301	Sequence 18301, A
9	42	47.2	174	2	US-09-854-133-426	Sequence 426, App
10	42	47.2	388	1	US-08-290-448A-80	Sequence 80, App1
11	42	47.2	388	1	US-08-290-448A-80	Sequence 80, App1
12	42	47.2	388	1	US-08-175-069A-80	Sequence 80, App1
13	42	47.2	388	2	US-08-461-939B-80	Sequence 80, App1
14	42	47.2	388	2	US-08-464-000-80	Sequence 80, App1
15	42	47.2	493	2	US-09-489-039A-12903	Sequence 12903, A
16	41	46.1	588	4	PCT-US95-13749-4	Sequence 4, App1
17	41	46.1	884	2	US-09-543-681A-7786	Sequence 7786, Ap
18	41	46.1	884	2	US-09-248-796A-20574	Sequence 20574, A
19	40.5	45.5	488	2	US-08-311-731A-29	Sequence 29, App1
20	40	44.9	392	2	US-08-252-991A-27798	Sequence 27798, A
21	40	44.9	497	2	US-09-489-039A-12027	Sequence 12027, A
22	40	44.9	576	2	US-09-367-206-1	Sequence 1, App1
23	40	44.9	576	2	US-09-367-206-21	Sequence 21, App1
24	40	44.9	576	2	US-09-367-206-22	Sequence 22, App1
25	40	44.9	576	2	US-09-367-206-23	Sequence 23, App1
26	40	44.9	576	2	US-09-298-404-1	Sequence 1, App1
27	40	44.9	576	2	US-09-298-404-21	Sequence 21, App1

28	40	44.9	576	2	US-09-298-404-22	Sequence 22, App1
29	40	44.9	576	2	US-09-298-404-23	Sequence 23, App1
30	40	44.9	776	2	US-09-165-396-3	Sequence 3, App1
31	39	43.8	13	1	US-08-321-625-44	Sequence 44, App1
32	39	43.8	13	2	US-09-181-083-44	Sequence 44, App1
33	39	43.8	13	2	US-09-750-754-44	Sequence 44, App1
34	39	43.8	93	2	US-09-072-596-272	Sequence 272, App
35	39	43.8	93	2	US-09-072-596-277	Sequence 277, App
36	39	43.8	93	2	US-10-193-002-272	Sequence 272, App
37	39	43.8	93	2	US-10-084-843-277	Sequence 277, App
38	39	43.8	141	2	US-09-902-540-14417	Sequence 14417, A
39	39	43.8	170	2	US-09-270-767-45277	Sequence 45277, A
40	39	43.8	194	2	US-09-489-039A-7558	Sequence 7558, Ap
41	39	43.8	226	2	US-09-004-731-8	Sequence 8, App1
42	39	43.8	226	2	US-08-749-699-8	Sequence 8, App1
43	39	43.8	226	2	US-09-004-729-8	Sequence 8, App1
44	39	43.8	258	2	US-09-134-000C-5594	Sequence 5594, Ap
45	39	43.8	286	2	US-09-248-796A-23020	Sequence 23020, A

## ALIGNMENTS

```
RESULT 1
US-09-489-039A-12532
; Sequence 12532, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12532
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12532

Query Match      53.9%; Score 48; DB 2; Length 229;
Best Local Similarity 57.1%; Pred. No. 7.8;
Matches      8; Conservative      1; Mismatches      5; Indels      0; Gaps      0;

QY      1 EPPDWLMGDRGALD 14
Db      32 ERSWCKMGDRFAID 45

RESULT 2
US-09-543-681A-7066
; Sequence 7066, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7066
; LENGTH: 614
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7066

Query Match      50.6%; Score 45; DB 2; Length 614;
```

Best Local Similarity 64.3%; Pred. No. 66;  
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EPDMLMGDRGALD 14  
DB 452 EDGWLRTGDAGALD 465

## RESULT 3

US-09-248-796A-22630  
; Sequence 22630, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 22630  
; LENGTH: 80  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-09-248-796A-22630

Query Match 49.4%; Score 44; DB 2; Length 80;  
Best Local Similarity 54.5%; Pred. No. 10;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 PDWLMGDRGA 12  
DB 12 PDWAVGSGQMA 22

## RESULT 4

US-09-303-518D-194  
; Sequence 194, Application US/09303518D  
; Patent No. 6914131  
; GENERAL INFORMATION:  
; APPLICANT: Scariato, Vincenzo  
; APPLICANT: Maignani, Vega  
; APPLICANT: Rappuoli, Rino  
; APPLICANT: Pizza, Mariagrazia  
; APPLICANT: Grandi, Guido  
; TITLE OF INVENTION: Neisserial Antigens  
; FILE REFERENCE: CHIR0160  
; CURRENT APPLICATION NUMBER: US/09/303,518D  
; CURRENT FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 1098  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 194  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-09-303-518D-194

Query Match 48.3%; Score 43; DB 2; Length 345;  
Best Local Similarity 70.0%; Pred. No. 72;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PDWLMGDRG 11  
DB 183 PEMLFGYRG 192

## RESULT 5

US-09-303-518D-196  
; Sequence 196, Application US/09303518D

; Patent No. 6914131  
; GENERAL INFORMATION:  
; APPLICANT: Scariato, Vincenzo  
; APPLICANT: Maignani, Vega  
; APPLICANT: Rappuoli, Rino  
; APPLICANT: Pizza, Mariagrazia  
; APPLICANT: Grandi, Guido  
; TITLE OF INVENTION: Neisserial Antigens  
; FILE REFERENCE: CHIR0160  
; CURRENT APPLICATION NUMBER: US/09/303,518D  
; CURRENT FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 1098  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 196  
; LENGTH: 383  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-303-518D-196

Query Match 48.3%; Score 43; DB 2; Length 383;  
Best Local Similarity 70.0%; Pred. No. 81;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PDWLMGDRG 11  
DB 181 PEMLFGYRG 190

## RESULT 6

US-09-949-016-9984  
; Sequence 9984, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: fastSeq for Windows Version 4.0  
; SEQ ID NO 9984  
; LENGTH: 638  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-9984

Query Match 48.3%; Score 43; DB 2; Length 638;  
Best Local Similarity 85.7%; Pred. No. 1.4e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EPDMLM 7  
DB 558 EPDWLTM 564

## RESULT 7

US-09-902-540-13627  
; Sequence 13627, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540  
CURRENT FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: 60/217,883  
PRIOR FILING DATE: 2000-07-10  
NUMBER OF SEQ ID NOS: 16825  
SEQ ID NO 13627  
LENGTH: 732  
TYPE: PRT  
ORGANISM: Myxococcus xanthus  
US-09-902-540-13627

Query Match 48.3%; Score 43; DB 2; Length 732;  
Best Local Similarity 63.6%; Pred. No. 1.6e+02;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 WLLMGDRGALD 14  
| | | | |  
| | | | |  
Db 126 WLLMGTRRAAE 136

RESULT 8  
US-09-252-991A-18301  
Sequence 18301, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 18301  
LENGTH: 320  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-18301

Query Match 47.8%; Score 42.5; DB 2; Length 320;  
Best Local Similarity 66.7%; Pred. No. 79;  
Matches 10; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 2 PDLWLGDRG-ALDV 15  
| | | | |  
| | | | |  
Db 254 PTLWLGDRDRVLDV 268

RESULT 9  
US-09-854-133-426  
Sequence 426, Application US/09854133  
Patent No. 6759308  
GENERAL INFORMATION:  
APPLICANT: Lodes, Michael J.  
APPLICANT: Mohamath, Raodoh  
APPLICANT: Henderson, Robert A.  
APPLICANT: Benson, Darin R.  
APPLICANT: Secrist, Heather  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR  
FILE REFERENCE: 210121.475C10  
CURRENT APPLICATION NUMBER: US/09/854,133  
CURRENT FILING DATE: 2001-05-11  
NUMBER OF SEQ ID NOS: 735  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 426  
LENGTH: 174  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-854-133-426

Query Match 47.2%; Score 42; DB 2; Length 174;  
Best Local Similarity 70.0%; Pred. No. 49;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EPDWLWMDR 10  
| | | | |  
| | | | |  
Db 124 DPGLWMDR 133

RESULT 10  
US-08-290-448A-80  
Sequence 80, Application US/08290448A  
Patent No. 5676954  
GENERAL INFORMATION:  
APPLICANT: Rogers, Bruce  
APPLICANT: Klapper, David G.  
APPLICANT: Rafnar, Thorunn  
APPLICANT: Kuo, Mei-chang  
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses  
NUMBER OF SEQUENCES: 93  
CORRESPONDENCE ADDRESS:  
ADDRESS: LAHIVE & COCKFIELD  
STREET: 60 State Street, suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/290,448A  
FILING DATE: August 15, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/529,951  
FILING DATE: May 29, 1990  
APPLICATION NUMBER: US 07/325,365  
FILING DATE: March 17, 1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Amy E. Mandragouras  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: IMI-018CN  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 80:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 388 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-290-448A-80

Query Match 47.2%; Score 42; DB 1; Length 388;  
Best Local Similarity 46.7%; Pred. No. 1.2e+02;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 EPDWLWMDR-ALDV 15  
| | | | |  
| | | | |  
Db 323 EPDMWTMWRDNDV 337

RESULT 11  
US-08-290-448A-80  
Sequence 80, Application US/08290448A  
Patent No. 5698204  
GENERAL INFORMATION:  
APPLICANT: Rogers, Bruce  
APPLICANT: Klapper, David G.  
APPLICANT: Rafnar, Thorunn

APPLICANT: Kuo, Mei-chang  
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses  
NUMBER OF SEQUENCES: 93  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/290,448A  
FILING DATE: August 15, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/529,951  
FILING DATE: May 29, 1990  
APPLICATION NUMBER: US 07/325,365  
FILING DATE: March 17, 1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Amy E. Mandragouras  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: IMI-018CN  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 80:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 388 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-290-448A-80

Query Match 47.2%; Score 42; DB 1; Length 388;  
Best Local Similarity 46.7%; Pred. No. 1.2e+02;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 EPDWLMDRGALDV 15  
||:|:|  
Db 323 EPEWMTNMRQNDV 337

RESULT 12  
US-08-175-069A-80  
Sequence 80, Application US/08175069A  
Patent No. 5776761  
GENERAL INFORMATION:  
APPLICANT: Rogers, Bruce  
APPLICANT: Klapper, David G.  
APPLICANT: Rafnar, Thorunn  
APPLICANT: Kuo, Mei-chang  
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses  
NUMBER OF SEQUENCES: 93  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/175,069A  
FILING DATE: December 29, 1993

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/529,951  
FILING DATE: May 29, 1990  
APPLICATION NUMBER: US 07/325,365  
FILING DATE: March 17, 1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Amy E. Mandragouras  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: IMI-018DV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 80:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 388 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-175-069A-80

Query Match 47.2%; Score 42; DB 1; Length 388;  
Best Local Similarity 46.7%; Pred. No. 1.2e+02;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 EPDWLMDRGALDV 15  
||:|:|  
Db 323 EPEWMTNMRQNDV 337

RESULT 13  
US-08-461-939B-80  
Sequence 80, Application US/08461939B  
Patent No. 6335019  
GENERAL INFORMATION:  
APPLICANT: Rogers, Bruce  
APPLICANT: Klapper, David G.  
APPLICANT: Rafnar, Thorunn  
APPLICANT: Kuo, Mei-chang  
TITLE OF INVENTION: Methods For Treating Sensitivity To A  
NUMBER OF SEQUENCES: 93  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,939B  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/464,000  
FILING DATE: 05-JUN-1995  
APPLICATION NUMBER: US 08/290,448  
FILING DATE: 15-AUG-1994  
APPLICATION NUMBER: US 07/529,951  
FILING DATE: 29-MAY-1990  
APPLICATION NUMBER: US 07/325,365  
FILING DATE: 17-MAR-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Amy E. Mandragouras  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: IMI-018CNDV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 80:

SEQUENCE CHARACTERISTICS:  
LENGTH: 388 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-461-939B-80

Query Match 47.2%; Score 42; DB 2; Length 388;  
Best Local Similarity 46.7%; Pred. No. 1.2e+02;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 EPDMLMGDRGALDV 15  
Db 323 EPEWMTWNRONDV 337

## RESULT 14

US-08-464-000-80  
Sequence 80, Application US/08464000  
Patent No. 6335020  
GENERAL INFORMATION:  
APPLICANT: Rogers, Bruce  
APPLICANT: Klapper, David G.  
APPLICANT: Rafnar, Thorunn  
APPLICANT: Kuo, Mei-chang  
TITLE OF INVENTION: Allergenic Peptides from Ragweed Pollen  
NUMBER OF SEQUENCES: 93  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/464,000  
FILING DATE: 05-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/290,448  
FILING DATE: 15-AUG-1994  
APPLICATION NUMBER: US 07/529,951  
FILING DATE: 29-MAY-1990  
APPLICATION NUMBER: US 07/325,365  
FILING DATE: 17-MAR-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Amy E. Mandragouras  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: IMI-018CN2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 80:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 388 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-464-000-80

Query Match 47.2%; Score 42; DB 2; Length 388;  
Best Local Similarity 46.7%; Pred. No. 1.2e+02;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 EPDMLMGDRGALDV 15  
Db 323 EPEWMTWNRONDV 337

RESULT 15  
US-09-489-039A-12903  
Sequence 12903, Application US/09489039A  
Patent No. 6610836  
GENERAL INFORMATION:  
APPLICANT: Gary Breton et. al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
FILE REFERENCE: 2709,2004001  
CURRENT FILING DATE: 2000-01-27  
CURRENT APPLICATION NUMBER: US/09/489,039A  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 14342  
SEQ ID NO 12903  
LENGTH: 493  
TYPE: PRN  
ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-12903

Query Match 47.2%; Score 42; DB 2; Length 493;  
Best Local Similarity 60.0%; Pred. No. 1.5e+02;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 WLLMGDRGAL 13  
Db 463 WLLMCGRGM 472

Search completed: December 4, 2005, 04:09:44  
Job time : 33.1875 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:07:28 / Search time 107.5 Seconds  
(without alignments)  
58.302 Million cell updates/sec

Title: US-10-632-706-197

Perfect score: 89  
Sequence: 1 EPPDWLMGDRGALDV 15

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Published Applications\_AA\_Main:\*  
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2: /cgn2\_6/prodata/1/pubppaa/US08\_PUBCOMB.pep.\*  
3: /cgn2\_6/prodata/1/pubppaa/US09\_PUBCOMB.pep.\*  
4: /cgn2\_6/prodata/1/pubppaa/US10\_PUBCOMB.pep.\*  
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6: /cgn2\_6/prodata/1/pubppaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	89	100.0	15	US-10-632-706-129	Sequence 129, App
2	89	100.0	15	US-10-632-706-130	Sequence 130, App
3	89	100.0	15	US-10-632-706-131	Sequence 131, App
4	89	100.0	15	US-10-632-706-194	Sequence 194, App
5	89	100.0	15	US-10-632-706-197	Sequence 197, App
6	89	100.0	15	US-10-632-706-200	Sequence 200, App
7	75	84.3	15	US-10-632-706-203	Sequence 203, App
8	51	57.3	334	US-10-450-763-50690	Sequence 50690, A
9	48	53.9	201	US-10-634-548-27	Sequence 27, Appl
10	48	53.9	775	US-10-159-257A-160	Sequence 160, App
11	47.5	53.4	992	US-10-437-963-134365	Sequence 134365, A
12	47	52.8	455	US-10-450-763-52883	Sequence 52883, A
13	47	52.8	904	US-10-369-493-12420	Sequence 12420, A
14	45	50.6	159	US-10-425-115-240160	Sequence 240160, A
15	45	50.6	372	US-10-282-122A-68332	Sequence 68332, A
16	44.5	50.0	203	US-10-767-701-42189	Sequence 42189, A
17	44.5	50.0	394	US-10-425-115-243524	Sequence 243524, A
18	44	49.4	472	US-10-117-161-1674	Sequence 1674, Ap
19	44	49.4	472	US-10-392-798-11334	Sequence 11334, Ap
20	44	49.4	505	US-10-437-963-178634	Sequence 178634, A
21	44	49.4	687	US-10-369-493-20876	Sequence 20876, A
22	43.5	48.9	77	US-10-425-115-263892	Sequence 263892, A
23	43	48.3	264	US-10-156-761-11420	Sequence 11420, A
24	43	48.3	368	US-10-437-963-115853	Sequence 115853, A
25	43	48.3	439	US-10-156-761-13497	Sequence 13497, A
26	43	48.3	616	US-10-808-522-8	Sequence 8, Appl
27	43	48.3	1975	US-10-437-963-140079	Sequence 140079, A

28	42.5	47.8	315	4	US-10-282-122A-43588	Sequence 43588, A
29	42	47.2	77	3	US-09-764-847-922	Sequence 922, App
30	42	47.2	77	4	US-10-092-154-922	Sequence 922, App
31	42	47.2	116	4	US-10-424-599-206981	Sequence 206981, A
32	42	47.2	131	3	US-09-864-408A-4566	Sequence 4566, Ap
33	42	47.2	154	4	US-10-312-354-26	Sequence 26, Appl
34	42	47.2	174	3	US-09-738-973-426	Sequence 426, App
35	42	47.2	174	3	US-09-854-133-426	Sequence 426, App
36	42	47.2	174	3	US-10-144-649A-426	Sequence 426, App
37	42	47.2	175	5	US-10-450-763-31629	Sequence 31629, A
38	42	47.2	198	4	US-10-767-701-34131	Sequence 34131, A
39	42	47.2	211	5	US-10-450-763-37978	Sequence 37978, A
40	42	47.2	245	4	US-10-437-963-108592	Sequence 108592, A
41	42	47.2	275	4	US-10-425-114-66625	Sequence 66625, A
42	42	47.2	363	4	US-10-282-122A-50322	Sequence 50322, A
43	42	47.2	380	4	US-10-369-493-20944	Sequence 20944, A
44	42	47.2	397	3	US-09-847-208-17	Sequence 17, Appl
45	42	47.2	397	5	US-10-809-689-97	Sequence 97, Appl

## ALIGNMENTS

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RESULT 1
US-10-632-706-129
; Sequence 129, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: AMERSDORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US/10/632,706
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 129
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-129
Query Match 100.0%; Score 89; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 EPPDWLMGDRGALDV 15
DB 1 EPPDWLMGDRGALDV 15
RESULT 2
US-10-632-706-130
; Sequence 130, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: AMERSDORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US/10/632,706
; PRIOR FILING DATE: 2002-08-01
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 129
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-130
Query Match 100.0%; Score 89; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 EPPDWLMGDRGALDV 15
DB 1 EPPDWLMGDRGALDV 15

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? PRIOR FILING DATE: 1998-08-31
? NUMBER OF SEQ ID NOS: 278
? SOFTWARE: PatentIn version 3.2
? SEQ ID NO: 130
? LENGTH: 15
? TYPE: PRT
? ORGANISM: Artificial
? FEATURE:
? OTHER INFORMATION: single chain antibody fragments
US-10-632-706-130

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Query Match	100.0%;	Score 89;	DB 4;	Length 15;
Best Local Similarity	100.0%;	Pred. No. 2.8e-06;		
Matches 15;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy		1	EPDWLLWGDRGALDV	15
Db		1	EPDWLLWGDRGALDV	15

```

: RESULT 3
: US-10-632-706-131
: Sequence 131, Application US/10632706
: Publication No. US20040175385A1
: GENERAL INFORMATION:
: APPLICANT: MARKS, JAMES D.
: APPLICANT: AMERSDORFER, PETER
: TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
: TITLE OF INVENTION: NEUROTOXINS
: FILE REFERENCE: 407T-895120US
: CURRENT APPLICATION NUMBER: US/10/632,706
: CURRENT FILING DATE: 2003-08-01
: PRIOR APPLICATION NUMBER: US 60/400,721
: PRIOR FILING DATE: 2002-08-01
: PRIOR APPLICATION NUMBER: US 09/144,806
: PRIOR FILING DATE: 1998-08-31
: NUMBER OF SEQ ID NOS: 278
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 131
: LENGTH: 15
: TYPE: PRT
: ORGANISM: Artificial
: FEATURE:
: OTHER INFORMATION: single chain antibody fragment
: US-10-632-706-131

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Query Match          100.0%   Score 89; DB 4; Length 15;
      Similarity    100.0%; Pred. No. 2.8e-06;
Beat Local          15; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Matches
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```

RESULT 4
US-10-632-706-194
: Sequence 194, Application US/10632706
: Publication No. US20040175385A1
: GENERAL INFORMATION:
: APPLICANT: MARKS, JAMES D.
: TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
: TITLE OF INVENTION: NEUROTOXINS
: FILE REFERENCE: 407T-895120US
: CURRENT APPLICATION NUMBER: US/10/632,706
: CURRENT FILING DATE: 2003-08-01
: PRIOR APPLICATION NUMBER: US 60/400,721
: PRIOR FILING DATE: 2002-08-01
: PRIOR APPLICATION NUMBER: US 09/144,806
: PRIOR FILING DATE: 1998-08-31
: NUMBER OF SEQ ID NOS: 278
: SOFTWARE: Patent in version 3.2

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? SEQ ID NO 194
? LENGTH: 15
? TYPE: PRT
? ORGANISM: Artificial
? FEATURES:
? OTHER INFORMATION: single chain antibody fragment
? OS=10-632-706-194

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Query Match	100.0%	Score 89;	DB 4;	Length 15;
Best Local Similarity	100.0%;	Pred. No. 2.8e-06;		
Matches 15; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY 1 EPDWLWGDRGALDV 15  
|||  
Db 1 EPDWLWGDRGALDV 15

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RESULT 5
US-10-632-706-197
; Sequence 197, Application US/106522706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; APPLICANT: AMERSDORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; TITLE OF INVENTION: NEUROTOXINS
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 197
; LENGTH: 15
; TYPE: PR1
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-197

```

```

Query Match          100.0%; Score 89; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Cy 1 EPDWLWNGDRGALDY 15
    |||||
Db 1 EPDWLWNGDRGALDY 15

```

```

RESULT 6
US-10-632-706-200
: Sequence 200. Application US/10632706
: Publication No. US20040175385A1
: GENERAL INFORMATION:
: APPLICANT: MARKS, JAMES D.
: APPLICANT: AMERSOORER, PETER
: TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
: TITLE OF INVENTION: NEUROTOXINS
: FILE REFERENCE: 407T-895120US
: CURRENT APPLICATION NUMBER: US/10/632,706
: CURRENT FILING DATE: 2003-08-01
: PRIOR APPLICATION NUMBER: US 60/400,721
: PRIOR FILING DATE: 2002-08-01
: PRIOR APPLICATION NUMBER: US 09/144,806
: PRIOR FILING DATE: 1998-08-31
: NUMBER OF SEQ ID NOS: 278
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 200
:
: LENGTH: 15
: TYPE: PRT
:

```

```

; ORGANISM: Artificial
;
; FEATURE:
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-200

```

Query Match	100.0%;	Score 89;	DB 4;	Length 15;
Best Local Similarity	100.0%;	Pred. No. 2.8e-06;		
Matches	15;	Conservative	0;	Mismatches 0;
			Indels	0;
Gy	1	EPDMLMGDRGALDV	15	
Db	1	EPDMLMGDRGALDV	15	

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1      RESULT 7
2      US-10-632-706-203
3      ; Sequence 203, Application US/10632706
4      ; Publication No. US20040175385A1
5      ; GENERAL INFORMATION:
6      ; APPLICANT: MARKS, JAMES D.
7      ; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
8      ; TITLE OF INVENTION: NEUROTOXINS
9      ; FILE REFERENCE: 407T-895120US
10     ; CURRENT APPLICATION NUMBER: US/10/632,706
11     ; CURRENT FILING DATE: 2003-08-01
12     ; PRIOR APPLICATION NUMBER: US 60/400,721
13     ; PRIOR FILING DATE: 2002-08-01
14     ; PRIOR APPLICATION NUMBER: US 09/144,806
15     ; PRIOR FILING DATE: 1998-08-31
16     ; NUMBER OF SEQ ID NOS: 278
17     ; SOFTWARE: PatentIn version 3.2
18     ; SEQ ID NO 203
19     ; LENGTH: 15
20     ; TYPE: PRT
21     ; ORGANISM: Artificial
22     ; FEATURE:
23     ; OTHER INFORMATION: single chain antibody fragment
24     ; US-10-632-706-203

```

Query Match	84.3%	Score 75;	DB 4;	Length 15;
Best Local Similarity	93.3%	Pred. No. 0.00033;		
Matches	14;	Conservative	0;	Mismatches 1;
				Indels 0;
				Gaps 0;
QY	1	EPDMLMGDRCALDV	15	
DB	1	EPDRLLMGDRGALDV	15	

```

/ RESULT 8
/ US-10-450-763-50690
/ Sequence 50690, Application US/10450763
/ Publication NO. US20050196754A1
/
/ GENERAL INFORMATION:
/
/ APPLICANT: Hyseq, Inc
/ TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
/ FILE REFERENCE: 790CIP/US
/ CURRENT APPLICATION NUMBER: US/10/450, 763
/ CURRENT FILING DATE: 2003-06-11
/ PRIOR APPLICATION NUMBER: PCT/US01/08631
/ PRIOR FILING DATE: 2001-03-30
/ PRIOR APPLICATION NUMBER: 09/540,217
/ PRIOR FILING DATE: 2000-03-31
/ PRIOR APPLICATION NUMBER: 09/649,167
/ PRIOR FILING DATE: 2000-08-23
/ NUMBER OF SEQ ID NOS: 60736
/ SOFTWARE: Custom
/
/ SEQ ID NO 50690
/
/ LENGTH: 334
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/
/ FEATURE:
/ NAME/KEY: DOMAIN
/

```

```

: LOCATION: (267)..(320)
: OTHER INFORMATION: Sodium:neurotransmitter symporter family proteins domain
: OTHER INFORMATION: Identified by eMARRIT, accession number BL00610D, p-value=2.000e-
: OTHER INFORMATION: 25, raw score of 20.97
: peptide.

```

Query Match	Score	DB	Length
Best Local Similarity	53.3%	21	334
Matches	8	Conservative	2
		Mismatches	5
		Indels	0
		Gaps	0

```

RESULT 9
US-10-634-548-27
; Sequence 27, Application US/10634548
; Publication No. US20040045051A1
; GENERAL INFORMATION:
; APPLICANT: No. US20040045051A1a1a, Susan R
; APPLICANT: Lincoln, Kim
; APPLICANT: Abad, Mark Scott
; APPLICANT: Eilers, Robert
; APPLICANT: Hartsuiker, Karen Kindle
; APPLICANT: Hirschberg, Joseph
; APPLICANT: Karunanandaa, Balasubramini
; APPLICANT: Moshiri, Farhad
; APPLICANT: Stein, Joshua C.
; APPLICANT: Valentin, Henry E.
; APPLICANT: Venkatesh, Tyamagondlu V.
; TITLE OF INVENTION: Tocopherol biosynthesis related genes and used thereof
; FILE REFERENCE: Ren-01-125
; CURRENT APPLICATION NUMBER: US/10/634,548
; CURRENT FILING DATE: 2003-08-05
; PRIOR APPLICATION NUMBER: us 60/400,689
; PRIOR FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 201
; TYPE: PR1
; ORGANISM: Prochlorococcus marinus-MIT9313
US-10-634-548-27

```

Query Match	53.9%	Score 40	DB 4	Length 201
Best local similarity	50.0%	Pred. No. 37		
Matches	6	Conservative	4	Mismatches 2
				Indels 0
				Gaps 0
QY	2	PDWLIMDRCAL	13	
		: : : : :	::	
Db	123	PWWLIMGQRKSI	134	

RESULT 10  
 US-10-159-257A-160  
 ; Sequence 160, Application US/10159257A  
 ; Publication No. US20040161828A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SHEN, BEN  
 ; APPLICANT: LIU, WEN  
 ; APPLICANT: CHRISTENSON, STEVEN D.  
 ; APPLICANT: STANDAGE, SCOTT  
 ; TITLE OF INVENTION: GENE CLUSTER FOR PRODUCTION OF THE ENEDIYNE ANTITUMOR

```
/ TITLE OF INVENTION: ANTIBIOTIC C-1027
/ FILE REFERENCE: 4077-896020US
/ CURRENT APPLICATION NUMBER: US/10/159,257A
/ CURRENT FILING DATE: 2002-05-31
/ PRIOR APPLICATION NUMBER: 09/478,188
/ PRIOR FILING DATE: 2000-01-05
/ PRIOR APPLICATION NUMBER: 60/115,434
/ PRIOR FILING DATE: 1999-01-06
/ NUMBER OF SEQ ID NOS: 207
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO: 160
/ LENGTH: 775
/ TYPE: PRT
/ ORGANISM: Streptomyces globisporus
/ FEATURE:
/ OTHER INFORMATION: orf(-1)
US-10-159-257A-160

Query Match          53.9%; Score 48; DB 4; Length 775;
Best Local Similarity 53.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      2 PDWLMGDRGALD 14
DB      195 PDWQIMAKSGRLD 207

RESULT 11
US-10-437-963-134365
/ Sequence 134365, Application US/10/437963
/ Publication No. US20040123343A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Wu, Wei
/ APPLICANT: Boukharov, Andrey A.
/ APPLICANT: Bardazuk, Brad
/ APPLICANT: Li, Ping
/ TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53221)B
/ CURRENT APPLICATION NUMBER: US/10/437,963
/ CURRENT FILING DATE: 2003-05-14
/ NUMBER OF SEQ ID NOS: 204966
/ SEQ ID NO: 134365
/ LENGTH: 992
/ TYPE: PRT
/ ORGANISM: Oryza sativa
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT4530_36146C.1.pep
US-10-437-963-134365

Query Match          53.4%; Score 47.5; DB 4; Length 992;
Best Local Similarity 50.0%; Pred. No. 2e+02;
Matches 9; Conservative 3; Mismatches 3; Indels 3; Gaps 1;

QY      1 EPDWL---MGDRGALDV 15
DB      551 EPNWLDWYWGDKGTGTV 568

RESULT 12
US-10-450-763-52883
/ Sequence 52883, Application US/10/450763
/ Publication No. US20050196754A1
/ GENERAL INFORMATION:
/ APPLICANT: HySeq, Inc
/ APPLICANT: Kovalic, David K.
/ TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
/ FILE REFERENCE: 790C19/US
/ CURRENT APPLICATION NUMBER: US/10/450,763
/ CURRENT FILING DATE: 2003-06-11
```

```
/ PRIOR APPLICATION NUMBER: PCT/US01/08631
/ PRIOR FILING DATE: 2001-03-30
/ PRIOR APPLICATION NUMBER: 09/540,217
/ PRIOR FILING DATE: 2000-03-31
/ PRIOR APPLICATION NUMBER: 09/649,167
/ PRIOR FILING DATE: 2000-08-23
/ NUMBER OF SEQ ID NOS: 60736
/ SOFTWARE: Custom
/ SEQ ID NO: 52883
/ LENGTH: 455
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc.feature
/ LOCATION: (1)...(455)
/ OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-52883

Query Match          52.8%; Score 47; DB 5; Length 455;
Best Local Similarity 53.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      1 EPDWLMGDRGAL 13
DB      93 EQNWLMWCEGVM 105

RESULT 13
US-10-369-493-12420
/ Sequence 12420, Application US/10369493
/ Publication No. US20030233675A1
/ GENERAL INFORMATION:
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Hinkle, Gregory J.
/ APPLICANT: Slater, Steven C.
/ APPLICANT: Goldman, Barry S.
/ APPLICANT: Chen, Xianfeng
/ TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
/ FILE REFERENCE: 38-10(52052)B
/ CURRENT APPLICATION NUMBER: US/10/369,493
/ CURRENT FILING DATE: 2003-02-28
/ PRIOR APPLICATION NUMBER: US 60/360,039
/ PRIOR FILING DATE: 2002-02-21
/ NUMBER OF SEQ ID NOS: 47374
/ SEQ ID NO: 12420
/ LENGTH: 904
/ TYPE: PRT
/ ORGANISM: Aspergillus nidulans
US-10-369-493-12420

Query Match          52.8%; Score 47; DB 4; Length 904;
Best Local Similarity 70.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      4 WLMGDRGAL 13
DB      460 WLMGDKTSL 469

RESULT 14
US-10-425-115-240160
/ Sequence 240160, Application US/10425115
/ Publication No. US20040214272A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
/ TITLE OF INVENTION: Plants
/ FILE REFERENCE: 38-21(53222)B
/ CURRENT APPLICATION NUMBER: US/10/425,115
```

```

; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 240160
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(159)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_150607C.1.pap
US-10-425-115-240160

```

```

Query Match      50.6%; Score 45; DB 4; Length 159;
Best Local Similarity 75.0%; Pred. No. 83;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      2 PDMLMGDRGAL 13
      |||||
DB      35 PGRLMGRRGAL 46

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RESULT 15
US-10-282-122A-68332
; Sequence 68332, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: EHTPA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68332
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Pseudomonas putida
US-10-282-122A-68332

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```

Query Match      50.6%; Score 45; DB 4; Length 372;
Best Local Similarity 70.0%; Pred. No. 1,86+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      2 PDMLMGDRG 11
      |||||
DB      221 PDMLMTPAG 230

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```

Search completed: December 4, 2005, 04:37:43
Job time : 121.5 secs

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**This Page Blank (uspdc)**

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: December 4, 2005, 04:08:08 ; Search time 4.375 Seconds  
(without alignments)  
16.417 Million cell updates/sec

Title: US-10-632-706-197  
Perfect score: 89  
Sequence: 1 EPDMLMGDRGALDV 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA-New:\*  
1: /cgn2\_6/prodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
2: /cgn2\_6/prodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
3: /cgn2\_6/prodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
4: /cgn2\_6/prodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
5: /cgn2\_6/prodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
6: /cgn2\_6/prodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
7: /cgn2\_6/prodata/1/pubpaa/US11\_NEW\_PUB.pep:\*  
8: /cgn2\_6/prodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	48.3	383	6	US-10-467-657-5602 Sequence 5602, Ap
2	41	46.1	251	7	US-11-054-515-1084 Sequence 1084, Ap
3	40.5	45.5	125	6	US-10-821-234-1277 Sequence 1277, Ap
4	38.5	43.3	1075	7	US-11-174-150-34 Sequence 34, Appl
5	38.5	43.3	1114	7	US-11-174-150-35 Sequence 35, Appl
6	38	42.7	248	7	US-11-054-515-1679 Sequence 1679, Ap
7	38	42.7	251	7	US-11-054-515-944 Sequence 944, Appl
8	37	41.6	344	6	US-10-967-527A-24 Sequence 24, Appl
9	36	40.4	225	6	US-10-821-234-1116 Sequence 1116, Ap
10	36	40.4	332	6	US-10-467-657-1006 Sequence 1006, Ap
11	36	40.4	438	6	US-10-793-626-484 Sequence 484, Appl
12	36	40.4	1857	7	US-11-057-058-60 Sequence 60, Appl
13	36	40.4	1857	7	US-11-057-058-61 Sequence 61, Appl
14	35.5	39.9	158	6	US-10-510-386-128 Sequence 128, Appl
15	35.5	39.9	247	6	US-10-793-626-1466 Sequence 1466, Ap
16	35.5	39.9	344	6	US-10-821-234-923 Sequence 923, Appl
17	35.5	39.9	380	6	US-10-624-932-20 Sequence 20, Appl
18	35	39.3	229	6	US-10-957-859-54 Sequence 54, Appl
19	35	39.3	350	6	US-10-467-657-5824 Sequence 5824, Ap
20	35	39.3	401	6	US-10-510-386-68 Sequence 68, Appl
21	35	39.3	530	6	US-10-980-388-62 Sequence 62, Appl
22	35	39.3	551	6	US-10-793-626-1668 Sequence 1668, Ap
23	34.5	38.8	1613	7	US-11-108-528-84 Sequence 84, Appl
24	34.5	38.8	1613	7	US-11-108-528-86 Sequence 86, Appl
25	34	38.2	251	7	US-11-054-515-1079 Sequence 1079, Ap

26	34	38.2	251	7	US-11-054-515-1793 Sequence 1793, Ap
27	34	38.2	253	7	US-11-015-546A-2 Sequence 2, Appl
28	34	38.2	253	7	US-11-054-515-1069 Sequence 1069, Ap
29	34	38.2	269	7	US-11-015-546A-10 Sequence 10, Appl
30	34	38.2	274	7	US-11-015-546A-12 Sequence 12, Appl
31	34	38.2	486	6	US-10-821-234-1063 Sequence 1063, Ap
32	34	38.2	613	6	US-10-131-826A-190 Sequence 190, Appl
33	34	38.2	616	6	US-10-131-826A-206 Sequence 206, Appl
34	34	38.2	820	7	US-11-147-047-31 Sequence 31, Appl
35	34	38.2	2725	7	US-11-113-424-52 Sequence 52, Appl
36	33.5	37.6	137	6	US-10-821-234-882 Sequence 882, Appl
37	33.5	37.6	249	7	US-11-054-515-649 Sequence 649, Ap
38	33	37.1	91	6	US-10-467-657-1052 Sequence 1052, Ap
39	33	37.1	177	6	US-10-980-388-95 Sequence 95, Appl
40	33	37.1	247	7	US-11-054-515-1307 Sequence 1307, Ap
41	33	37.1	248	7	US-11-054-515-877 Sequence 877, Appl
42	33	37.1	248	7	US-11-054-515-953 Sequence 953, Appl
43	33	37.1	248	7	US-11-054-515-965 Sequence 965, Appl
44	33	37.1	248	7	US-11-054-515-980 Sequence 980, Appl
45	33	37.1	248	7	US-11-054-515-984 Sequence 984, Appl

## ALIGNMENTS

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RESULT 1
US-10-467-657-5602
; Sequence 5602, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5602
; LENGTH: 383
; TYPE: PRP
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5602

Query Match      48.3% Score 43; DB 6; Length 383;
Best Local Similarity 70.0%; Pred. No. 3.8;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 PDMLMGDRG 11
      |:|:|:|
Db      181 PEWLIFGYRG 190

RESULT 2
US-11-054-515-1084
; Sequence 1084, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
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/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 1084
/ LENGTH: 251
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-054-515-1084
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Query Match          46.1%; Score 41; DB 7; Length 251;
Best Local Similarity 46.2%; Pred. No. 5.1;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 2 PDWLWGDGRGALD 14
DB 45 PEMWGMINRGSD 57
```

```
RESULT 3
US-10-821-234-1277
/ Sequence 1277, Application US/10821234
/ Publication No. US20050255114A1
/ GENERAL INFORMATION:
/ APPLICANT: Labac, Ivan
/ APPLICANT: Stache-Crain, Birgit
/ APPLICANT: Andarmani, Susan
/ APPLICANT: Tang, Y. Tom
/ TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
/ FILE REFERENCE: 821A
/ CURRENT APPLICATION NUMBER: US/10/821,234
/ CURRENT FILING DATE: 2004-04-07
/ PRIOR APPLICATION NUMBER: US 60/462,047
/ PRIOR FILING DATE: 2003-04-07
/ NUMBER OF SEQ ID NOS: 1704
/ SOFTWARE: pc_seq_genes Version 1.0
/ SEQ ID NO 1277
/ LENGTH: 125
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-821-234-1277
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Query Match          45.5%; Score 40.5; DB 6; Length 125;
Best Local Similarity 63.6%; Pred. No. 3.1;
Matches 7; Conservative 3; Mismatches 0; Indels 1; Gaps 1;
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```
QY 1 EPDWLWGDGRG 11
DB 101 DDDWLI-GERG 110
```

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RESULT 4
US-11-174-150-34
/ Sequence 34, Application US/11174150
/ Publication No. US20050260714A1
/ GENERAL INFORMATION:
/ APPLICANT: Agarwal, Pankaj
/ APPLICANT: Murdoch, Paul R.
/ APPLICANT: Rizvi, Safia K.
/ APPLICANT: Smith, Randall F.
```

```
/ APPLICANT: Xiang, Zhaoying
/ TITLE OF INVENTION: NOVEL COMPOUNDS
/ FILE REFERENCE: GP50022
/ CURRENT APPLICATION NUMBER: US/11/174,150
/ CURRENT FILING DATE: 2005-07-01
/ PRIOR APPLICATION NUMBER: US/10/257,174
/ PRIOR FILING DATE: 2002-10-10
/ PRIOR APPLICATION NUMBER: PCT/US01/11797
/ PRIOR FILING DATE: 2001-04-11
/ PRIOR APPLICATION NUMBER: 60/196,603
/ PRIOR FILING DATE: 2000-04-13
/ PRIOR APPLICATION NUMBER: 60/199,417
/ PRIOR FILING DATE: 2000-04-24
/ NUMBER OF SEQ ID NOS: 48
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 34
/ LENGTH: 1075
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-174-150-34
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Query Match          43.3%; Score 38.5; DB 7; Length 1075;
Best Local Similarity 53.8%; Pred. No. 5.1;
Matches 7; Conservative 2; Mismatches 1; Indels 3; Gaps 1;
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```
QY 3 DWLWLG---DRGA 12
DB 922 EMSVWGSWYDRGA 934
```

```
RESULT 5
US-11-174-150-35
/ Sequence 35, Application US/11174150
/ Publication No. US20050260714A1
/ GENERAL INFORMATION:
/ APPLICANT: Agarwal, Pankaj
/ APPLICANT: Murdoch, Paul R.
/ APPLICANT: Rizvi, Safia K.
/ APPLICANT: Smith, Randall F.
/ APPLICANT: Xiang, Zhaoying
/ TITLE OF INVENTION: NOVEL COMPOUNDS
/ FILE REFERENCE: GP50022
/ CURRENT APPLICATION NUMBER: US/11/174,150
/ CURRENT FILING DATE: 2005-07-01
/ PRIOR APPLICATION NUMBER: US/10/257,174
/ PRIOR FILING DATE: 2002-10-10
/ PRIOR APPLICATION NUMBER: PCT/US01/11797
/ PRIOR FILING DATE: 2001-04-11
/ PRIOR APPLICATION NUMBER: 60/196,603
/ PRIOR FILING DATE: 2000-04-13
/ PRIOR APPLICATION NUMBER: 60/199,417
/ PRIOR FILING DATE: 2000-04-24
/ NUMBER OF SEQ ID NOS: 48
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 35
/ LENGTH: 1114
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-174-150-35
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Query Match          43.3%; Score 38.5; DB 7; Length 1114;
Best Local Similarity 53.8%; Pred. No. 5.3;
Matches 7; Conservative 2; Mismatches 1; Indels 3; Gaps 1;
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```
QY 3 DWLWLG---DRGA 12
DB 961 EMSVWGSWYDRGA 973
```

```
RESULT 6
US-11-054-515-1679
/ Sequence 1679, Application US/11054515
/ Publication No. US2005025532A1
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```
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1679
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1679

Query Match          42.7%; Score 38; DB 7; Length 248;
Best Local Similarity 42.9%; Pred. No. 15;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy      1 EPDWLMGDRGALD 14
||:|:|:|:|:|
Db      44 EPDMGWMINGSGSD 57

RESULT 7
US-11-054-515-944
; Sequence 944, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
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; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 944
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-944

Query Match          42.7%; Score 38; DB 7; Length 251;
Best Local Similarity 42.9%; Pred. No. 15;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy      1 EPDWLMGDRGALD 14
||:|:|:|:|:|
Db      44 EPDMGWMINGSGSD 57

RESULT 8
US-10-967-527A-24
; Sequence 24, Application US/10967527A
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Holloway, James L.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Zcnf14, A Tumor Necrosis Factor
; FILE REFERENCE: 03-17
; CURRENT APPLICATION NUMBER: US/10/967,527A
; CURRENT FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 344
; TYPE: PRT
; ORGANISM: mus musculus
US-10-967-527A-24

Query Match          41.6%; Score 37; DB 6; Length 344;
Best Local Similarity 83.3%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 PDWLMW 7
|||
Db      3 PSWLMW 8

RESULT 9
US-10-821-234-1116
; Sequence 1116, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1116
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1116

Query Match          40.4%; Score 36; DB 6; Length 225;
```

Best Local Similarity 62.5%; Pred. No. 27;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 WLMGDRG 11  
Db 74 WRMGRG 81

## RESULT 10

US-10-467-657-1006  
; Sequence 1006, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SPA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASTIGNANI Vega  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqMin9, version 1.04  
; SEQ ID NO 1006  
; LENGTH: 322  
; TYPE: PRT  
; ORGANISM: *Neisseria gonorrhoeae*  
US-10-467-657-1006

Query Match 40.4%; Score 36; DB 6; Length 322;  
Best Local Similarity 63.6%; Pred. No. 38;  
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 PDWLMGDRGA 12  
Db 251 PDWFLVLDRSA 261

## RESULT 11

US-10-793-626-484  
; Sequence 484, Application US/10793626  
; Publication No. US20050255478A1  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PU348005  
; CURRENT APPLICATION NUMBER: US/10/793,626  
; CURRENT FILING DATE: 2004-03-04  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 484  
; LENGTH: 428  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-10-793-626-484

Query Match 40.4%; Score 36; DB 6; Length 428;  
Best Local Similarity 62.5%; Pred. No. 50;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 7 WGDGRGALD 14  
Db 333 WGDKGVD 340

RESULT 12  
US-11-057-058-60  
; Sequence 60, Application US/11057058  
; Publication No. US20050244400A1  
; GENERAL INFORMATION:  
; APPLICANT: Lebowitz, Jonathan  
; APPLICANT: Maga, John  
; TITLE OF INVENTION: ACID ALPHA-GLUCOSIDASE AND FRAGMENTS THEREOF  
; FILE REFERENCE: SW-011  
; CURRENT APPLICATION NUMBER: US/11/057,058  
; CURRENT FILING DATE: 2005-02-10  
; PRIOR APPLICATION NUMBER: US 60/543,812  
; PRIOR FILING DATE: 2004-02-10  
; NUMBER OF SEQ ID NOS: 68  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 60  
; LENGTH: 1857  
; TYPE: PRT  
; ORGANISM: *Homo sapiens*  
US-11-057-058-60

Query Match 40.4%; Score 36; DB 7; Length 1857;  
Best Local Similarity 45.5%; Pred. No. 2.1e+02;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 4 WLMGDRGALD 14  
Db 1749 WLFWDGQSID 1759

## RESULT 13

US-11-057-058-61  
; Sequence 61, Application US/11057058  
; Publication No. US20050244400A1  
; GENERAL INFORMATION:  
; APPLICANT: Lebowitz, Jonathan  
; APPLICANT: Maga, John  
; TITLE OF INVENTION: ACID ALPHA-GLUCOSIDASE AND FRAGMENTS THEREOF  
; FILE REFERENCE: SW-011  
; CURRENT APPLICATION NUMBER: US/11/057,058  
; CURRENT FILING DATE: 2005-02-10  
; PRIOR APPLICATION NUMBER: US 60/543,812  
; PRIOR FILING DATE: 2004-02-10  
; NUMBER OF SEQ ID NOS: 68  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 61  
; LENGTH: 1857  
; TYPE: PRT  
; ORGANISM: *Homo sapiens*  
US-11-057-058-61

Query Match 40.4%; Score 36; DB 7; Length 1857;  
Best Local Similarity 45.5%; Pred. No. 2.1e+02;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 4 WLMGDRGALD 14  
Db 1749 WLFWDGQSID 1759

## RESULT 14

US-10-510-386-128  
; Sequence 128, Application US/10510386  
; Publication No. US20050244922A1  
; GENERAL INFORMATION:  
; APPLICANT: Andersen, Jens Tonne  
; APPLICANT: Clausen, Ib Groth  
; APPLICANT: Jorgensen, Steen Troels  
; APPLICANT: Olsen, Peter Bjarke  
; APPLICANT: Rasmussen, Michael Dolberg  
; TITLE OF INVENTION: Improved Bacillus Host Cell  
; FILE REFERENCE: 10294.204-US  
; CURRENT APPLICATION NUMBER: US/10/510,386

; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 248  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 128  
; LENGTH: 158  
; TYPE: PRF  
; ORGANISM: Bacillus licheniformis  
US-10-510-386-128

Query Match 39.9%; Score 35.5; DB 6; Length 158;  
Best Local Similarity 72.7%; Pred. No. 23;  
Matches 8; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 5 LLM-GDRGALD 14  
| | | | |  
Db 65 LYWTGDRGKLD 75

RESULT 15  
US-10-793-626-1466  
; Sequence 1466, Application US/107931626  
; Publication No. US20050255478A1  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PU3480US  
; CURRENT APPLICATION NUMBER: US/10/793,626  
; CURRENT FILING DATE: 2004-03-04  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1466  
; LENGTH: 247  
; TYPE: PRF  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: amino acid sequence  
US-10-793-626-1466

Query Match 39.9%; Score 35.5; DB 6; Length 247;  
Best Local Similarity 63.6%; Pred. No. 35;  
Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 4 WL-LMGDRGAL 13  
| : | | | | |  
Db 186 WMLMGNGVGL 196

Search completed: December 4, 2005, 04:37:50  
Job time : 5.375 secs

**This Page Blank (usp10)**

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: December 4, 2005, 04:09:54 ; Search time 95.5625 Seconds  
(without alignments)  
50.576 Million cell updates/sec

Title: US-10-632-706-198

Sequence: 1 WGGGTTVTWSS 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

1: A\_Geneseq\_21.\*  
2: geneseqp19806.\*  
3: geneseqp19908.\*  
4: geneseqp20008.\*  
5: geneseqp20015.\*  
6: geneseqp20028.\*  
7: geneseqp20035.\*  
8: geneseqp20048.\*  
9: geneseqp20058.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	11	2	AAR85166
2	59	100.0	11	2	AAR85166
3	59	100.0	11	4	AAR85166
4	59	100.0	11	5	AAR85166
5	59	100.0	11	5	AAR85166
6	59	100.0	11	5	AAR85166
7	59	100.0	11	5	AAR85166
8	59	100.0	11	5	AAR85166
9	59	100.0	11	6	AAR85166
10	59	100.0	11	6	AAR85166
11	59	100.0	11	7	AAR85166
12	59	100.0	11	7	AAR85166
13	59	100.0	11	8	AAR85166
14	59	100.0	11	8	AAR85166
15	59	100.0	11	8	AAR85166
16	59	100.0	11	8	AAR85166
17	59	100.0	11	8	AAR85166
18	59	100.0	11	8	AAR85166
19	59	100.0	11	8	AAR85166
20	59	100.0	11	8	AAR85166
21	59	100.0	11	8	AAR85166
22	59	100.0	11	8	AAR85166
23	59	100.0	11	8	AAR85166
24	59	100.0	11	9	AAR85166

25	59	100.0	11	9	ADM07407	Adw07407 Heavy cha
26	59	100.0	11	9	ADM07423	Adw07423 Heavy cha
27	59	100.0	11	9	ADM07427	Adw07427 Heavy cha
28	59	100.0	11	9	ADM07435	Adw07435 Heavy cha
29	59	100.0	11	9	ADM07439	Adw07439 Heavy cha
30	59	100.0	11	9	ADM07411	Adw07411 Heavy cha
31	59	100.0	11	9	ADM07443	Adw07443 Heavy cha
32	59	100.0	11	9	ADM07451	Adw07451 Heavy cha
33	59	100.0	11	9	ADM07415	Adw07415 Heavy cha
34	59	100.0	11	9	ADM07447	Adw07447 Heavy cha
35	59	100.0	11	9	ADM07431	Adw07431 Heavy cha
36	59	100.0	11	9	ADY31581	Ady31581 Human ant
37	59	100.0	11	9	ADZ35850	Adz35850 Anti-glyc
38	59	100.0	11	9	ADZ83544	Adz83544 CD3 const
39	59	100.0	11	9	ADZ83542	Adz83542 CD3 const
40	59	100.0	11	9	ADZ83545	Adz83545 CD3 const
41	59	100.0	11	9	ADZ83543	Adz83543 CD3 const
42	59	100.0	11	9	AEA21481	Aea21481 Human ant
43	59	100.0	11	9	AEA21445	Aea21445 Human ant
44	59	100.0	11	9	AEA45691	Aea45691 Apolipop
45	59	100.0	11	9	AEA44171	Aea44171 Anti-TPO

## ALIGNMENTS

### RESULT 1

AAR85166 standard; protein; 11 AA.

AAR85166;

18-JAN-1996 (first entry)

Human ONS-M21 antibody heavy variable region FR 4.

Human, ONS-M21 antibody; heavy variable region; chimeric protein; framework region; FR 4; medulloblastoma; brain tumour; treatment; diagnosis.

OS Homo sapiens.

PN WO9514041-A1.

PD 26-MAY-1995.

PF 19-OCT-1994; 94WO-JP001763.

PR 19-NOV-1993; 93JP-00291078.

PA (CHUS) CHUGAI SEIYAKU KK.

PI Ohtomo T, Sato K, Tsuchiya M;

WPI; 1995-200347/26.

Reconstituted antibody against human medulloblastoma cells - contains high proportion of human antibody origin and has low antigenicity.

Claim 18; Page 102; 120pp; Japanese.

AAR85163-R85166 are human antibody ONS-M21 heavy variable region framework regions (FRs). They were used in the construction of a human/murine chimeric antibody, reactive with human medulloblastoma (a brain tumour) cells. The chimeric antibody can be used in the diagnosis and treatment of this disease.

Sequence 11 AA;

Query Match 100.0%; Score 59; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WGGGTTTVSS 11  
|||  
DB 1 WGGGTTTVSS 11

## RESULT 2

AAR97333  
ID AAR97333 standard; peptide; 11 AA.

XX AAR97333;

DT 15-OCT-1996 (first entry)

DE Humanised monoclonal antibody heavy chain framework region.

XX Monoclonal antibody; humanised; mouse; framework region; FR; CDR;  
XX complementary determining region; anti-carcinomyonic antigen; CEA;  
XX diagnosis; imaging; therapy; immune response.

OS Homo sapiens.

PN WO9611013-A1.

PD 18-APR-1996.

PF 28-SEP-1995; 95WO-US011964.

PR 05-OCT-1994; 94US-00318157.

PA (IMMU-) IMMUNOMEDICS INC.

PI Hansen HJ, Armour KL;

DR WPI; 1996-209653/21.

PT New humanised anti-CEA monoclonal antibody - having engrafted murine  
CDRs, used for diagnosis, imaging and therapy of CEA-producing cancers.

PS Claim 7; Page 40; 62pp; English.

XX New humanised monoclonal antibodies (MAbs) comprising the complementary  
CC determining regions (CDRs) of a parental murine class III anti-  
CC carcinoembryonic (CEA) MAb engrafted to the framework regions (FRs) of a  
CC heterologous antibody which can be derived from any species including  
CC human, retain the anti-CEA binding specificity of the parental murine MAb  
CC but are less immunogenic in a human subject than the parental MAb. The  
CC humanised antibodies can be used in diagnosis, imaging and therapy of CEA  
CC -producing cancers and patients receiving the humanised antibodies and  
CC conjugates show improved therapeutic results, decreased immune responses  
CC and decreased immune-mediated adverse effects compared to the parent  
CC antibody. This sequence corresponds to the fourth framework region of the  
CC heavy chain of the humanised MAb. See AAR97333-97333

XX Sequence 11 AA;

Query Match 100.0%; Score 59; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.011;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WGGGTTTVSS 11  
|||  
DB 1 WGGGTTTVSS 11

## RESULT 3

AAU07452  
ID AAU07452 standard; peptide; 11 AA.

XX AAU07452;

DT 24-OCT-2001 (first entry)

XX Synthetic peptide H-FR4-F8.

XX H-FR4-F8; antimicrobial; antiviral; cytostatic; immunomodulatory;  
XX antibody; gene therapy; HIV; human immunodeficiency virus; tumour;  
XX metabolic disorder; immune disorder; auto-immune disorder.

OS Synthetic.

PN WO200149713-A2.

PD 12-JUL-2001.

PF 29-DEC-2000; 2000WO-IT000554.

PR 30-DEC-1999; 99IT-RM000803.

PA (CNEN) ENEA ENTERNOVE TECNOLOGIE ENERGIA.  
XX (CONS-) SOC CONSORTILE METAPONTUM AGROBIOS SRL.

PI Benvenuto E, Franconi R, Desiderio A, Tavladoraki P;

DR WPI; 2001-502555/55.

DR N-P5DB; AAS11874.

PT Peptides which are able to confer stability and solubility to an antibody  
comprising these peptides, useful for treating pathologies (e.g. tumor)  
associated with accumulation of a molecule inside or outside a human, or  
animal cell.

PS Claim 1; Page 57; 109pp; English.

XX The invention relates to peptides which are able to confer stability and  
CC solubility to an antibody comprising these peptides. The peptides are  
CC especially H-FR1, H-FR2, HP-R3, HPR4, L-FR1, L-FR2, L-FR3 or L-FR4  
CC present within a variable region of an antibody which makes the antibody  
CC soluble and stable in cytoplasm. Peptides having the sequences of HFR1 to  
CC H-FR4 are present within the variable region of the heavy chain of an  
CC antibody, covalently linked to the H-CDR1, H-CDR2, H-CDR3 in the order (H  
CC -FR1)-(H-CDR1)-(H-FR2)-(H-CDR2)-(H-FR3)-(H-CDR3)-(H-CDR4) and peptides  
CC having the sequences of L-FR1 to L-FR4 are present within the variable  
CC region of the light chain of an antibody, covalently linked to the L-  
CC CDR1, L-CDR2, L-CDR3 in the order (L-FR1)-(L-CDR1)-(L-FR2)-(L-CDR2)-(L-  
CC -FR3)-(L-CDR3)-(L-FR4). The antibodies and polynucleotides are useful  
CC (e.g. by gene therapy) for the manufacture of a medicament for the  
CC treatment of pathologies associated with accumulation of a molecule  
CC inside or outside a human, animal cell or plant cell. The pathologies are  
CC infectious (e.g. viral infections) such as HIV, human immunodeficiency  
CC virus, infections), tumour, metabolic and immune (especially auto-immune)  
CC pathologies. The present sequence represents the peptide H-FR4-F8 (also  
CC known as H-FR4)

XX Sequence 11 AA;

Query Match 100.0%; Score 59; DB 4; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.011;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WGGGTTTVSS 11  
|||  
DB 1 WGGGTTTVSS 11

## RESULT 4

AAE28561  
ID AAE28561 standard; peptide; 11 AA.

XX AAE28561;

DT 27-DEC-2002 (first entry)

XX scFv antibody heavy chain frame work region 4 from S18 clone.

XX Human; sugar-nucleic acid interaction; single chain human antibody; scFv;  
XX Human; sugar-nucleic acid interaction; single chain human antibody; scFv;  
XX L-peptide binder; D-nucleic acid binder; sugar-protein interaction; FR4;

KM frame work region 4.  
XX  
XX Homo sapiens.  
OS  
XX MO200267860-A2.  
PN  
XX  
PD 06-SEP-2002.  
XX  
PF 22-FEB-2002; 2002WO-US005193.  
XX  
PR 22-FEB-2001; 2001US-0271377P.  
XX  
PA (SCRI ) SCRIPPS RES INST.  
XX  
PI Wong C;  
XX  
DR MPI; 2002-691633/74.  
XX  
PT Selecting L-peptide or D-nucleic acid binders that binds to enantiomers  
PT of naturally occurring carbohydrate, comprises providing enantiomers of  
PT naturally occurring carbohydrate, and screening library against  
PT enantiomers.  
XX  
PS Disclosure; Fig 6B; 46pp; English.  
XX  
XX The present invention relates to a novel method of selecting L-peptide or  
CC D-nucleic acid binders that bind to enantiomers of naturally occurring  
CC sugar or carbohydrate. The method involves providing enantiomers of  
CC naturally occurring sugar or carbohydrate employable for screening the  
CC library and then screening the library against the enantiomers for  
CC identifying a L-peptide binder or D-nucleic acid binder having binding  
CC activity with respect to enantiomers. The method is useful for selecting  
CC L-peptide binder or D-nucleic acid binder that binds to enantiomer of  
CC naturally occurring sugar or carbohydrate. It is useful for selecting L-  
CC peptide binders and/or L-nucleic acid binders that are resistant to  
CC enzymatic degradation due to their non-naturally occurring chirality, for  
CC blocking or activating the biological function of the naturally occurring  
CC sugar or carbohydrate to which they are targeted. The naturally occurring  
CC sugars and carbohydrates include bacterial or viral cell surface sugars  
CC or carbohydrates, heparin sulphates involved in viral entry, thrombos-  
CC and angiogenesis. The method is useful for identifying D-peptides, for  
CC studying sugar-protein and sugar-nucleic acid interaction and for  
CC designing high-affinity and hydrolyase resistant molecules as artificial  
CC receptors capable of binding natural carbohydrates. The immobilised  
CC enantiomers are useful for screening phases expressing a peptide library  
CC on the coat proteins to identify specific clones that bind to an  
CC immobilised enantiomer. The present sequence is single chain human  
CC antibody (scFv) heavy chain frame work region 4 (FR4) from S18 clone.  
XX This sequence is used to illustrate the method of the invention  
XX  
SQ Sequence 11 AA;  
XX  
Query Match 100.0%; Score 59; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 WGGGTTTVSS 11  
Db 1 WGGGTTTVSS 11  
XX  
RESULT 5  
AAU70517  
ID AAU70517 standard; peptide; 11 AA.  
XX  
XX AAU70517;  
AC  
XX 14-FEB-2002 (first entry)  
XX  
XX Mouse heavy chain immunoglobulin framework region 4 #11.  
DE  
XX  
XX Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;  
KM complementarity determining region; framework region; IGBP;  
KM

KM transgenic plant; immunoglobulin binding protein array; IGM; IGG; IGA;  
XX IGD; IGE; IGF; IGM; kappa; lambda; CHBP.  
XX  
XX Mus musculus.  
OS  
XX MO200183806-A1.  
PN  
XX  
PD 08-NOV-2001.  
XX  
PF 02-MAY-2001; 2001WO-US014349.  
XX  
PR 02-MAY-2000; 2000US-00563222.  
XX  
PA (EPIC-) EPICYTE PHARM INC.  
XX  
PI Hiact AC, Hein MB;  
XX  
DR MPI; 2002-055482/07.  
XX  
PT Preparing immunoglobulin binding protein array in plant cells by  
PT transforming the cells with different polynucleotides encoding binding  
PT protein polypeptides specific to ligand, selecting plant cells for  
PT preparing array.  
XX  
PS Disclosure; Fig 1B; 129pp; English.  
XX  
XX The invention relates to transforming a population of cells (e.g. plant  
CC cells), comprising using a library of two different polynucleotides  
CC encoding different immunoglobulin binding protein (IGBP) polypeptides  
CC that specifically bind to a ligand or form one or more disulphide bonds  
CC with polypeptides in transfected cells, to generate an IGBP that binds to  
CC a ligand, and transformed plant cells are selected, and preparing an IGBP  
CC array in plant cells. At least one peptide sequence has at least 75%  
CC sequence identity to a framework region (FR) of a native IGM, IGG, IGA,  
CC IGD, IGE, IGF, kappa or lambda immunoglobulin molecule. The method is  
CC useful for preparing an immunoglobulin binding protein array, preferably  
CC heavy chain binding protein (CHBP) array in eukaryotic cells especially  
CC plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic  
CC cells (e.g. insect cells or mammalian cells). The CHBP is useful for  
CC discovery of e.g. screening assays of IGBPs having desired  
CC characteristics. The present sequence is a mammalian immunoglobulin  
CC derived peptide that may be incorporated into an IGBP of the invention  
XX  
SQ Sequence 11 AA;  
XX  
Query Match 100.0%; Score 59; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 WGGGTTTVSS 11  
Db 1 WGGGTTTVSS 11  
XX  
RESULT 6  
AAU70501  
ID AAU70501 standard; peptide; 11 AA.  
XX  
XX AAU70501;  
AC  
XX 14-FEB-2002 (first entry)  
XX  
XX Mouse heavy chain immunoglobulin framework region 4 #7.  
DE  
XX  
XX Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;  
KM complementarity determining region; framework region; IGBP;  
KM transgenic plant; immunoglobulin binding protein array; IGM; IGG; IGA;  
XX IGD; IGE; IGF; IGM; kappa; lambda; CHBP.  
XX  
XX Mus musculus.  
OS  
XX  
XX MO200183806-A1.  
PN

```
PD 08-NOV-2001.
XX
XX 02-MAY-2001; 2001WO-US014349.
XX
XX 02-MAY-2000; 2000US-00563222.
XX
XX (EPIC-) EPICYTE PHARM INC.
XX
XX Hiact AC, Hein MB;
XX
XX WPI, 2002-055482/07.
XX
XX Preparing immunoglobulin binding protein array in plant cells by
XX transforming the cells with different polynucleotides encoding binding
XX protein polypeptides specific to ligand, selecting plant cells for
XX preparing array.
XX
XX Disclosure; Fig 1B; 129pp; English.
XX
XX The invention relates to transforming a population of cells (e.g. plant
XX cells), comprising using a library of two different polynucleotides
XX encoding different immunoglobulin binding protein (IGBP) polypeptides
XX that specifically bind to a ligand or form one or more disulphide bonds
XX with polypeptides in transfected cells, to generate an IGBP that binds to
XX a ligand, and transformed plant cells are selected, and preparing an IGBP
XX array in plant cells. At least one peptide sequence has at least 75%
XX sequence identity to a framework region (FR) of a native Igm, IgG, IgA,
XX IgD, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is
XX useful for preparing an immunoglobulin binding protein array, preferably
XX heavy chain binding protein (CHBP) array in eukaryotic cells especially
XX plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic
XX cells (e.g. insect cells or mammalian cells). The CHBP is useful for
XX discovery of e.g. screening assays of IGbps having desired
XX characteristics. The present sequence is a mammalian immunoglobulin
XX derived peptide that may be incorporated into an IGBP of the invention
XX
XX Sequence 11 AA;
XX
XX Query Match 100.0%; Score 59; DB 5; Length 11;
XX Best Local Similarity 100.0%; Pred. No. 0.011;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 WGGGTTVTSS 11
XX |||||
XX 1 WGGGTTVTSS 11
XX
XX DB
XX
XX RESULT 7
XX AAU70485
XX ID AAU70485 standard; peptide; 11 AA.
XX
XX AC AAU70485;
XX
XX DT 14-FEB-2002 (first entry)
XX
XX DE Mouse heavy chain immunoglobulin framework region 4 #3.
XX
XX KW Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
XX complementarity determining region; framework region; IGBP;
XX transgenic plant; immunoglobulin binding protein array; Igm; IgG; IgA;
XX IgD; IgE; IgY; Igm; kappa; lambda; CHBP.
XX
XX OS Mus musculus.
XX
XX PN WO200183806-A1.
XX
XX PD 08-NOV-2001.
XX
XX PF 02-MAY-2001; 2001WO-US014349.
XX
XX PR 02-MAY-2000; 2000US-00563222.
XX
XX (EPIC-) EPICYTE PHARM INC.
XX
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XX
XX Hiact AC, Hein MB;
XX
XX WPI, 2002-055482/07.
XX
XX Preparing immunoglobulin binding protein array in plant cells by
XX transforming the cells with different polynucleotides encoding binding
XX protein polypeptides specific to ligand, selecting plant cells for
XX preparing array.
XX
XX Disclosure; Fig 1B; 129pp; English.
XX
XX The invention relates to transforming a population of cells (e.g. plant
XX cells), comprising using a library of two different polynucleotides
XX encoding different immunoglobulin binding protein (IGBP) polypeptides
XX that specifically bind to a ligand or form one or more disulphide bonds
XX with polypeptides in transfected cells, to generate an IGBP that binds to
XX a ligand, and transformed plant cells are selected, and preparing an IGBP
XX array in plant cells. At least one peptide sequence has at least 75%
XX sequence identity to a framework region (FR) of a native Igm, IgG, IgA,
XX IgD, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is
XX useful for preparing an immunoglobulin binding protein array, preferably
XX heavy chain binding protein (CHBP) array in eukaryotic cells especially
XX plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic
XX cells (e.g. insect cells or mammalian cells). The CHBP is useful for
XX discovery of e.g. screening assays of IGbps having desired
XX characteristics. The present sequence is a mammalian immunoglobulin
XX derived peptide that may be incorporated into an IGBP of the invention
XX
XX Sequence 11 AA;
XX
XX Query Match 100.0%; Score 59; DB 5; Length 11;
XX Best Local Similarity 100.0%; Pred. No. 0.011;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 WGGGTTVTSS 11
XX |||||
XX 1 WGGGTTVTSS 11
XX
XX DB
XX
XX RESULT 8
XX AAU70477
XX ID AAU70477 standard; peptide; 11 AA.
XX
XX AC AAU70477;
XX
XX DT 14-FEB-2002 (first entry)
XX
XX DE Mouse heavy chain immunoglobulin framework region 4 #1.
XX
XX KW Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
XX complementarity determining region; framework region; IGBP;
XX transgenic plant; immunoglobulin binding protein array; Igm; IgG; IgA;
XX IgD; IgE; IgY; Igm; kappa; lambda; CHBP.
XX
XX OS Mus musculus.
XX
XX PN WO200183806-A1.
XX
XX PD 08-NOV-2001.
XX
XX PF 02-MAY-2001; 2001WO-US014349.
XX
XX PR 02-MAY-2000; 2000US-00563222.
XX
XX (EPIC-) EPICYTE PHARM INC.
XX
XX Hiact AC, Hein MB;
XX
XX WPI, 2002-055482/07.
XX
XX Preparing immunoglobulin binding protein array in plant cells by
XX transforming the cells with different polynucleotides encoding binding
```



PT protein polypeptides specific to ligand, selecting plant cells for  
PT preparing array.

PS Disclosure; Fig 1B; 129pp; English.

XX  
XX  
XX The invention relates to transforming a population of cells (e.g. plant  
CC cells), comprising using a library of two different polynucleotides  
CC encoding different immunoglobulin binding protein (IgBP) polypeptides  
CC that specifically bind to a ligand or form one or more disulphide bonds  
CC with polypeptides in transfected cells, to generate an IgBP that binds to  
CC a ligand, and transformed plant cells are selected, and preparing an IgBP  
CC array in plant cells. At least one peptide sequence has at least 75%  
CC sequence identity to a framework region (FR) of a native IgM, IgG, IgA,  
CC IgD, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is  
CC useful for preparing an immunoglobulin binding protein array, preferably  
CC heavy chain binding protein (CHBP) array in eukaryotic cells especially  
CC plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic  
CC cells (e.g. insect cells or mammalian cells). The CHBP is useful for  
CC discovery of e.g. screening assays of IgBPs having desired  
CC characteristics. The present sequence is a mammalian immunoglobulin  
CC derived peptide that may be incorporated into an IgBP of the invention

XX  
SQ Sequence 11 AA;

Query Match 100.0%; Score 59; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTVTWSS 11  
|||  
Db 1 WGGGTTVTWSS 11

RESULT 9

ID ABO10719 standard; peptide; 11 AA.

XX ABO10719;

DT 20-AUG-2003 (first entry)

XX Deimmunised murine J415-4 antibody framework sequence VHFR4.

XX Modified antibody; deimmunised antibody; anti-PSMA antibody;  
XX prostate specific membrane antigen; immunogenic; CDR; murine;  
XX complementary determining region; J591; J415; J533; E99; mouse;  
XX prostatic disorder; cancerous disorder; genitourinary inflammation;  
XX prostatitis; benign enlargement; prostatic cancer; testicular cancer;  
XX solid tumour; soft tissue tumour; metastatic lesion; pain; analgesic;  
XX antiinflammatory; cytostatic; framework region; variable heavy chain;  
XX variable light chain; VH; VL; variable region; mutant; mutein.

OS Mus musculus.

XX Synthetic.

XX WO200298897-A2.

XX 12-DEC-2002.

XX 30-MAY-2002; 2002WO-US017068.

XX 01-JUN-2001; 2001US-0295214P.

XX 20-SEP-2001; 2001US-0323585P.

XX 08-MAR-2002; 2002US-0362810P.

XX (CORR ) CORNELL RES FOUND INC.

XX Bander N, Carr FJ, Hamilton A;

XX WPI; 2003-156839/15.

XX New modified anti-prostate specific membrane antigen (PSMA)  
PT immunoglobulins, useful for treating or preventing a prostatic or

PT cancerous disorder, e.g. genitourinary inflammation, prostatitis, or  
PT prostatic or testicular cancer.

PS Disclosure; Page 21; 254pp; English.

XX  
XX  
XX The present invention relates to modified (e.g. deimmunised) antibodies  
CC to prostate specific membrane antigen (PSMA). The modified anti-PSMA  
CC antibodies are less immunogenic compared to the unmodified anti-PSMA  
CC antibodies. The modified antibodies comprise complementarity determining  
CC regions (CDRs) from a non-human antibody (e.g. murine antibody J591, J415,  
CC J533 or E99), and framework sequences that are less immunogenic in humans  
CC (e.g. less antigenic than the murine frameworks in which a murine CDR  
CC naturally occurs). The modified antibodies bind with PSMA, preferably  
CC human PSMA, with high affinity and specificity. The anti-PSMA antibodies  
CC are useful for treating or preventing a prostatic or cancerous disorder,  
CC e.g. genitourinary inflammation, prostatitis, benign enlargement,  
CC prostatic cancer or testicular cancer, or solid tumours, soft tissue  
CC tumours or metastatic lesions, and its associated pain. The present  
CC sequence represents a deimmunised murine framework region

XX  
SQ Sequence 11 AA;

Query Match 100.0%; Score 59; DB 6; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTVTWSS 11  
|||  
Db 1 WGGGTTVTWSS 11

RESULT 10

ID ABR44663 standard; peptide; 11 AA.

XX ABR44663;

DT 25-JUL-2003 (first entry)

XX Murine J415-4 antibody VH FR4 amino acid sequence SEQ ID NO:40.

XX Mouse; murine; antibody; skin disorder; binding agent; PSMA; cytostatic;  
XX prostate specific membrane antigen; antipsoriatic; antiarthritic;  
XX dermatological; antiinflammatory; antiallergic; vaccine; dermal disorder;  
XX epidermal disorder; psoriasis; inflammatory disorder; epidermis; dermis;  
XX neoplastic disorder.

OS Mus musculus.

XX Synthetic.

XX WO2003024388-A2.

XX 27-MAR-2003.

XX 30-MAY-2002; 2002WO-US017204.

XX 20-SEP-2001; 2001US-0324100P.

XX 08-MAR-2002; 2002US-0362612P.

XX (CORR ) CORNELL RES FOUND INC.

XX Bander N;

XX WPI; 2003-313319/30.

XX Ablating/killing aberrant prostate specific membrane antigen-expressing  
PT cells for treating skin disorders, by contacting the cell with an  
PT antibody that binds to the extracellular domain of prostate specific  
PT membrane antigen.

XX Disclosure; Page 68; 225pp; English.

XX The present invention describes a method (M1) for ablating or killing an



CC excessive T cell or neutrophil activity. Accordingly, these IL-9  
CC antagonists exhibit antiallergic, antiasthmatic and cytostatic  
CC activities. This peptide sequence is a peptide from the human heavy chain  
CC framework region 4, used in an exemplification of the invention.

XX Sequence 11 AA;

Query Match 100.0%; Score 59; DB 7; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11  
|||  
DB 1 WGGGTTTVSS 11

#### RESULT 13

ADH17960  
ID ADH17960 standard; peptide; 11 AA.

XX ADH17960;

DT 11-MAR-2004 (first entry)

XX Human modified 15H12/19D12 HCA framework region 4 peptide.

XX insulin-like growth factor receptor 1; IGFRI; cytostatic; osteopathic;  
XX antiatherosclerotic; antiproliferative; vasotropic; antidiarrhoeal;  
XX acromegaly; bladder cancer; Wilm's tumour; ovarian; pancreatic;  
XX benign prostatic hyperplasia; breast; prostate; bone; lung; colorectal;  
XX cervical; synovial sarcoma; diarrhoea; carcinoma syndrome;  
XX vasoactive intestinal peptide; gigantism; psoriasis; atherosclerosis;  
XX smooth muscle restenosis; blood vessel; microvascular proliferation;  
XX gene therapy; human; 15H12/19D12; heavy chain A; HCA; framework region.

XX Synthetic.

OS Homo sapiens.

XX WO2003100008-A2.

PD 04-DEC-2003.

PP 22-MAY-2003; 2003WO-US016283.

XX 24-MAY-2002; 2002US-0383459P.

PR 02-JUL-2002; 2002US-0393214P.

PR 23-DEC-2002; 2002US-0436254P.

XX (SCHE) SCHERING CORP.

XX Wang Y, Greenberg R, Presta L, Pachter JA, Hailey J, Brams P;  
PI Williams D, Srinivasan M, Feingersh D;  
XX WPI: 2004-042807/04.  
DR N-PSDB; ADH17959.

XX New binding composition that specifically binds to insulin-like growth  
PT factor receptor 1, useful for treating or preventing a medical condition  
PT that is mediated by elevated expression or activity of IGFRI.

XX Disclosure; SEQ ID NO 69; 144pp; English.

XX The invention relates to a novel binding composition that specifically  
CC binds to insulin-like growth factor receptor 1 (IGFRI). The composition  
CC of the invention demonstrates cytostatic, osteopathic,  
CC antiatherosclerotic, antiproliferative, vasotropic and antidiarrhoeal  
CC activities and may be useful for preventing or treating a medical  
CC condition selected from acromegaly, bladder cancer, Wilm's cancer,  
CC ovarian cancer, pancreatic cancer, benign prostatic hyperplasia, breast  
CC cancer, prostate cancer, bone cancer, lung cancer, colorectal cancer,  
CC cervical cancer, synovial sarcoma, diarrhoea associated with carcinoma  
CC syndrome, vasoactive intestinal peptide secreting tumours, gigantism,  
CC psoriasis, atherosclerosis, smooth muscle restenosis of blood vessels and

CC inappropriate microvascular proliferation. The composition may also have  
CC gene therapy applications. The current sequence is that of the human  
CC 15H12/19D12 heavy chain A (HCA) framework region peptide of the  
CC invention.

XX Sequence 11 AA;

Query Match 100.0%; Score 59; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11  
|||  
DB 1 WGGGTTTVSS 11

#### RESULT 14

ADH18011  
ID ADH18011 standard; peptide; 11 AA.

XX ADH18011;

DT 11-MAR-2004 (first entry)

XX Human modified 15H12/19D12 HCB framework region 4 peptide.

XX insulin-like growth factor receptor 1; IGFRI; cytostatic; osteopathic;  
XX antiatherosclerotic; antiproliferative; vasotropic; antidiarrhoeal;  
XX acromegaly; bladder cancer; Wilm's tumour; ovarian; pancreatic;  
XX benign prostatic hyperplasia; breast; prostate; bone; lung; colorectal;  
XX cervical; synovial sarcoma; diarrhoea; carcinoma syndrome;  
XX vasoactive intestinal peptide; gigantism; psoriasis; atherosclerosis;  
XX smooth muscle restenosis; blood vessel; microvascular proliferation;  
XX gene therapy; human; 15H12/19D12; heavy chain B; HCB; framework region.

XX Synthetic.

OS Homo sapiens.

XX WO2003100008-A2.

PD 04-DEC-2003.

PP 22-MAY-2003; 2003WO-US016283.

XX 24-MAY-2002; 2002US-0383459P.

PR 02-JUL-2002; 2002US-0393214P.

PR 23-DEC-2002; 2002US-0436254P.

XX (SCHE) SCHERING CORP.

XX Wang Y, Greenberg R, Presta L, Pachter JA, Hailey J, Brams P;  
PI Williams D, Srinivasan M, Feingersh D;  
XX WPI: 2004-042807/04.  
DR N-PSDB; ADH18010.

XX New binding composition that specifically binds to insulin-like growth  
PT factor receptor 1, useful for treating or preventing a medical condition  
PT that is mediated by elevated expression or activity of IGFRI.

XX Disclosure; SEQ ID NO 120; 144pp; English.

XX The invention relates to a novel binding composition that specifically  
CC binds to insulin-like growth factor receptor 1 (IGFRI). The composition  
CC of the invention demonstrates cytostatic, osteopathic,  
CC antiatherosclerotic, antiproliferative, vasotropic and antidiarrhoeal  
CC activities and may be useful for preventing or treating a medical  
CC condition selected from acromegaly, bladder cancer, Wilm's cancer,  
CC ovarian cancer, pancreatic cancer, benign prostatic hyperplasia, breast  
CC cancer, prostate cancer, bone cancer, lung cancer, colorectal cancer,  
CC cervical cancer, synovial sarcoma, diarrhoea associated with carcinoma  
CC syndrome, vasoactive intestinal peptide secreting tumours, gigantism,  
CC psoriasis, atherosclerosis, smooth muscle restenosis of blood vessels and

CC inappropriate microvascular proliferation. The composition may also have  
 CC gene therapy applications. The current sequence is that of the human  
 CC 15H12/19D12 heavy chain B (HCB) framework region peptide of the  
 CC invention.

XX  
 SQ Sequence 11 AA;

Query Match 100.0%; Score 59; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.011;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVVSS 11  
 |||||  
 Db 1 WGGGTTTVVSS 11

RESULT 15

ADQ90791  
 ID ADQ90791 standard; protein; 11 AA.

AC ADQ90791;

XX  
 DT 07-OCT-2004 (first entry)

XX Artificially deimmunised framework sequence #14.

XX insulin-related disorder; prostate specific membrane antigen; PSMA;  
 XX obesity; hyperglycaemia; hypoglycaemia; hyperinsulinaemia;  
 XX insulin-resistance; impaired glucose tolerance; impaired fasting glucose;  
 XX Type 1 diabetes mellitus; Type 2 diabetes mellitus; gestational diabetes.  
 OS Synthetic.

XX US2004136998-A1.

XX PD 15-JUL-2004.

XX PF 17-OCT-2003; 2003US-00688015.

XX PR 30-OCT-2002; 2002US-0422396P.

XX PA (BAND/) BANDER N H.

XX PI Bander NH;

XX DR WPI; 2004-533338/51.

XX Use of anti-prostate specific membrane antigen antibodies for treating or  
 PT preventing insulin-related disorders, e.g. obesity, hyperglycemia,  
 PT hypoglycemia, hyperinsulinemia, insulin-resistance, or Type 1 or 2  
 PT diabetes mellitus.

XX Disclosure; SEQ ID NO 40; 89pp; English.

XX The invention relates to a method of treating or preventing an insulin-  
 CC related disorder in a subject which comprises administering an antibody  
 CC or its antigen-binding portion specific for prostate specific membrane  
 CC antigen (PSMA). The method is useful for treating an insulin-related  
 CC disorder, including obesity, hyperglycaemia, hypoglycaemia,  
 CC hyperinsulinaemia, insulin-resistance, impaired glucose tolerance,  
 CC impaired fasting glucose, Type 1 diabetes mellitus, Type 2 diabetes  
 CC mellitus, and gestational diabetes. The present sequence represents an  
 CC artificially deimmunised framework sequence.

XX SQ Sequence 11 AA;

Query Match 100.0%; Score 59; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.011;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVVSS 11  
 |||||  
 Db 1 WGGGTTTVVSS 11

Search completed: December 4, 2005, 04:45:01  
 Job time : 97.5625 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 4, 2005, 04:31:45 ; Search time 15.5833 Seconds  
(without alignment)  
67.918 Million cell updates/sec

Title: US-10-632-706-198  
Perfect score: 59  
Sequence: 1 WGGGTTTVSS 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	74	2 S26793	Ig heavy chain V r
2	59	100.0	110	2 PH1655	Ig heavy chain V r
3	59	100.0	113	2 S55533	Ig heavy chain V r
4	59	100.0	113	2 S55535	Ig heavy chain V r
5	59	100.0	113	2 S55530	Ig heavy chain V r
6	59	100.0	113	2 S55534	Ig heavy chain V r
7	59	100.0	113	2 S55528	Ig heavy chain V r
8	59	100.0	113	2 S55532	Ig heavy chain V r
9	59	100.0	113	2 S55531	Ig heavy chain V r
10	59	100.0	114	2 S46392	Ig heavy chain V r
11	59	100.0	114	2 S20707	Ig heavy chain V r
12	59	100.0	115	2 S20706	Ig heavy chain V r
13	59	100.0	116	2 S15672	Ig heavy chain V r
14	59	100.0	116	2 S55542	Ig heavy chain V r
15	59	100.0	117	2 S55541	Ig heavy chain V r
16	59	100.0	118	2 PH1666	Ig heavy chain V r
17	59	100.0	118	2 PH1660	Ig heavy chain V r
18	59	100.0	118	2 S32786	Ig heavy chain V r
19	59	100.0	119	2 PH0961	Ig heavy chain (an
20	59	100.0	120	2 PH1650	Ig heavy chain V r
21	59	100.0	120	2 B49590	Ig heavy chain V r
22	59	100.0	120	2 PD0008	Ig heavy chain V r
23	59	100.0	120	2 S55538	Ig heavy chain V r
24	59	100.0	120	2 S55539	Ig heavy chain V r
25	59	100.0	120	2 S55537	Ig heavy chain V r
26	59	100.0	120	2 S55536	Ig heavy chain V r
27	59	100.0	120	2 S12953	Ig heavy chain V r
28	59	100.0	121	2 S31106	Ig heavy chain - h
29	59	100.0	121	2 S55540	Ig heavy chain V r

30	59	100.0	122	2 E36005	Ig heavy chain V r
31	59	100.0	122	2 PH0958	Ig heavy chain V r
32	59	100.0	123	2 S26794	Ig heavy chain V r
33	59	100.0	124	2 S20775	Ig heavy chain V r
34	59	100.0	125	2 S37455	Ig mu chain - huma
35	59	100.0	125	2 S24686	Ig heavy chain V6
36	59	100.0	127	2 S56213	Ig heavy chain V r
37	59	100.0	127	2 S24689	Ig heavy chain V6
38	59	100.0	128	2 S48797	Ig heavy chain V r
39	59	100.0	131	2 S66537	Ig heavy chain V r
40	59	100.0	132	2 PH0954	Ig heavy chain V r
41	59	100.0	133	2 C33548	Ig heavy chain V-1
42	59	100.0	135	2 B32274	Ig heavy chain pre
43	59	100.0	135	2 S78051	Ig heavy chain pre
44	59	100.0	136	2 PH0960	Ig heavy chain V r
45	59	100.0	137	2 S31676	Ig heavy chain V r

## ALIGNMENTS

RESULT 1  
S26793  
Ig heavy chain V region - human  
C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Jun-2000  
C/Accession: S26793  
R/Morlat, F.; Newcom, J.A.; Wang, J.Y.; Schroeder Jr., H.W.  
Eur. J. Immunol. 22, 241-245, 1992  
A/Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene fam1  
A/Reference number: S26786; MUID:92111632; PMID:1730251  
A/Accession: S26793  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-74 <MOR>  
A/Cross-references: UNIPARC:UPI000115FCA; EMBL:X61019; NID:932787; PIDN:CAA43353.1; PID  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin

Query Match 100.0%; Score 59; DB 2; Length 74;  
Best Local Similarity 100.0%; Pred. No. 0.0021;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11  
|||||||  
DB 64 WGGGTTTVSS 74

## RESULT 2

PH1655  
Ig heavy chain V region (clone 2E8) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 16-Aug-1996  
C/Accession: PH1655  
R/Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Saseo, E.H.  
J. Exp. Med. 178, 331-336, 1993  
A/Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphyloc  
A/Reference number: PH1642; MUID:93301610; PMID:8315388  
A/Accession: PH1655  
A/Molecule type: mRNA  
A/Residues: 1-110 <HIL>  
A/Cross-references: UNIPARC:UPI000176BDC  
A/Experimental source: B cell  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F/7-90/Domain: immunoglobulin homology <IMW>

Query Match 100.0%; Score 59; DB 2; Length 110;  
Best Local Similarity 100.0%; Pred. No. 0.0032;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11  
|||||||

Db 100 WGGGTTTVSS 110

## RESULT 3

S55533

Ig heavy chain V region pe25 - mouse (fragment)  
C:Species: Mus musculus (house mouse)

CjDate: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 21-Jan-2000

CjAccession: S55533

RjBoettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.

J. Mol. Biol. 247, 932-946, 1995

AjTitle: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using  
A:Reference number: S55528; MUID:95239763; PMID:7536850

A:Accession: S55533

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-113 &lt;BOB&gt;

AjCross-references: UNIPARC:UPI0000116205; EMBL:X82594; NID:9854314; PIDN:CAA57930.1; PI

CjSuperfamily: immunoglobulin V region; immunoglobulin homology

CjKeywords: heterotrimer; immunoglobulin

Fj14-97/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 113;

Best Local Similarity 100.0%; Pred. No. 0.0033;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVSS 11

Db 103 WGGGTTTVSS 113

## RESULT 4

S55535

Ig heavy chain V region pe23 - mouse (fragment)  
C:Species: Mus musculus (house mouse)

CjDate: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 21-Jan-2000

CjAccession: S55535

RjBoettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.

J. Mol. Biol. 247, 932-946, 1995

AjTitle: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using  
A:Reference number: S55528; MUID:95239763; PMID:7536850

A:Accession: S55535

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-113 &lt;BOB&gt;

AjCross-references: UNIPARC:UPI0000116203; EMBL:X82592; NID:9854310; PIDN:CAA57928.1; PI

CjSuperfamily: immunoglobulin V region; immunoglobulin homology

CjKeywords: heterotrimer; immunoglobulin

Fj14-97/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 113;

Best Local Similarity 100.0%; Pred. No. 0.0033;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVSS 11

Db 103 WGGGTTTVSS 113

## RESULT 5

S55530

Ig heavy chain V region pe17 - mouse (fragment)  
C:Species: Mus musculus (house mouse)

CjDate: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 21-Jan-2000

CjAccession: S55530

RjBoettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.

J. Mol. Biol. 247, 932-946, 1995

AjTitle: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using  
A:Reference number: S55528; MUID:95239763; PMID:7536850

A:Accession: S55530

A:Status: preliminary  
A:Molecule type: mRNA

A:Residues: 1-113 <BOB>

AjCross-references: UNIPARC:UPI00001161FP; EMBL:X82586; NID:9854296; PIDN:CAA57922.1; PI

CjSuperfamily: immunoglobulin V region; immunoglobulin homology

CjKeywords: heterotrimer; immunoglobulin

Fj14-97/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 113;

Best Local Similarity 100.0%; Pred. No. 0.0033;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVSS 11

Db 103 WGGGTTTVSS 113

## RESULT 6

S55534

Ig heavy chain V region pe15 - mouse (fragment)  
C:Species: Mus musculus (house mouse)

CjDate: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 21-Jan-2000

CjAccession: S55534

RjBoettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.

J. Mol. Biol. 247, 932-946, 1995

AjTitle: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using  
A:Reference number: S55528; MUID:95239763; PMID:7536850

A:Accession: S55534

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-113 &lt;BOB&gt;

AjCross-references: UNIPARC:UPI00001161FC; EMBL:X82584; NID:9854292; PIDN:CAA57920.1; PI

CjSuperfamily: immunoglobulin V region; immunoglobulin homology

CjKeywords: heterotrimer; immunoglobulin

Fj14-97/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 113;

Best Local Similarity 100.0%; Pred. No. 0.0033;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVSS 11

Db 103 WGGGTTTVSS 113

## RESULT 7

S55528

Ig heavy chain V region (pe16/pe14) - mouse (fragment)  
C:Species: Mus musculus (house mouse)

CjDate: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 21-Jan-2000

CjAccession: S55528

RjBoettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.

J. Mol. Biol. 247, 932-946, 1995

AjTitle: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using  
A:Reference number: S55528; MUID:95239763; PMID:7536850

A:Accession: S55528

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-113 &lt;BOB&gt;

AjCross-references: UNIPARC:UPI00001161FB; EMBL:X82585; NID:9854294; PIDN:CAA57921.1; PI

CjSuperfamily: immunoglobulin V region; immunoglobulin homology

CjKeywords: heterotrimer; immunoglobulin

Fj14-97/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 113;

Best Local Similarity 100.0%; Pred. No. 0.0033;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVSS 11

Db 103 WGGGTTTVSS 113

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTVTYSS 11  
|||||

Db 103 WGGGTTVTYSS 113

## RESULT 8

S55532

Ig heavy chain V region pe19 - mouse (fragment)

C:Species: Mus musculus (house mouse)

C&gt;Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 21-Jan-2000

C:Accession: S55532

R:Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.

J. Mol. Biol. 247, 932-946, 1995

A:Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using

A:Reference number: S55528; PMID:95239763; PMID:7536850

A:Accession: S55532

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-113 &lt;BOE&gt;

C:Cross-references: UNIPARC:UPI00001161PF; EMBL:X82588; NID:9854300; PIDN:CAA57924.1; PI

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:14-97/Domain: immunoglobulin homology &lt;IMM&gt;

## Query Match

Best Local Similarity 100.0%; Score 59; DB 2; Length 113;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTVTYSS 11  
|||||

Db 103 WGGGTTVTYSS 113

## RESULT 9

S55531

Ig heavy chain V region pe18 - mouse (fragment)

C:Species: Mus musculus (house mouse)

C&gt;Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 21-Jan-2000

C:Accession: S55531

R:Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.

J. Mol. Biol. 247, 932-946, 1995

A:Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using

A:Reference number: S55528; PMID:95239763; PMID:7536850

A:Accession: S55531

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-113 &lt;BOE&gt;

C:Cross-references: UNIPARC:UPI00001161FE; EMBL:X82587; NID:9854298; PIDN:CAA57923.1; PI

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:14-97/Domain: immunoglobulin homology &lt;IMM&gt;

## Query Match

Best Local Similarity 100.0%; Score 59; DB 2; Length 113;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTVTYSS 11  
|||||

Db 103 WGGGTTVTYSS 113

## RESULT 10

S46392

Ig heavy chain V region (VH-28) - human

C:Species: Homo sapiens (man)

C&gt;Date: 27-Jan-1995 #sequence\_revision 27-Jan-1995 #text\_change 20-Jun-2000

C:Accession: S46392

R:Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.

J. Mol. Biol. 239, 66-78, 1994

A:Title: In vitro assembly of repertoires of antibody chains on the surface of phage by

A:Reference number: S46390; PMID:94254092; PMID:8196048

A:Accession: S46392

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-114 &lt;FIG&gt;

C:Cross-references: UNIPARC:UPI00001137D6; EMBL:Z31688; NID:9499306; PIDN:CAA83493.1; PI

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:15-98/Domain: immunoglobulin homology &lt;IMM&gt;

## Query Match

Best Local Similarity 100.0%; Score 59; DB 2; Length 114;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTVTYSS 11  
|||||

Db 104 WGGGTTVTYSS 114

## RESULT 11

S20707

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C&gt;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jan-2000

C:Accession: S20707

R:Brennan, D.M.; Hinds, M.G.; Welsh, J.H.; Tempest, P.R.; Harris, W.J.; Carr, F.J.; Oeb

submitted to the EMBL Data Library, April 1992

A:Description: Binding specificity and variable region sequences of two monoclonal anti

A:Reference number: S20706

A:Accession: S20707

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-114 &lt;BRE&gt;

C:Cross-references: UNIPARC:UPI0000176B37; EMBL:Z11916

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:12-95/Domain: immunoglobulin homology &lt;IMM&gt;

## Query Match

Best Local Similarity 100.0%; Score 59; DB 2; Length 114;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTVTYSS 11  
|||||

Db 104 WGGGTTVTYSS 114

## RESULT 12

S20706

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C&gt;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004

C:Accession: S20706

R:Brennan, D.M.; Hinds, M.G.; Welsh, J.H.; Tempest, P.R.; Harris, W.J.; Carr, F.J.; Oeb

submitted to the EMBL Data Library, April 1992

A:Description: Binding specificity and variable region sequences of two monoclonal anti

A:Reference number: S20706

A:Accession: S20706

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-115 &lt;BRE&gt;

C:Cross-references: UNIPARC:Q8R3V9; UNIPARC:UPI0000176C45; EMBL:Z11914

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:12-97/Domain: immunoglobulin homology &lt;IMM&gt;

## Query Match

Best Local Similarity 100.0%; Score 59; DB 2; Length 115;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTVTYSS 11  
|||||

DB 105 WCGTTVTSS 115

## RESULT 13

IG heavy chain V region - mouse (fragment)  
S15672  
C:Species: Mus musculus (house mouse)  
C:Date: 18-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000  
C:Accession: S15672  
R:Tempest, P.R.; Bremner, P.; Lambert, M.; Taylor, G.; Furze, J.M.; Carr, F.J.; Harris, B.O./Technology 9, 266-271, 1991  
A:Title: Reshaping a human monoclonal antibody to inhibit human respiratory syncytial virus  
A:Reference number: S15672; MUID:91337412; PMID:1367535  
A:Accession: S15672  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-116 <TM>  
A:Cross-references: UNIPARC:UPI0000115F4C; EMBL:X58835; NID:G51978; PIDN:CAA41644.1; PID  
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
C:Keywords: heterotetramer; Immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 116;  
Best Local Similarity 100.0%; Pred. No. 0.0033;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGTTVTSS 11  
|||||  
DB 106 WCGTTVTSS 116

## RESULT 14

S55542  
IG heavy chain V region pa2 - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S55542  
R:Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.  
J. Mol. Biol. 247, 932-946, 1995  
A:Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using  
variations in the variable region genes.  
A:Reference number: S55528; MUID:95239763; PMID:7536850  
A:Accession: S55542  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-116 <BO>  
A:Cross-references: UNIPARC:UPI00001161F9; EMBL:X82581; NID:G854302; PIDN:CAA57917.1; PI  
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
C:Keywords: heterotetramer; Immunoglobulin  
F:14-97/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 116;  
Best Local Similarity 100.0%; Pred. No. 0.0033;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGTTVTSS 11  
|||||  
DB 106 WCGTTVTSS 116

## RESULT 15

S55541  
IG heavy chain V region pa1 - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S55541  
R:Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.  
J. Mol. Biol. 247, 932-946, 1995  
A:Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using  
variations in the variable region genes.  
A:Reference number: S55528; MUID:95239763; PMID:7536850  
A:Accession: S55541  
A:Status: preliminary

A:Molecule type: mRNA  
A:Residues: 1-117 <BO>  
A:Cross-references: UNIPARC:UPI00001161F8; EMBL:X82580; NID:G854286; PIDN:CAA57916.1; PI  
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
C:Keywords: heterotetramer; Immunoglobulin  
F:14-97/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 117;  
Best Local Similarity 100.0%; Pred. No. 0.0034;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGTTVTSS 11  
|||||  
DB 107 WCGTTVTSS 117

Search completed: December 4, 2005, 04:53:46  
Job time : 15.5833 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:31:36 ; Search time 100.375 Seconds  
(without alignment)  
77.318 Million cell updates/sec

Title: US-10-632-706-198  
Perfect score: 59  
Sequence: 1 MGCGTTVTWSS 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : uniprot\_05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	119	2 Q9GYZ2_MOUSE	Q9GYZ2 mus musculus
2	59	100.0	121	2 Q8CGS2_MOUSE	Q8CGS2 mus musculus
3	59	100.0	146	1 HV21_HUMAN	P06331 homo sapien
4	59	100.0	147	1 HV1C_HUMAN	P01744 homo sapien
5	59	100.0	147	2 Q925S3_MOUSE	Q925S3 mus musculus
6	59	100.0	159	2 Q968S0_HUMAN	Q968S0 homo sapien
7	59	100.0	170	2 Q925S2_MOUSE	Q925S2 mus musculus
8	59	100.0	218	2 Q925S1_MOUSE	Q925S1 mus musculus
9	59	100.0	241	2 Q921A6_MOUSE	Q921A6 mus musculus
10	59	100.0	348	2 Q6PYX1_HUMAN	Q6PYX1 homo sapien
11	59	100.0	416	2 Q9NBP6_HUMAN	Q9NBP6 homo sapien
12	59	100.0	472	2 Q6N089_HUMAN	Q6N089 homo sapien
13	59	100.0	573	2 Q8W038_HUMAN	Q8W038 homo sapien
14	59	100.0	576	2 Q6P418_HUMAN	Q6P418 homo sapien
15	59	100.0	595	2 Q8WUX4_HUMAN	Q8WUX4 homo sapien
16	59	100.0	597	2 Q9BUI1_HUMAN	Q9BUI1 homo sapien
17	59	100.0	597	2 Q9BOB8_HUMAN	Q9BOB8 homo sapien
18	59	100.0	597	2 Q6GKX5_HUMAN	Q6GKX5 homo sapien
19	59	100.0	606	2 Q6GMT2_HUMAN	Q6GMT2 homo sapien
20	59	100.0	625	2 Q96A66_HUMAN	Q96A66 homo sapien
21	58	98.3	465	2 Q6PJB2_MOUSE	Q6PJB2 mus musculus
22	58	98.3	468	2 Q6P9W9_MOUSE	Q6P9W9 mus musculus
23	58	98.3	468	2 Q505N9_MOUSE	Q505N9 mus musculus
24	58	98.3	471	2 Q6K044_MOUSE	Q6K044 mus musculus
25	58	98.3	472	2 Q6PJA7_MOUSE	Q6PJA7 mus musculus
26	58	98.3	473	2 Q91205_MOUSE	Q91205 mus musculus
27	58	98.3	476	2 Q569X1_MOUSE	Q569X1 mus musculus
28	58	98.3	477	2 Q58B56_MOUSE	Q58B56 mus musculus
29	58	98.3	486	2 Q91207_MOUSE	Q91207 mus musculus
30	58	98.3	487	2 Q99KA4_MOUSE	Q99KA4 mus musculus
31	56	94.9	109	2 Q9JL75_MOUSE	Q9JL75 mus musculus

32	56	94.9	111	1 HV35_MOUSE	P01804 mus musculus
33	56	94.9	114	2 Q9JL81_MOUSE	Q9JL81 mus musculus
34	56	94.9	117	2 Q9QXFO_MOUSE	Q9QXFO mus musculus
35	56	94.9	118	1 HV39_MOUSE	P01809 mus musculus
36	56	94.9	118	2 Q921C4_MOUSE	Q921C4 mus musculus
37	56	94.9	120	1 HV03_MOUSE	P01747 mus musculus
38	56	94.9	121	1 HV01_MOUSE	P01745 mus musculus
39	56	94.9	134	2 Q65ZF6_MOUSE	Q65ZF6 mus musculus
40	56	94.9	136	1 HV15_MOUSE	P01759 mus musculus
41	56	94.9	137	1 HV46_MOUSE	P01755 mus musculus
42	56	94.9	137	1 HV46_MOUSE	P01822 mus musculus
43	56	94.9	137	2 Q924R6_MOUSE	Q924R6 mus musculus
44	56	94.9	139	1 HV07_MOUSE	P01751 mus musculus
45	56	94.9	140	2 Q924F8_MOUSE	Q924F8 mus musculus

## ALIGNMENTS

```

RESULT 1
Q9GYZ2_MOUSE
AC Q9GYZ2_MOUSE PRELIMINARY; PRT; 119 AA.
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Monoclonal anti-idiotypic Schistosoma japonicum antibody NP30 heavy
DE chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Song X.T., Feng Z.Q., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the heavy chain
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT Schistosoma japonicum."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF282622; AAG01452.1; -, mRNA.
DR HSSP; P01751; 1A6W.
DR SMR; Q9GYZ2; 1-119.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IG_V.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER
FT NON_TER
FT NON_TER
SQ SEQUENCE 119 AA; 13567 MW; BA893873F05FA6AB CRC64;

Query Match 100.0%; Score 59; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGCGTTVTWSS 11
Db 109 MGCGTTVTWSS 119

RESULT 2
Q8CGS2_MOUSE
ID Q8CGS2_MOUSE PRELIMINARY; PRT; 121 AA.
AC Q8CGS2;
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Anti-deoxythymineol scfv lambda heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.

```

OK NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN-BALB/C;  
RA Wang Z., Munshi K., Osawa F., Pescka J.J., Hart L.P.,  
RL Submitted (SEP-2002) to the EMBL/GenBank/DBD databases.  
DR EMBL; AY151140; AAN7452.1; -, mRNA.  
DR HSSP; P01751; INOB.  
DR Ensembl; ENSMUSG00000021155; Mus musculus.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 121  
SQ SEQUENCE 121 AA; 13475 MW; 84FE6CFA8053F5D6 CRC64;  
  
Query Match 100.0%; Score 59; DB 2; Length 121;  
Best Local Similarity 100.0%; Pred. No. 0.0054;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 WGGGTTVTSS 11  
DB 111 WGGGTTVTSS 121  
  
RESULT 3  
HY2I\_HUMAN STANDARD; PRT; 146 AA.  
AC P06331;  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DS Ig heavy chain V-II region ARH-77 precursor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=8520532; PubMed=3922855; DOI=10.1016/0378-1119(85)90092-7;  
RA Kudo A., Ishihara T., Nishimura Y., Watanabe T.;  
RT "A cloned human immunoglobulin heavy chain gene with a novel direct-  
RT repeat sequence in 5' flanking region.";  
RL Gene 33:181-189 (1985).  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC PIR; A02101; G1H0H2.  
DR HSSP; P01825; 7FAB.  
DR SMR; P06331; 21-146.  
DR GO; GO:0005576; C:extracellular region; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin domain; Immunoglobulin V region; Signal.  
FT SIGNAL 1  
FT CHAIN 19  
FT CHAIN 20  
FT REGION 20 146 Ig heavy chain V-II region ARH-77.  
FT REGION 118 127 D segment.  
FT REGION 128 146 J segment.  
FT DISULFID 42 115 By similarity.  
FT NON\_TER 146  
SQ SEQUENCE 146 AA; 16228 MW; 8D7FD52B8218171F CRC64;

Query Match 100.0%; Score 59; DB 1; Length 146;  
Best Local Similarity 100.0%; Pred. No. 0.0066;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 WGGGTTVTSS 11  
DB 136 WGGGTTVTSS 146  
  
RESULT 4  
HY1C\_HUMAN STANDARD; PRT; 147 AA.  
ID HY1C\_HUMAN STANDARD; PRT; 147 AA.  
AC P01744;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DS Ig heavy chain V-I region ND precursor (fragments).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=83065234; PubMed=6815656;  
RA Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,  
RA Bell L.O., Gould H.J.;  
RT "Cloning and sequence determination of the gene for the human  
RT immunoglobulin epsilon chain expressed in a myeloma cell line.";  
RT Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665 (1982).  
RN [2]  
RP PROTEIN SEQUENCE OF 20-147.  
RA Benrich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;  
RL (in) Bach M.K. (eds.);  
RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,  
RL Marcel Dekker, New York (1978).  
RL -1- MISCELLANEOUS: This epsilon chain was isolated from a myeloma  
CC protein.  
CC -----  
CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC HSSP; P01751; INOB.  
DR GO; GO:0005576; C:extracellular region; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Direct protein sequencing; Immunoglobulin domain;  
KW Immunoglobulin V region; Pyroglutamate carboxylic acid; Signal.  
FT SIGNAL 1  
FT CHAIN 19  
FT CHAIN 20 147 Ig heavy chain V-I region ND.  
FT DOMAIN 20 131 Ig-like.  
FT MOD\_RES 20 20 Pyroglutamate carboxylic acid.  
FT DISULFID 41 115  
FT CONFLICT 21 21 T -> V (in Ref. 2).  
FT CONFLICT 53 54 IH -> HI (in Ref. 2).  
FT CONFLICT 67 68 VG -> GV (in Ref. 2).  
FT CONFLICT 125 125 Missing (in Ref. 2).  
FT NON\_TER 147  
FT NON\_TER 147  
SQ SEQUENCE 147 AA; 16496 MW; 948F9F72A536C20 CRC64;  
  
Query Match 100.0%; Score 59; DB 1; Length 147;  
Best Local Similarity 100.0%; Pred. No. 0.0067;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 WGGGTTVTSS 11

Db 137 WGGGTTTVSS 147

## RESULT 5

Q925S3\_MOUSE PRELIMINARY; PRT; 147 AA.

AC Q925S3; 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

MRP3

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

NCBI\_TaxID=10090;

OX [1]

NP NUCLEOTIDE SEQUENCE.

RC STRAIN=BALB/c;

RX PubMed=11819679;

RA Cui D.X., Zeng G.Y., Wang F., Xu J.R., Ren D.Q., Guo Y.H., Tian F.R.,

Yan X.J., Hou Y., Su C.Z.;

RT "Mechanism of exogenous nucleic acids and their precursors improving

the repair of intestinal epithelium after gamma-irradiation in mice.,"

World J. Gastroenterol. 6:709-717(2000).

RL [2]

RN NUCLEOTIDE SEQUENCE.

RP STRAIN=BALB/c;

RC Cui D., Zeng G., Yan X., Li X., Su C.;

RT "Cloning of mouse genes related to repairing of intestinal epithelium

of the irradiated mice by treatment with the intestinal RNA of mice of

the same strain."

Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).

DR EMBL; AF240166; AKK43731.1; -; mRNA.

DR HSSP; P01751; 1A6W.

DR SMR; Q925S3; 3-139.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig\_v.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG LIKE; 1.

KW Immunoglobulin domain.

SQ SEQUENCE 147 AA; 16274 MW; 800594A12B97191F CRC64;

QY

1 WGGGTTTVSS 11

Db 111 WGGGTTTVSS 121

## RESULT 6

Q96QSO\_HUMAN

ID Q96QSO\_MOUSE PRELIMINARY; PRT; 159 AA.

AC Q96QSO; 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Putative matrix cell adhesion molecule-3.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;

OC Homo

NCBI\_TaxID=9606;

OX [1]

NP NUCLEOTIDE SEQUENCE.

RP TILSON M.D.;

RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY339025; AAK82649.1; -; mRNA.

DR HSSP; P01869; 1A66.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; IG\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin domain.  
SQ SEQUENCE 159 AA; 17497 MW; 5D29537E881FAF02 CRC64;

Query Match 100.0%; Score 59; DB 2; Length 159;  
Best Local Similarity 100.0%; Pred. No. 0.0073;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11  
Db 139 WGGGTTTVSS 149

## RESULT 7

Q925S2\_MOUSE PRELIMINARY; PRT; 170 AA.

AC Q925S2; 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

MRP4.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

NCBI\_TaxID=10090;

OX [1]

NP NUCLEOTIDE SEQUENCE.

RC STRAIN=BALB/c;

RX PubMed=11819679;

RA Cui D.X., Zeng G.Y., Wang F., Xu J.R., Ren D.Q., Guo Y.H., Tian F.R.,

Yan X.J., Hou Y., Su C.Z.;

RT "Mechanism of exogenous nucleic acids and their precursors improving

the repair of intestinal epithelium after gamma-irradiation in mice.,"

World J. Gastroenterol. 6:709-717(2000).

RL [2]

RN NUCLEOTIDE SEQUENCE.

RP STRAIN=BALB/c;

RC Cui D., Zeng G., Yan X., Li X., Su C.;

RT "Cloning of mouse genes related to repairing of intestinal epithelium

of the irradiated mice by treatment with the intestinal RNA of mice of

the same strain."

Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).

DR EMBL; AF240167; AAK43732.1; -; mRNA.

DR HSSP; P01751; 1A6W.

DR SMR; Q925S2; 3-124.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig\_v.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG LIKE; 1.

KW Immunoglobulin domain.

SQ SEQUENCE 170 AA; 17978 MW; 5042823CC6C10F38 CRC64;

Query Match 100.0%; Score 59; DB 2; Length 170;  
Best Local Similarity 100.0%; Pred. No. 0.0078;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11  
Db 113 WGGGTTTVSS 123

## RESULT 8

Q925S1\_MOUSE PRELIMINARY; PRT; 218 AA.

AC Q925S1; 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

MRP5 (Fragment).

OS Mus musculus (Mouse).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c;
RX PubMed=11819679;
RA Cui D.X., Zeng G.Y., Wang F., Xu J.R., Ren D.Q., Guo Y.H., Tian P.R.,
RT "Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after gamma-irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
[2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
RT of the irradiated mice by treatment with the intestinal RNA of mice of
RT the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR HSPF; P01665; 1QNZ.
DR Ensembl; ENSMUSG0000058040; Mus musculus.
DR InterPro; IPR007110; IG_1like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER
SQ SEQUENCE 218 AA; 23013 MW; 527E4FA8F7982817 CRC64;

Query Match
Best Local Similarity 100.0%; Score 59; DB 2; Length 218;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVVSS 11
DB 110 WGGGTTTVVSS 120

RESULT 9
Q921A6_MOUSE
ID Q921A6_MOUSE PRELIMINARY; PRT; 241 AA.
AC Q921A6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-CEA 79 single chain Fv (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98170165; PubMed=9509426;
RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
RT "Cloning and characterization of cDNAs encoding VH and VL of a
RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RT generation of a single-chain Fv molecule (scFv).";
RL Mol. Cells 7:816-819(1997).
[2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=9141421; PubMed=1908510; DOI=10.1084/jem.174.3.613;
RA Stark S.E., Caton A.J.;
RT "Antibodies that are specific for a single amino acid interchange in a
RT protein epitope use structurally distinct variable regions.";
RL J. Exp. Med. 174:613-624(1991)
EMBL; U8067; AAA8044.1; -; mRNA.
DR PIR; S1965; S1965.
DR PIR; S1967; S1967.
DR PIR; S1968; S1968.

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DR PIR; S26325; S26325.
DR HSPF; P01607; 1BMW.
DR Ensembl; ENSMUSG00000021155; Mus musculus.
DR InterPro; IPR007110; IG_1like.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS00835; IG_LIKE; 2.
FT NON_TER
SQ SEQUENCE 241 AA; 26086 MW; 0276887248B9C771 CRC64;

Query Match
Best Local Similarity 100.0%; Score 59; DB 2; Length 241;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVVSS 11
DB 108 WGGGTTTVVSS 118

RESULT 10
Q6PYX1_HUMAN
ID Q6PYX1_HUMAN PRELIMINARY; PRT; 348 AA.
AC Q6PYX1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hepatitis B virus receptor binding protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
OX NCBI_TaxId=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Zhu N.S., Chen Y.Y.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY570731; AAS88328.1; -; mRNA.
DR PDB; 1T89; X-ray; A/B=-.
DR SMR; Q6PYX1; 3-348.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003066; IG_MHC.
DR Pfam; PF07654; C1-setc; 3.
DR SMART; SM00407; IGV; 3.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Receptor.
FT NON_TER
SQ SEQUENCE 348 AA; 38162 MW; DD96C3D7E0B5E845 CRC64;

Query Match
Best Local Similarity 100.0%; Score 59; DB 2; Length 348;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVVSS 11
DB 8 WGGGTTTVVSS 18

RESULT 11
Q9NPP6_HUMAN
ID Q9NPP6_HUMAN PRELIMINARY; PRT; 416 AA.
AC Q9NPP6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Immunoglobulin heavy chain variant (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.

```

```

OX NCBI_TaxID=9606;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RA Auffray C., Anseorge W., Ballabio A., Estivill X., Gibson K.,
RA Lehrach H., Poustka A., Lundeberg J.
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Pluvinet R., Estivill X., Escarceller M., Sumoy L.
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL389978; CAB97534.1; -; mRNA.
DR HSSP; P01876; 10M0.
DR SMR; Q9NPPE; 186-394.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
FT NON TER 1
SQ SEQUENCE 416 AA; 44786 MW; 8C41708B8AB4687 CRC64;

Query Match 100.0%; Score 59; DB 2; Length 416;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTVTYSS 11
DB 66 WGGGTTVTYSS 76

RESULT 12
Q6N089_HUMAN PRELIMINARY; PRT; 472 AA.
ID Q6N089_HUMAN
AC Q6N089;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686P15220.
GN Name=DKFZp686P15220;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
OX NCBI_TaxID=9606;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Rectum tumor;
RA The German cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Oeanger A.,
RA Fobio G., Han M., Wiemann S.
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640627; CAE45781.1; -; mRNA.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
DR Hypothetical protein.
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 100.0%; Score 59; DB 2; Length 472;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 1 WGGGTTVTYSS 11
DB 132 WGGGTTVTYSS 142

RESULT 13
Q8WU38_HUMAN PRELIMINARY; PRT; 573 AA.
ID Q8WU38_HUMAN
AC Q8WU38;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGH domain protein.
GN Name=IGH;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
OX NCBI_TaxID=9606;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klaunder R.D., Collins F.S., Zeeberg B., Bueltow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.U., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huij S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN (2)
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RA Director MGC Project;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN (3)
RP PROTEIN SEQUENCE.
RX PubMed=1555592;
RA Makiya R., Stigbrand T.
RT "Placental alkaline phosphatase has a binding site for the human
RT immunoglobulin-G Fc portion."
RL Eur. J. Biochem. 205:341-345 (1992).
DR EMBL; BC021276; AAH21276.1; -; mRNA.
DR PIR; S21205; S21205.
DR PIR; S30532; S30532.
DR HSSP; P18529; 118K.
DR InterPro; ENSG00000196122; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
DR Immunoglobulin domain. Repeat.
SQ SEQUENCE 573 AA; 62967 MW; FD072344033AC530 CRC64;
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Query Match 100.0%; Score 59; DB 2; Length 595;  
Best Local Similarity 100.0%; Pred. No. 0.032;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGQGTTVTVSS 11  
|||  
Db 141 MGQGTTVTVSS 151

Search completed: December 4, 2005, 04:52:27  
Job time : 102.375 secs

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## OM protein - protein search, using sw model

Run on: December 4, 2005, 03:59:51 ; Search time 23.6042 Seconds  
(without alignments)  
38.528 Million cell updates/sec

Title: US-10-632-706-198

Perfect score: 59

Sequence: 1 WGGQTTVVSS 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

572060

Minimum DB seq length: 0  
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/iaa/5-COMB.pep:\*  
2: /cgn2\_6/prodata/1/iaa/6-COMB.pep:\*  
3: /cgn2\_6/prodata/1/iaa/H-COMB.pep:\*  
4: /cgn2\_6/prodata/1/iaa/PCTUS-COMB.pep:\*  
5: /cgn2\_6/prodata/1/iaa/RE-COMB.pep:\*  
6: /cgn2\_6/prodata/1/iaa/backfillset1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	11	1	US-08-471-780C-120
2	59	100.0	11	1	US-08-467-282B-120
3	59	100.0	11	1	US-08-471-282A-120
4	59	100.0	11	1	US-08-318-157B-40
5	59	100.0	11	1	US-08-466-710C-120
6	59	100.0	11	2	US-08-468-739C-120
7	59	100.0	11	2	US-08-646-265A-114
8	59	100.0	11	2	US-08-646-265A-129
9	59	100.0	11	2	US-09-253-794-40
10	59	100.0	11	2	US-09-563-222C-146
11	59	100.0	11	2	US-09-563-222C-169
12	59	100.0	11	2	US-09-269-921-137
13	59	100.0	11	2	US-09-293-769A-120
14	59	100.0	13	6	5189147-14
15	59	100.0	15	1	US-08-765-179B-8
16	59	100.0	15	6	5189147-20
17	59	100.0	16	4	PCT-US91-02942-91
18	59	100.0	20	2	US-10-194-975-107
19	59	100.0	22	4	PCT-US91-02942-100
20	59	100.0	29	1	US-08-053-131-73
21	59	100.0	29	1	US-08-645-641-73
22	59	100.0	29	1	US-07-853-408B-73
23	59	100.0	29	1	US-08-096-762-73
24	59	100.0	29	1	US-08-308-865-73
25	59	100.0	29	2	US-09-042-353-270
26	59	100.0	29	2	US-08-758-417A-118
27	59	100.0	29	4	PCT-US92-10983-73

28	59	100.0	31	1	US-08-053-131-83	Sequence 83, App1
29	59	100.0	31	1	US-08-645-641-83	Sequence 83, App1
30	59	100.0	31	1	US-07-853-408B-83	Sequence 83, App1
31	59	100.0	31	1	US-08-096-762-83	Sequence 83, App1
32	59	100.0	31	1	US-08-308-865-83	Sequence 83, App1
33	59	100.0	31	2	US-09-042-353-280	Sequence 280, App
34	59	100.0	31	2	US-08-758-417A-128	Sequence 128, App
35	59	100.0	31	4	PCT-US92-10983-83	Sequence 83, App1
36	59	100.0	32	1	US-08-053-131-92	Sequence 92, App1
37	59	100.0	32	1	US-08-645-641-92	Sequence 92, App1
38	59	100.0	32	1	US-07-853-408B-92	Sequence 92, App1
39	59	100.0	32	1	US-08-096-762-92	Sequence 92, App1
40	59	100.0	32	1	US-08-308-865-92	Sequence 92, App1
41	59	100.0	32	2	US-09-042-353-289	Sequence 289, App
42	59	100.0	32	2	US-08-758-417A-137	Sequence 137, App
43	59	100.0	32	4	PCT-US92-10983-92	Sequence 92, App1
44	59	100.0	33	1	US-08-053-131-89	Sequence 89, App1
45	59	100.0	33	1	US-08-645-641-89	Sequence 89, App1

## ALIGNMENTS

RESULT 1  
US-08-471-780C-120  
; Sequence 120, Application US/08471780C  
; Patent No. 5759808  
; GENERAL INFORMATION:  
; APPLICANT: Casterman, Cecile  
; APPLICANT: Hamers, Raymond  
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains  
; NUMBER OF SEQUENCES: 130  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner  
; STREET: 1300 I Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/471,780C  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/106,944  
; FILING DATE: 17-AUG-1993  
; APPLICATION NUMBER: FR 92402326.0  
; FILING DATE: 21-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 93401310.3  
; FILING DATE: 21-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Potter, Jane E.R.  
; REGISTRATION NUMBER: 33,332  
; REFERENCE/DOCKET NUMBER: 04958-0008-00000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 120:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULAR TYPE: peptide  
US-08-471-780C-120  
Query Match 100.0%; Score 59; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0017;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 WGGGTTTVSS 11  
Db 1 WGGGTTTVSS 11

RESULT 2  
US-08-467-282B-120  
; Sequence 120, Application US/08467282B  
; Patent No. 5800988  
; GENERAL INFORMATION:  
; APPLICANT: Casterman, Cecile  
; APPLICANT: Hamers, Raymond  
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains  
; NUMBER OF SEQUENCES: 130  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner  
; STREET: 1300 I Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/467,282B  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/106,944  
; FILING DATE: 17-AUG-1993  
; APPLICATION NUMBER: FR 92402326.0  
; FILING DATE: 21-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 93401310.3  
; FILING DATE: 21-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Potier, Jane E.R.  
; REGISTRATION NUMBER: 33,332  
; REFERENCE/DOCKET NUMBER: 04958, 0008-00000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 120:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-467-282B-120

Query Match 100.0%; Score 59; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0017;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVSS 11  
Db 1 WGGGTTTVSS 11

RESULT 3  
US-08-471-282A-120  
; Sequence 120, Application US/08471282A  
; Patent No. 5840853  
; GENERAL INFORMATION:  
; APPLICANT: Casterman, Cecile  
; APPLICANT: Hamers, Raymond  
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains  
; NUMBER OF SEQUENCES: 130

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner  
; STREET: 1300 I Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/471,282A  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/106,944  
; FILING DATE: 17-AUG-1993  
; APPLICATION NUMBER: FR 92402326.0  
; FILING DATE: 21-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 93401310.3  
; FILING DATE: 21-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Potier, Jane E.R.  
; REGISTRATION NUMBER: 33,332  
; REFERENCE/DOCKET NUMBER: 04958, 0008-00000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 120:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-471-282A-120

Query Match 100.0%; Score 59; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0017;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVSS 11  
Db 1 WGGGTTTVSS 11

RESULT 4  
US-08-318-157B-40  
; Sequence 40, Application US/08318157B  
; Patent No. 5874540  
; GENERAL INFORMATION:  
; APPLICANT: HANSEN, Hans J.  
; APPLICANT: ARMOUR, Kathryn L.  
; TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CBA HUMANIZED  
; TITLE OF INVENTION: MOUSE MONOCLONAL ANTIBODIES  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/318,157B  
; FILING DATE: 05-OCT-1994

CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Saxe, Bernard D.  
REGISTRATION NUMBER: 28,665  
REFERENCE/DOCKET NUMBER: 18733/464  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-318-157B-40

Query Match 100.0%; Score 59; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0017;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGTTTVSS 11  
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Db 1 WGGTTTVSS 11

RESULT 5  
US-08-466-710C-120  
Sequence 120, Application US/08466710C  
Patent No. 5874541  
GENERAL INFORMATION:  
APPLICANT: Castelman, Cecile  
TITLE OF INVENTION: Immunoglobulins devoid of light chains  
NUMBER OF SEQUENCES: 130  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,710C  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/106,944  
FILING DATE: 17-AUG-1993  
APPLICATION NUMBER: FR 92402326.0  
FILING DATE: 21-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 93401310.3  
FILING DATE: 21-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Potier, Jane E.R.  
REGISTRATION NUMBER: 33,332  
REFERENCE/DOCKET NUMBER: 04958, 0008-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 120:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

US-08-466-710C-120

Query Match 100.0%; Score 59; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0017;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGTTTVSS 11  
|||  
Db 1 WGGTTTVSS 11

RESULT 6  
US-08-468-739C-120  
Sequence 120, Application US/08468739C  
Patent No. 6015695  
GENERAL INFORMATION:  
APPLICANT: Castelman, Cecile  
TITLE OF INVENTION: Immunoglobulins devoid of light chains  
NUMBER OF SEQUENCES: 130  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,739C  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/106,944  
FILING DATE: 17-AUG-1993  
APPLICATION NUMBER: FR 92402326.0  
FILING DATE: 21-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 93401310.3  
FILING DATE: 21-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Potier, Jane E.R.  
REGISTRATION NUMBER: 33,332  
REFERENCE/DOCKET NUMBER: 04958, 0008-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 120:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-468-739C-120

Query Match 100.0%; Score 59; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0017;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGTTTVSS 11  
|||  
Db 1 WGGTTTVSS 11

RESULT 7  
US-08-646-265A-114  
Sequence 114, Application US/08646265A  
Patent No. 6214973  
GENERAL INFORMATION:

APPLICANT: OHTOMO, Toshiniko  
APPLICANT: SATO, Koh  
APPLICANT: TSUCHIYA, Masayuki  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
NUMBER OF SEQUENCES: 132  
CORRESPONDENCE ADDRESS:  
ADDRESS: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,265A  
FILING DATE: 09-SEP-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/JP94/01763  
FILING DATE: 19-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-291078  
FILING DATE: 19-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/184  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 114:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-646-265A-114

Query Match 100.0%; Score 59; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0017;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11  
Db 1 WGGGTTTVSS 11

RESULT 8  
US-08-646-265A-129  
Sequence 129, Application US/08646265A  
Patent No. 6214973  
GENERAL INFORMATION:  
APPLICANT: OHTOMO, Toshiniko  
APPLICANT: SATO, Koh  
APPLICANT: TSUCHIYA, Masayuki  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
NUMBER OF SEQUENCES: 132  
CORRESPONDENCE ADDRESS:  
ADDRESS: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,265A  
FILING DATE: 09-SEP-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/JP94/01763  
FILING DATE: 19-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-291078  
FILING DATE: 19-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/184  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 129:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-646-265A-129

Query Match 100.0%; Score 59; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0017;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11  
Db 1 WGGGTTTVSS 11

RESULT 9  
US-09-253-794-40  
Sequence 40, Application US/09253794  
Patent No. 6676924  
GENERAL INFORMATION:  
APPLICANT: HANSEN, Hans J.  
TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESS: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/253,794  
FILING DATE: 22-Feb-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/318,157  
FILING DATE: 05-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: SAYE, Bernhard D.  
REGISTRATION NUMBER: 28,665  
REFERENCE/DOCKET NUMBER: 18733/464  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300

```

;
; TELEFAX: (202) 672-5399
;
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 11 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: <Unknown>
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-253-794-40

Query Match          100.0%; Score 59; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WGGGTTTVSS 11
      |||||
Db      1 WGGGTTTVSS 11

RESULT 10
US-09-563-222C-146
; Sequence 146, Application US/09563222C
; Patent No. 6696620
; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MITCH B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/09/563,222C
; CURRENT FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 146
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-563-222C-146

Query Match          100.0%; Score 59; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WGGGTTTVSS 11
      |||||
Db      1 WGGGTTTVSS 11

RESULT 11
US-09-563-222C-169
; Sequence 169, Application US/09563222C
; Patent No. 6696620
; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MITCH B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/09/563,222C
; CURRENT FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
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;
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-563-222C-169

Query Match          100.0%; Score 59; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WGGGTTTVSS 11
      |||||
Db      1 WGGGTTTVSS 11

RESULT 12
US-09-269-921-137
; Sequence 137, Application US/09269921
; Patent No. 6699974
; GENERAL INFORMATION:
; APPLICANT: Ono, Koichiyo
; APPLICANT: Ono, Koichiyo
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yoshimura, Yasushi
; APPLICANT: Koishihara, Yasuo
; TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY
; FILE REFERENCE: 35029-20007.00
; CURRENT APPLICATION NUMBER: US/09/269,921
; CURRENT FILING DATE: 1999-04-01
; EARLIER APPLICATION NUMBER: PCT/JP97/03553
; EARLIER FILING DATE: 1997-10-03
; EARLIER APPLICATION NUMBER: JP 8-264756
; EARLIER FILING DATE: 1996-10-04
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 137
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: JH6
; PUBLICATION INFORMATION:
; AUTHORS: Ravetch, J. et al.
; JOURNAL: CELL
; VOLUME: 27
; PAGES: 583-591
; DATE: 1981
US-09-269-921-137

Query Match          100.0%; Score 59; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WGGGTTTVSS 11
      |||||
Db      1 WGGGTTTVSS 11

RESULT 13
US-09-293-769A-120
; Sequence 120, Application US/09293769A
; Patent No. 6765087
; GENERAL INFORMATION:
; APPLICANT: CASTERMAN, CECILE
; APPLICANT: HAMERS, RAYMOND
; TITLE OF INVENTION: IMMUNOGLOBULINS DEVOID OF LIGHT CHAINS
; FILE REFERENCE: 04958.0008-07000
; CURRENT APPLICATION NUMBER: US/09/293,769A
; CURRENT FILING DATE: 1999-04-19
; PRIOR APPLICATION NUMBER: 08/471,284
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 07/106,944
; PRIOR FILING DATE: 1987-10-15
; PRIOR APPLICATION NUMBER: EPO 92403236.0
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/ PRIOR FILING DATE: 1992-08-21  
/ PRIOR APPLICATION NUMBER: EPO 93401310.3  
/ PRIOR FILING DATE: 1993-05-21  
/ NUMBER OF SEQ ID NOS: 130  
/ SOFTWARE: Patent In Ver. 2.1  
/ SEQ ID NO 120  
/ LENGTH: 11  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-09-293-769A-120

Query Match 100.0%; Score 59; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0017;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11  
|||  
Db 1 WGGGTTTVSS 11

RESULT 14  
5189147-14  
/ Patent No. 5189147  
/ APPLICANT: SAITO, HARUO; KRANZ, DAVID M.; ELSSEN, HERMAN N.;  
/ TONEGAWA, SUSUMU  
/ TITLE OF INVENTION: METEORODIMERIC T LYMPHOCYTE RECEPTOR  
/ ANTI-BODY  
/ NUMBER OF SEQUENCES: 21  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/07/271,216  
/ FILING DATE: 14-NOV-1988  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: 666,988  
/ FILING DATE: 31-OCT-1984  
/ APPLICATION NUMBER: 620,122  
/ FILING DATE: 13-JUN-1984  
/ SEQ ID NO:14  
/ LENGTH: 13  
5189147-14

Query Match 100.0%; Score 59; DB 6; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.002;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11  
|||  
Db 3 WGGGTTTVSS 13

RESULT 15  
US-08-765-179B-8  
/ Sequence 8, Application US/08765179B  
/ Patent No. 5854027  
/ GENERAL INFORMATION:  
/ APPLICANT: STEIBE, Boris  
/ APPLICANT: STEINBACHER, Stefan  
/ TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY  
/ TITLE OF INVENTION: OF ANTIBODIES  
/ NUMBER OF SEQUENCES: 28  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Nikaido, Marmelestein, Murray & Oram LLP  
/ STREET: 655 Fifteenth Street N.W. Suite 330  
/ CITY: Washington  
/ STATE: D.C.  
/ COUNTRY: U.S.A.  
/ ZIP: 20005-5701  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: Patent In Release #1.0, Version #1.30  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/765.179B

/ FILING DATE: 14-JAN-1997  
/ CLASSIFICATION: 435  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: PCT/EP95/02626  
/ FILING DATE: 06-JUL-1995  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: DE P 44 25 115.7  
/ FILING DATE: 15-JUL-1994  
/ INFORMATION FOR SEQ ID NO: 8:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 15 amino acids  
/ TYPE: amino acid  
/ STRANDEDNESS:  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: protein  
US-08-765-179B-8

Query Match 100.0%; Score 59; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.0023;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11  
|||  
Db 5 WGGGTTTVSS 15

Search completed: December 4, 2005, 04:09:45  
Job time : 24.6042 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: December 4, 2005, 04:07:28 ; Search time 78.8333 Seconds  
(without alignments)  
58.302 Million cell updates/sec

Title: US-10-632-706-198

Perfect score: 59

Sequence: 1 WGGGTTTVSS 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA.Main:\*  
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2: /cgn2\_6/prodata/1/pubppaa/US08\_PUBCOMB.pep:\*  
3: /cgn2\_6/prodata/1/pubppaa/US09\_PUBCOMB.pep:\*  
4: /cgn2\_6/prodata/1/pubppaa/US10\_PUBCOMB.pep:\*  
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6: /cgn2\_6/prodata/1/pubppaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	100.0	11	3	US-09-253-794-40 Sequence 40, Appl
2	59	100.0	11	3	US-09-828-708-78 Sequence 78, Appl
3	59	100.0	11	3	US-09-749-873-114 Sequence 114, Appl
4	59	100.0	11	3	US-09-749-873-129 Sequence 129, Appl
5	59	100.0	11	3	US-09-669-921-137 Sequence 137, Appl
6	59	100.0	11	3	US-09-663-222-157 Sequence 157, Appl
7	59	100.0	11	3	US-09-663-222-165 Sequence 165, Appl
8	59	100.0	11	3	US-09-663-222-181 Sequence 181, Appl
9	59	100.0	11	3	US-09-663-222-197 Sequence 197, Appl
10	59	100.0	11	3	US-09-509-098-179 Sequence 179, Appl
11	59	100.0	11	4	US-10-218-253-137 Sequence 137, Appl
12	59	100.0	11	4	US-10-169-351-4 Sequence 4, Appl
13	59	100.0	11	4	US-10-160-506-40 Sequence 40, Appl
14	59	100.0	11	4	US-10-310-113-26 Sequence 26, Appl
15	59	100.0	11	4	US-10-310-113-147 Sequence 147, Appl
16	59	100.0	11	4	US-10-310-113-148 Sequence 148, Appl
17	59	100.0	11	4	US-10-310-113-149 Sequence 149, Appl
18	59	100.0	11	4	US-10-310-113-150 Sequence 150, Appl
19	59	100.0	11	4	US-10-310-113-151 Sequence 151, Appl
20	59	100.0	11	4	US-10-310-113-152 Sequence 152, Appl
21	59	100.0	11	4	US-10-310-113-153 Sequence 153, Appl
22	59	100.0	11	4	US-10-310-113-154 Sequence 154, Appl
23	59	100.0	11	4	US-10-310-113-155 Sequence 155, Appl
24	59	100.0	11	4	US-10-310-113-156 Sequence 156, Appl
25	59	100.0	11	4	US-10-310-113-157 Sequence 157, Appl
26	59	100.0	11	4	US-10-310-113-158 Sequence 158, Appl
27	59	100.0	11	4	US-10-310-113-159 Sequence 159, Appl

## ALIGNMENTS

28	59	100.0	11	4	US-10-412-703A-135	Sequence 135, App
29	59	100.0	11	4	US-10-443-466A-69	Sequence 69, Appl
30	59	100.0	11	4	US-10-443-466A-120	Sequence 120, Appl
31	59	100.0	11	4	US-10-449-379-40	Sequence 40, Appl
32	59	100.0	11	4	US-10-688-015-40	Sequence 195, Appl
33	59	100.0	11	4	US-10-632-706-195	Sequence 198, Appl
34	59	100.0	11	4	US-10-632-706-198	Sequence 201, App
35	59	100.0	11	4	US-10-632-706-201	Sequence 204, App
36	59	100.0	11	4	US-10-632-706-204	Sequence 146, App
37	59	100.0	11	4	US-10-783-950-146	Sequence 166, App
38	59	100.0	11	4	US-10-783-950-169	Sequence 40, Appl
39	59	100.0	11	4	US-10-160-505-40	Sequence 120, App
40	59	100.0	11	5	US-10-751-826-120	Sequence 413, App
41	59	100.0	11	5	US-10-922-068-413	Sequence 78, Appl
42	59	100.0	11	5	US-10-630-009-78	Sequence 40, Appl
43	59	100.0	11	5	US-10-755-382-40	Sequence 9, Appl
44	59	100.0	11	5	US-10-984-960A-9	Sequence 45, Appl
45	59	100.0	11	5	US-10-984-960A-45	

RESULT 1  
US-09-253-794-40  
; Sequence 40, Application US/09253794  
; Patent No. US2002018750A1  
; GENERAL INFORMATION:  
; APPLICANT: HANSEN, Hans J.  
; ARMOUR, Kathryn L.  
; TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/253,794  
; FILING DATE: 22-Feb-1999  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/318,157  
; FILING DATE: 05-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saxe, Bernhard D.  
; REGISTRATION NUMBER: 28,665  
; REFERENCE/DOCKET NUMBER: 18733/464  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 672-5300  
; TELEFAX: (202) 672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 40:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; MOLECULE TYPE: protein  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:  
US-09-253-794-40  
Query Match 100.0%; Score 59; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.01;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGTTTVSS 11  
| | | | |  
Db 1 WGGTTTVSS 11

## RESULT 2

US-09-828-708-78  
Sequence 78, Application US/09828708  
Patent No. US20020146753A1  
GENERAL INFORMATION:  
APPLICANT: Ditzel, H.  
APPLICANT: Burton, D.  
TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici

TITLE OF INVENTION: autoimmune disease  
FILE REFERENCE: 1361.005US1  
CURRENT APPLICATION NUMBER: US/09/828,708  
CURRENT FILING DATE: 2001-09-24  
NUMBER OF SEQ ID NOS: 123  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 78  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-828-708-78

Query Match 100.0%; Score 59; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.01;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGTTTVSS 11  
| | | | |  
Db 1 WGGTTTVSS 11

## RESULT 3

US-09-749-873-114  
Sequence 114, Application US/09749873  
Publication No. US20030023045A1  
GENERAL INFORMATION:  
APPLICANT: OHTOMO, Toshihiko  
SATO, Koh  
TSUCHIYA, Masayuki

TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
MEDULOBLASTOMA CELLS  
NUMBER OF SEQUENCES: 132  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/749,873  
FILING DATE: 29-Dec-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/646,265  
FILING DATE: 1996-09-09  
APPLICATION NUMBER: JP 5-291078  
FILING DATE: 19-NOV-1993

ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/184  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136

INFORMATION FOR SEQ ID NO: 114:

SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 114:

US-09-749-873-114

Query Match 100.0%; Score 59; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.01;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGTTTVSS 11  
| | | | |  
Db 1 WGGTTTVSS 11

## RESULT 4

US-09-749-873-129  
Sequence 129, Application US/09749873  
Publication No. US20030023045A1  
GENERAL INFORMATION:  
APPLICANT: OHTOMO, Toshihiko  
SATO, Koh  
TSUCHIYA, Masayuki

TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
MEDULOBLASTOMA CELLS  
NUMBER OF SEQUENCES: 132  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/749,873  
FILING DATE: 29-Dec-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/646,265  
FILING DATE: 1996-09-09  
APPLICATION NUMBER: JP 5-291078  
FILING DATE: 19-NOV-1993

ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/184  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136

INFORMATION FOR SEQ ID NO: 129:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 129:

US-09-749-873-129

Query Match 100.0%; Score 59; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.01;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



OY 1 WGGGTTTVSS 11  
| | | | |  
Db 1 WGGGTTTVSS 11

## RESULT 5

US-09-269-921-137  
; Sequence 137, Application US/09269921  
; Publication No. US20030045691A1  
; GENERAL INFORMATION:  
; APPLICANT: Ono, Koichiro  
; APPLICANT: Ohtomo, Toshiniko  
; APPLICANT: Tsuchiya, Masayuki  
; APPLICANT: Yoshimura, Yasushi  
; APPLICANT: Koshihara, Yasuo  
; TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY  
; FILE REFERENCE: 35029-20007.00  
; CURRENT APPLICATION NUMBER: US/09/269,921  
; CURRENT FILING DATE: 1999-04-01  
; EARLIER APPLICATION NUMBER: PCT/JP97/03553  
; EARLIER FILING DATE: 1997-10-03  
; EARLIER APPLICATION NUMBER: JP 8-264756  
; EARLIER FILING DATE: 1996-10-04  
; NUMBER OF SEQ ID NOS: 137  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 137  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: JH6  
; PUBLICATION INFORMATION:  
; AUTHORS: Ravetch, J. et al.  
; JOURNAL: CELL  
; VOLUME: 27  
; PAGES: 583-591  
; DATE: 1981  
US-09-269-921-137

Query Match 100.0%; Score 59; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.01;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WGGGTTTVSS 11  
| | | | |  
Db 1 WGGGTTTVSS 11

## RESULT 6

US-09-563-222-157  
; Sequence 157, Application US/09563222  
; Publication No. US20030079253A1  
; GENERAL INFORMATION:  
; APPLICANT: Hiatt, Andrew  
; APPLICANT: Hein, Mich B.  
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN  
; TITLE OF INVENTION: EUKARYOTIC CELLS  
; FILE REFERENCE: 310098.406  
; CURRENT APPLICATION NUMBER: US/09/563,222  
; CURRENT FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 197  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 157  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-563-222-157

Query Match 100.0%; Score 59; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.01;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WGGGTTTVSS 11  
| | | | |  
Db 1 WGGGTTTVSS 11

## RESULT 7

US-09-563-222-165  
; Sequence 165, Application US/09563222  
; Publication No. US20030079253A1  
; GENERAL INFORMATION:  
; APPLICANT: Hiatt, Andrew  
; APPLICANT: Hein, Mich B.  
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN  
; TITLE OF INVENTION: EUKARYOTIC CELLS  
; FILE REFERENCE: 310098.406  
; CURRENT APPLICATION NUMBER: US/09/563,222  
; CURRENT FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 197  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 165  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-563-222-165

Query Match 100.0%; Score 59; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.01;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WGGGTTTVSS 11  
| | | | |  
Db 1 WGGGTTTVSS 11

## RESULT 8

US-09-563-222-181  
; Sequence 181, Application US/09563222  
; Publication No. US20030079253A1  
; GENERAL INFORMATION:  
; APPLICANT: Hiatt, Andrew  
; APPLICANT: Hein, Mich B.  
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN  
; TITLE OF INVENTION: EUKARYOTIC CELLS  
; FILE REFERENCE: 310098.406  
; CURRENT APPLICATION NUMBER: US/09/563,222  
; CURRENT FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 197  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 181  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-563-222-181

Query Match 100.0%; Score 59; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.01;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WGGGTTTVSS 11  
| | | | |  
Db 1 WGGGTTTVSS 11

## RESULT 9

US-09-563-222-197  
; Sequence 197, Application US/09563222  
; Publication No. US20030079253A1  
; GENERAL INFORMATION:  
; APPLICANT: Hiatt, Andrew  
; APPLICANT: Hein, Mich B.  
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN  
; TITLE OF INVENTION: EUKARYOTIC CELLS  
; FILE REFERENCE: 310098.406  
US-09-563-222-197

/ CURRENT APPLICATION NUMBER: US/09/563,222  
/ CURRENT FILING DATE: 2000-05-02  
/ NUMBER OF SEQ ID NOS: 197  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO: 197  
/ LENGTH: 11  
/ TYPE: PRT  
/ ORGANISM: Mus musculus  
US-09-563-222-197

Query Match 100.0%; Score 59; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.01;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVSS 11  
|||  
Db 1 WGGGTTTVSS 11

RESULT 10  
US-09-509-098-179  
/ Sequence 179, Application US/09509098  
/ Publication No. US20030103970A1  
/ GENERAL INFORMATION:  
/ APPLICANT: TSUCHIYA, MASAYUKI  
/ TITLE OF INVENTION: NATURAL HUMANIZED ANTIBODY  
/ FILE REFERENCE: 053466/0274  
/ CURRENT APPLICATION NUMBER: US/09/509,098  
/ PRIOR FILING DATE: 2000-03-22  
/ PRIOR APPLICATION NUMBER: PCT/JP98/04469  
/ PRIOR FILING DATE: 1998-10-02  
/ PRIOR APPLICATION NUMBER: JP 9-271726  
/ PRIOR FILING DATE: 1997-10-03  
/ NUMBER OF SEQ ID NOS: 203  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO: 179  
/ LENGTH: 11  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence: Amino acid  
/ OTHER INFORMATION: Sequence of the H chain V region JH6  
US-09-509-098-179

Query Match 100.0%; Score 59; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.01;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVSS 11  
|||  
Db 1 WGGGTTTVSS 11

RESULT 11  
US-10-218-253-137  
/ Sequence 137, Application US/10218253  
/ Publication No. US20030129185A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Ono, Koichiro  
/ APPLICANT: Ohtomo, Toshihiko  
/ APPLICANT: Tsuchiya, Masayuki  
/ APPLICANT: Yoshimura, Yasushi  
/ APPLICANT: Koshihara, Yasuo  
/ TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY  
/ FILE REFERENCE: 35029-20007.00  
/ CURRENT APPLICATION NUMBER: US/10/218,253  
/ PRIOR FILING DATE: 2002-11-21  
/ PRIOR APPLICATION NUMBER: US/09/269,921  
/ PRIOR FILING DATE: 1999-04-01  
/ PRIOR APPLICATION NUMBER: PCT/JP97/03553  
/ PRIOR FILING DATE: 1997-10-03  
/ PRIOR APPLICATION NUMBER: JP 8-264756  
/ PRIOR FILING DATE: 1996-10-04

/ NUMBER OF SEQ ID NOS: 137  
/ SOFTWARE: PatentIn Ver. 2.0  
/ SEQ ID NO: 137  
/ LENGTH: 11  
/ TYPE: PRT  
/ ORGANISM: Unknown  
/ FEATURE:  
/ OTHER INFORMATION: Description of Unknown Organism: JH6  
/ PUBLICATION INFORMATION:  
/ AUTHORS: Ravetch, J. et al.  
/ JOURNAL: CELL  
/ VOLUME: 27  
/ PAGES: 583-591  
/ DATE: 1981  
US-10-218-253-137

Query Match 100.0%; Score 59; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.01;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVSS 11  
|||  
Db 1 WGGGTTTVSS 11

RESULT 12  
US-10-169-351-4  
/ Sequence 4, Application US/10169351  
/ Publication No. US20030157090A1  
/ GENERAL INFORMATION:  
/ APPLICANT: BENVENTO, EUGENIO  
/ APPLICANT: FRANCONI, ROSELLA  
/ APPLICANT: DESIDERIO, ANGIOLA  
/ APPLICANT: TAVLABORAKI, PARASKEVI  
/ TITLE OF INVENTION: STABILIZING PEPTIDES, POLYPEPTIDES AND ANTIBODIES  
/ TITLE OF INVENTION: WHICH INCLUDE THEM  
/ FILE REFERENCE: 4161-4  
/ CURRENT APPLICATION NUMBER: US/10/169,351  
/ PRIOR FILING DATE: 2002-10-29  
/ PRIOR APPLICATION NUMBER: PCT/IT00/00554  
/ PRIOR FILING DATE: 2000-12-29  
/ PRIOR APPLICATION NUMBER: IT RM99A000803  
/ PRIOR FILING DATE: 1999-12-30  
/ NUMBER OF SEQ ID NOS: 118  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO: 4  
/ LENGTH: 11  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
/ OTHER INFORMATION: peptide  
US-10-169-351-4

Query Match 100.0%; Score 59; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.01;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVSS 11  
|||  
Db 1 WGGGTTTVSS 11

RESULT 13  
US-10-160-506-40  
/ Sequence 40, Application US/10160506  
/ Publication No. US20030161832A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Bander, Neil H.  
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING  
/ TITLE OF INVENTION: SKIN DISORDERS USING BINDING AGENTS SPECIFIC FOR  
/ TITLE OF INVENTION: PROSTATE SPECIFIC MEMBRANE ANTIGEN  
/ FILE REFERENCE: 10448-162001

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; CURRENT APPLICATION NUMBER: US/10/160,506
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/324,100
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/362,612
; PRIOR FILING DATE: 2002-03-08
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: deimmunized heavy chain J415-4
US-10-160-506-40
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Query Match      100.0%; Score 59; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 WGGGTTVTSS 11
        |||||
Db      1 WGGGTTVTSS 11
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RESULT 14
US-10-310-113-26
; Sequence 26, Application US/10310113
; Publication No. US2003017664A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: KONG, HING C.
; APPLICANT: NIEVES, ESPERANZA LILIANA
; TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING
; TITLE OF INVENTION: THROMBOSES
; FILE REFERENCE: 58122(71758)
; CURRENT APPLICATION NUMBER: US/10/310,113
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 08/814,806
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-310-113-26
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```
Query Match      100.0%; Score 59; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 WGGGTTVTSS 11
        |||||
Db      1 WGGGTTVTSS 11
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```
RESULT 15
US-10-310-113-147
; Sequence 147, Application US/10310113
; Publication No. US2003017664A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: KONG, HING C.
; APPLICANT: NIEVES, ESPERANZA LILIANA
; APPLICANT: MOSQUERA, LUIS A.
```

```
; TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING
; TITLE OF INVENTION: THROMBOSES
; FILE REFERENCE: 58122(71758)
; CURRENT APPLICATION NUMBER: US/10/310,113
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 08/814,806
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 147
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: humanized HC-01 FR4 amino acid sequence
US-10-310-113-147
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Query Match      100.0%; Score 59; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 WGGGTTVTSS 11
        |||||
Db      1 WGGGTTVTSS 11
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Job time : 79.8333 secs
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